

173999

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Monday, December 12, 2005 2:44 PM
To: Zeman, Mary; STIC-Biotech/ChemLib
Subject: RE: Rush Seq Search 09/924400

Please ~~rush~~. Thanks. Chris

URFS

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Zeman, Mary
Sent: Monday, December 12, 2005 1:32 PM
To: Chan, Christina
Subject: Rush Seq Search 09/924400

This amended application may soon be allowable.
Please search SEQ ID NO: 302, 303 in ALL files including interference
Please do an OLIGO search of SEQ ID NO: 302, 303 in all files. Minimum 10
contiguous nucleotides.
Paper printout please
Thank you, Mary Z

Mary K. Zeman
Primary Examiner, 1631
571-272-0723
Remsen 2D61
MAILBOX: REM 2C70
mary.zeman@uspto.gov

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 12/13/05
Date completed: 12/28/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 024
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:05:29 ; Search time 10111.9 Seconds
(without alignments)
11242.903 Million cell updates/sec

Title: US-09-924-400-302

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11752642

Minimum DB seq length: 10
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2000	100.0	2000	6	AR218479
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4	2000	100.0	2000	6	AR367175
5	2000	100.0	2000	6	AR371071
6	2000	100.0	2000	6	AR400211
7	2000	100.0	2000	6	AR405478
8	2000	100.0	2000	6	AR433319
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20	2000	100.0	2000	6	AX316965	Sequence
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23	1551	77.5	2040	6	AR350944	Sequence
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25	1551	77.5	2040	6	AR371072	Sequence
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ALIGNMENTS

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DEFINITION	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.				
ACCESSION	BD242272				
VERSION	BD242272.1	GI:33052042			
KEYWORDS	JP 2002520054-A/359.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2000)				
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2002520054-A 359 09-JUL-2002;				
COMMENT	CORIXA CORP				
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PD	09-JUL-2002				
PF	14-JUL-1999 JP 2000560247				
PR	14-JUL-1998 US 09/115453, 14-JUL-1998 US 09/116134 PR				
23-SEP-1998 US 09/159822, 23-SEP-1998 US 09/159812 PR					
15-JAN-1999 US 09/232880, 15-JAN-1999 US 09/232149 PR					
09-APR-1999 US 09/288946					
PI	DAVIN CLIFFORD DILLON, SUSAN LOUISE HARLOCKER, JIANG YUGU, PI				
JIANGCHUN XU, LYNN MITCHAM					
PC	CI2N15/09, A61K38/00, A61K39/00, A61K39/395, C07K14/47, C07K16/30,				
PC	CI2N15/10,				
PC	CI2P21/08, CI2Q1/68, G01N33/574, G01N33/68//A61P35/00, CI2N15/00,				
PC	A61K37/02,				
PC	CI2N5/00				
CC	Compounds for immunotherapy and diagnosis of prostate cancer				
CC	and methods				
CC	for their use				
CC	key				
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ORIGIN

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 DEFINITION Sequence 374 from patent US 6512094.
 ACCESSION AR278479
 VERSION AR278479.1 GI:29712725
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 2000)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
 Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,T.A.W.,
 Hepler,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate
 cancer
 JOURNAL Patent: US 6512094-A 374 28-JAN-2003;
 Corixa Corporation; Seattle, WA
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 Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR367175 Sequence 374 from patent US 6329505.
DEFINITION AR367175
ACCESSION AR367175 GI:34600150
VERSION AR367175.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6329505-A 374 11-DEC-2001;
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source 1.2000
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 374 from patent US 6395278.
ACCESSION AR371071
VERSION AR371071.1 GI:34607964
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 2000)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yudin, J.
TITLE Prostate specific fusion protein compositions
JOURNAL Patent: US 6395278-A 374 28-MAY-2002;
Corixa Corporation; Seattle, WA

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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR400211 2000 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 374 from patent US 6620922.
ACCESSION AR400211
VERSION AR400211.1 GI:40143375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaleo,M.D., Fenger,G.R., Retzer,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 374 16-SEP-2003;
Corixa Corporation; Seattle, WA
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source location/Qualifiers
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR405478 2000 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 374 from patent US 6630305.
ACCESSION AR405478
VERSION AR405478.1 GI:40154315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate
cancer
PATENT: US 6630305-A 374 07-OCT-2003;
CORIXA Corporation; Seattle, WA;
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Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 8
AR433319 2000 bp DNA linear PAT 18-DEC-2003
LOCUS AR433319
DEFINITION Sequence 302 from patent US 6656480.
ACCESSION AR433319
VERSION AR433319.1 GI:40196101
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 2000)
Rettner M.W. and Dillon P.C.
TITLE
Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL
Patent: US 6656480-A 302 02-DEC-2003;
Corixa Corporation; Seattle, WA
FEATURES
source
1..2000
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 9
AR563858 2000 bp DNA linear PART 08-OCT-2004
LOCUS AR563858
DEFINITION Sequence 374 from patent US 6759515.
ACCESSION AR563858
VERSION AR563858.1 GI:53978909
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2000)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocke,S.L., Jiang,Y.,
Kaloos,M.D., Fanger,G.R., Retter,M.W., Stoik,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,

QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
AR588844
LOCUS AR588844
DEFINITION Sequence 374 from patent US 6800746.
ACCESSION AR588844
VERSION AR588844.1 GI:56635741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kales,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6800746-A 374 05-OCT-2004;
Corixa Corporation; Seattle, WA
FEATURES
source 1..2000
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1981 AAAAAAAAAAAAAAAAAA 2000
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Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 11
AR605664
LOCUS AR605664 Sequence 374 f.com patent US 6818751. DNA linear PAT 15-DEC-2004
DEFINITION
ACCESSION AR605664
VERSION AR605664.1 GI:56657328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalog,M.D., Fanger,G.R., Reister,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 374 16-NOV-2004;
FEATURES
source Corixa Corporation; Seattle, WA
Location/Qualifiers
1..2000
/organism="Unknown"
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ORIGIN
Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGCCATTGGTTC 60
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Db 1 ATGCTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGCCATTGGTTC 60
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Db 241 GGGCTTTGAGAGACAGACACTGCTATGAAGCACTCAGAAACAAGATGGCAAG 300
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QY 1981 AAAAAAAAAAAAAAAAAA 2000
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Db 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 12
AR615063
LOCUS AR615063
DEFINITION Sequence 302 from patent US 6828431.
ACCESSION AR615063
VERSION AR615063.1 GI:56671467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Prudekis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
TITLE Retzer,M.W., Wang,A., Skeiky,Y.A.W. and Harlocke,S.L.
JOURNAL Compositions and methods for the therapy and diagnosis of breast
Patent: US 6828431-A 302 07-DEC-2004;
Corixa Corporation; Seattle, WA
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/organism="unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AR642105 2000 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 302 from patent US 6861506.
ACCESSION AR642105
VERSION AR642105.1 GI:62778253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Prudakis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and
Dillon,D.C.
TITLE Conditions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6861506-A 302 01-MAR-2005;
Corixa Corporation; Seattle, WA
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LOCUS ARE57003 2000 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 374 from patent US 6894146.
ACCESSION ARE57003
VERSION ARE57003.1 GI:67590123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kalog M.D., Fanger G.R., Retter M.W., Stoik J.A., Day C.H.,
Vedick T.S., Carter D., Li S.X., Wang A., Skelky Y.A.W.,
Hepler W.T. and Henderson R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6894146-A 374 17-MAY-2005;
Corixa Corporation; Seattle, WA
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 DEFINITION Sequence 374 from Patent WO0125272.
 ACCESSION AX106593
 VERSION AX106593.1 GI:13922264
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 Xu, J., Skelky, Y.A., Reed, S.G. and Cheever, M.A.
 AUTHORS Compositions and methods for therapy and diagnosis of prostate cancer
 TITLE Patent: WO 0125272-A 374 12-APR-2001;
 JOURNAL CORIXA CORPORATION (US)
 FEATURES location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 2000; DB 6; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 121 AGCAAGTGTGGCACTTCTGAGACCAAGAGACTCTGCTATGAAGCACTCAGAGCAAG 180
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 QY 181 ATGGGCAAGTGTGGCGGCACTGCTTCCCTGCTGACGAGGAGGTGGCAAGCAACGTC 240
 Db 181 ATGGGCAAGTGTGGCGGCACTGCTTCCCTGCTGACGAGGAGGTGGCAAGCAACGTC 240

QY 241 GCGCTTCTGAGACCAAGCACTGCTATGAAACA CTGAGAAACAAGATGGGCAAG 300
DB 241 GGGGCTTTGGAGACCAAGCACTGCTATGAAACA CTGAGAAACAAGATGGGCAAG 300
QY 301 TGGTGTCCCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGTCCCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GAGACCTACGATGACAGTGGCTTCAATGAGCCCAAGGTACCAAGTCCGCTGAGAAAGATCTG 420
DB 361 GAGACCTACGATGACAGTGGCTTCAATGAGCCCAAGGTACCAAGTCCGCTGAGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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DB 481 CTCAGAGCACTGACGCTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
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DB 781 TATGTGCTGATATGCAATCAAAAACAAGATGAGCTCACAACAATGTTACTTGGTGA 840
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Search completed: December 19, 2005, 15:33:32
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 01:50:48 ; Search time 1194.55 Seconds
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Title: US-09-924-400-302

Perfect score: 2000
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9978348

Minimum DB seq length: 10
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2000	100.0	2000	3 AAC81012	AAC81012 Human B11
2	2000	100.0	2000	4 AAH93715	AAH93715 Human pro
3	2000	100.0	2000	4 AA167212	AA167212 B305D iso
4	2000	100.0	2000	4 AAB63808	AAB63808 Human pro
5	2000	100.0	2000	4 AAH02780	AAH02780 Prostate
6	2000	100.0	2000	4 ACA59616	ACA59616 Prostate
7	2000	100.0	2000	5 AAB85029	AAB85029 Human pro
8	2000	100.0	2000	6 AAB95179	AAB95179 Human B30
9	2000	100.0	2000	6 AAC99857	AAC99857 Breast tu
10	2000	100.0	2000	8 AAC95343	AAC95343 Prostate
11	2000	100.0	2000	8 ADA11381	ADA11381 Human bre
12	2000	100.0	2000	10 ADC15354	ADC15354 Human bre
13	2000	100.0	2000	10 ADB13824	ADB13824 Human pro
14	2000	100.0	2000	10 ADG26240	ADG26240 Human pro
15	1949	97.5	2000	3 AAH06599	AAH06599 Human imm
16	1551	77.5	2040	4 AAC81013	AAC81013 Human B11
17	1551	77.5	2040	4 AAH93716	AAH93716 Human pro
18	1551	77.5	2040	4 AA167213	AA167213 B305D iso
19	1551	77.5	2040	4 AAB63809	AAB63809 Human pro

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21	1551	77.5	2040	5 AAB85030	AAB85030 Human pro
22	1551	77.5	2040	5 AAC95617	AAC95617 Prostate
23	1551	77.5	2040	6 AAB195180	AAB195180 Human B30
24	1551	77.5	2040	6 AAC99859	AAC99859 Breast tu
25	1551	77.5	2040	8 AAC95344	AAC95344 Prostate
26	1551	77.5	2040	8 ADA11382	ADA11382 Human bre
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38	1128	56.4	1155	5 AAB95178	AAB95178 Human B30
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40	1128	56.4	1155	6 AAC95342	AAC95342 Prostate
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ALIGNMENTS

RESULT 1	
AAC81012	AAC81012 standard; cDNA, 2000 BP.
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XX	AAC81012;
AC	13-FEB-2001 (first entry)
XX	
DT	Human B11Ag1 antigen splice isoform B11C-8 cDNA.
DE	Human; breast tumour-specific antigen; cytostatic; vaccine;
XX	
KW	breast cancer; B18Ag1, B11Ag1, B15Ag1; ss.
KW	
OS	Homo sapiens.
PN	WO20061753-A2.
XX	
PD	19-OCT-2000.
XX	
PF	07-APR-2000; 2000WO-US009312.
XX	
PR	09-APR-1999; 99US-00289198.
PR	28-OCT-1999; 99US-00429755.
PR	23-MAR-2000; 2000US-00534825.
XX	
XX	(CORI-) CORIXA CORP.
XX	
DR	Prudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
DR	WPI. 2000-628403/60.
DR	P-PSDB; AAB28629.
XX	
PT	An isolated polypeptide comprising an immunogenic portion of a breast
PT	tumor protein used for inhibiting the development of cancer, especially
PT	breast cancer, and monitoring cancer progression in a patient.
XX	
PS	Claim 4; Page 177-178; 187pp; English.
XX	
CC	The present sequence is given in a specification relating to compositions
CC	and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC	sequences that are preferentially expressed in breast tumour tissue, and
CC	the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
ID AAH93715 standard; cDNA; 2000 BP.
AAH93715;

04-OCT-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #9.

Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.

OS Homo sapiens.

PN WO200151633-A2.

PD 19-JUL-2001.

PF 16-JAN-2001; 2001WO-US001574.

PR 14-JAN-2000; 2000US-00483672.

(CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
PI Wang A, Meagher MJ;

XX MPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.

PS Claim 1: Page 347-348; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTATTCATTCGAGCGGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
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```
Db 1201 ATGTCTCAAGAACAGAAATAAATAGATGTGTAGAGAGGTGAGAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACTGTAAGTGTGCACTGTGGC 1320
Db 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACTGTAAGTGTGCACTGTGGC 1320
Qy 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGACACTGTAATATGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGACACTGTAATATGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAGTAATGACAAATTTGGGAATTAATTTCTGACATCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAGTAATGACAAATTTGGGAATTAATTTCTGACATCAAGAA 1440
Qy 1441 AAACAGATGCCAAATTAATCTTCTGAAAAAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
Qy 1501 TCAGAGAAAGAGTCAAGAAAGCTTGAGGCGAGTGAATGGCCAGCAGAGCTAGAAAAAT 1560
Db 1501 TCAGAGAAAGAGTCAAGAAAGCTTGAGGCGAGTGAATGGCCAGCAGAGCTAGAAAAAT 1560
Qy 1561 TTTATGGCTATGCAAGAAATGAAGAGCAGGAAAGTACTATGTCCGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATGCAAGAAATGAAGAGCAGGAAAGTACTATGTCCGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATAGTGCCTGCTGGCAATGTGATGATTAATTTCTCCCAAGAAAGAGC 1680
Db 1621 CTGACTAATAGTGCCTGCTGGCAATGTGATGATTAATTTCTCCCAAGAAAGAGC 1680
Qy 1681 AGAACACTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAACAGTCGAA 1740
Db 1681 AGAACACTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAACAGTCGAA 1740
Qy 1741 CAAAAAGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACACGATGAG 1800
Db 1741 CAAAAAGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTACACGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAGAAATGAATTTCTGAGCTTTC 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAGAAATGAATTTCTGAGCTTTC 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGACATGAATAATAGTACGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGACATGAATAATAGTACGTTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTTAAGACTGAGCTAGACAAATGAACATCAAGCCAGCTTAAGAAAGAAAG 1980
Db 1921 GCCATGCTTAAGACTGAGCTAGACAAATGAACATCAAGCCAGCTTAAGAAAGAAAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3
AA167212 ID AA167212 standard; cDNA; 2000 BP.
XX AC AA167212;
XX DT 11-FEB-2002 (first entry)
XX DE B305D isoform C splice variant 2 encoding cDNA.
XX KM Genetic substructure; DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..1971
XX FT /tag= a
```

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FT /product= "B305D isoform C splice variant"
XX MO200175171-A2.
PN 11-OCT-2001.
XX 02-APR-2001; 2001WO-US010631.
XX PF 03-APR-2000; 2000US-0194241P.
PR 27-JUL-2000; 2000US-0219862P.
PR 27-JUL-2000; 2000US-0221300P.
XX PR 18-DEC-2000; 2000US-0256592P.
XX (CORI-) CORIXA CORP.
XX PA Houghton RI, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;
PI WPI; 2001-626449/72.
XX DR P-PSDB; AAG65977.
XX DR
XX PT Identifying tissue (tumor)-specific polynucleotides overexpressed in
PT tissue of interest, as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction.
XX PS Claim 4; Page 94; 127p; English.
XX CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic substructure to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (Sp1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on Sp1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant
XX SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2000; DB 4; Length 2000;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTGTGAAGAGCAATTTGCTTC 60
Db 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTGTGAAGAGCAATTTGCTTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGAGACAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGACAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCACTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGAGGAGAGTGGCAAGCACTG 240
Qy 241 GGGGCTTCTGAGAGACAGCAAGCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGGCTTCTGAGAGACAGCAAGCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Qy 301 TGTGTCTGCACTGCTTCCCTGCTGAGAGGAGAGGAGAGCAAGGTGGGCTTGG 360
Db 301 TGTGTCTGCACTGCTTCCCTGCTGAGAGGAGAGGAGAGCAAGGTGGGCTTGG 360
Qy 361 GGAGACTAGATGAGAGTGCCTTTCATGAGGCCAGGTACACAGTCCGTGGAAGATCTG 420
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Db 361 GGAGGCTAAGATGACAGTGCTTCATGAGCCAGGTACACGTCCTGGAGGAAGTCTG 420
Qy 421 GACAGCTTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAGCTTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Qy 481 CTCAGGGAACCTGACCTGAAACAAGAGACACAGCAAAAGAGACTCTCTACATCTGGCC 540
Db 481 CTCAGGGAACCTGACCTGAAACAAGAGACACAGCAAAAGAGACTCTCTACATCTGGCC 540
Qy 541 TCTGCAATGAGGAATTCAGAAAGTAAATCTCTGTCGACAGAGATGTCATCTTAAT 600
Db 541 TCTGCAATGAGGAATTCAGAAAGTAAATCTCTGTCGACAGAGATGTCATCTTAAT 600
Qy 601 GTCTTGTACAAACAAAAGAGAGACAGCTGTATTAAGCCGTACATGCCAGGAAGATGA 660
Db 601 GTCTTGTACAAACAAAAGAGAGACAGCTGTATTAAGCCGTACATGCCAGGAAGATGA 660
Qy 661 TGTGCTTAATGTTGCTGGAACTGGCACTGATCCAAATTTCCAGATGATGTGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACTGGCACTGATCCAAATTTCCAGATGATGTGAAT 720
Qy 721 ACCACTGTGCACTAGCTATCTTAATGAAGATTAATGAGCCAAAGACTGCTCTTA 780
Db 721 ACCACTGTGCACTAGCTATCTTAATGAAGATTAATGAGCCAAAGACTGCTCTTA 780
Qy 781 TATGCTGTATATTCGAATCAAAAAACAAGCATGGCTCACAACCTGTTACTTGTGTGA 840
Db 781 TATGCTGTATATTCGAATCAAAAAACAAGCATGGCTCACAACCTGTTACTTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGAACTGCGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAACTGCGAAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGAGAGAGCTGCTCATATCTGTATGTTGTTGAGATCAGCAATATA 960
Db 901 CTGATAGATATGAGAGAGAGCTGCTCATATCTGTATGTTGTTGAGATCAGCAATATA 960
Qy 961 GTGAGCTTCTATCTTGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTATCTTGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATATCTTCTGAAAAACAAGATCCAAACAAGCTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATATCTTCTGAAAAACAAGATCCAAACAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCATGTAATTTGACGACAGAGAAA 1200
Db 1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCATGTAATTTGACGACAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATTAATGAGGATTAATCTAGAAAACTGATATGTTGCTGCTGAC 1320
Db 1261 AAGCATGAAGATTAATTAATGAGGATTAATCTAGAAAACTGATATGTTGCTGCTGAC 1320
Qy 1321 AATGTGATTAATGATTAATCTTCAAGAGAAAGAGAGAACTGTAATTCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTTCAAGAGAAAGAGAGAACTGTAATTCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATTCACAAATTTTGGCAATTTGTTCTGATCAAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATTCACAAATTTTGGCAATTTGTTCTGATCAAAAGAA 1440
Qy 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAAGCTGACA 1500
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Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGAGTCAAAAAGCTTTAGAGGCACTGAAATATGSCACAGCTAGAAAAAT 1560
Db 1501 TCAGAGAAAGAGTCAAAAAGCTTTAGAGGCACTGAAATATGSCACAGCTAGAAAAAT 1560
Qy 1561 TTTATGCTATGAGAAAGAAATGAAGAGACGGAAGTCACTCATGTGGATTTCCAGAAAC 1620
Db 1561 TTTATGCTATGAGAAAGAAATGAAGAGACGGAAGTCACTCATGTGGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGATGTCACCTGCTGGCAATGATGATGATTAATTTCTCAAGAAAGAGC 1680
Db 1621 CTGACTAATGATGTCACCTGCTGGCAATGATGATGATTAATTTCTCAAGAAAGAGC 1680
Qy 1681 AGAAGACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGACGA 1740
Db 1681 AGAAGACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCAGATGACGA 1740
Qy 1741 CAAATGATATCTCAGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Db 1741 CAAATGATATCTCAGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGAGAGATGAGATGATGATGATGATGATGATGATGATGAT 1860
Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGATGATGATGATGATGATGATGATGATGAT 1860
Qy 1861 CTTAGTTGTAGAAAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGAT 1920
Db 1861 CTTAGTTGTAGAAAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGAT 1920
Qy 1921 GCCATGCTTAAGCTGAGAGTACACATATGAAACATCAGAGCAGTAAATTAATTAAT 1980
Db 1921 GCCATGCTTAAGCTGAGAGTACACATATGAAACATCAGAGCAGTAAATTAATTAAT 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 4
ID AAS63808 strand: cdna; 2000 BP.
XX AAS63808;
AC XX
XX XX
DT 29-JAN-2002 (first entry)
XX
XX Human prostate cDNA clone B305D splice variant #9.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX
XX WO200173032-A2.
XX
PD 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00651236.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
XX
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PI Xu J, Dillon DC, Mutcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
XX P-PsDB: AAU69778.
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX
PS Claim 1; Page 349-350; 579pp; English.
CC The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
XX
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No.0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGGTGATTCATGCGCGTGCCCTCTTGTGAGAAAGCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGGTGATTCATGCGCGTGCCCTCTTGTGAGAAAGCATTTGGTCTC 60
QY 61 AGGAGCAATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAAGAGCGGCAAG 120
DB 61 AGGAGCAATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACGACGACGACTGTGTAAGACCTCGAGGACAAG 180
DB 121 AGCAACGTGGGCACTTGTGAGACGACGACGACTGTGTAAGACCTCGAGGACAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACAGT 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACAGT 240
QY 241 GGGGCTTTGAGAGACGACGACGACTGTGTAAGACACTGAGAACTGGGCAAG 300
DB 241 GGGGCTTTGAGAGACGACGACGACTGTGTAAGACACTGAGAACTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGAAGCAAGGTGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGAAGCAAGGTGGCGCTTGG 360
QY 361 GAGAGCTAGATGAGTGTGCTTATGAGCCGAGGTACACGCTCCGTGAGAGATCTG 420
DB 361 GAGAGCTAGATGAGTGTGCTTATGAGCCGAGGTACACGCTCCGTGAGAGATCTG 420
QY 421 GACAGCTGACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTGACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGACCTGAGCTGAGCAAGAGCAAGCAAAAGATCTCTTACATCTGGCC 540
DB 481 CTCAGGGACCTGAGCTGAGCAAGAGCAAGCAAAAGATCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTGAGAGTAAATCTCTGCTGAGACGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTGAGAGTAAATCTCTGCTGAGACGAGATGCACTTAAT 600
QY 601 GTCTTTGACAAACAAAGAGACAGCTTGATTAAGCGGTACATGCGAAGATGAA 660
DB 601 GTCTTTGACAAACAAAGAGACAGCTTGATTAAGCGGTACATGCGAAGATGAA 660

DB 601 GTCTTTGACAAACAAAGAGACAGCTTGATTAAGCGGTACATGCGAAGATGAA 660
QY 661 TGTGGTTAAATGTGTGGAACAATGCACTGTATCCAAATATCCAGATGAGTAAT 720
DB 661 TGTGGTTAAATGTGTGGAACAATGCACTGTATCCAAATATCCAGATGAGTAAT 720
QY 721 ACCACTGTGACCTAGCTATCTATAAGATTAATATGAGCCAAAGCTGCTCTTA 780
DB 721 ACCACTGTGACCTAGCTATCTATAAGATTAATATGAGCCAAAGCTGCTCTTA 780
QY 781 TATGTGCTGATATGATCAAAAAAGCAATGCGCTCAGACCACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATGATCAAAAAAGCAATGCGCTCAGACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGTGAAATTTTAACTCAAGAAAAAGCGAATTTAATGCA 900
DB 841 CATGAGCAAAAAAGCAAGTGTGAAATTTTAACTCAAGAAAAAGCGAATTTAATGCA 900
QY 901 CTGATATGATATGAGAGACTGCTCTCATCTGCTGATATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAGAGACTGCTCTCATCTGCTGATATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATCTAAATCTCTTGTGAAAAAGCAATCCAGAACAAAGCTTTAAG 1140
DB 1081 AAGAGAAAAAGATCTAAATCTCTTGTGAAAAAGCAATCCAGAACAAAGCTTTAAG 1140
QY 1141 CTGACATCAGAGAAAGTCACAAAGTTCAAAGGCAAGTAAATGCCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAAAGTCACAAAGTTCAAAGGCAAGTAAATGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGATTAATGAGTAACTGAGAAAAGCTGATGCTGAC 1320
DB 1261 AAGCATGAAAGTAAATATGATGATTAATGAGTAACTGAGAAAAGCTGATGCTGAC 1320
QY 1321 AATGTGATATGATTAATTCCTCAAGAGAAAGACAAACCTGAAATATGCAATTT 1380
DB 1321 AATGTGATATGATTAATTCCTCAAGAGAAAGACAAACCTGAAATATGCAATTT 1380
QY 1381 CCTGACAAAGAGTAAAGATATCAAGAAATTTGGAATTTGTTCTGACTTCAAGAAA 1440
DB 1381 CCTGACAAAGAGTAAAGATATCAAGAAATTTGGAATTTGTTCTGACTTCAAGAAA 1440
QY 1441 AAAAGATGCGCAAAATACTCTTCTGAAAAAGCAAAAGCAAGCAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCGCAAAATACTCTTCTGAAAAAGCAAAAGCAAGCAAGCTTAAAGCTGACA 1500
QY 1501 TGAAGAGAAAGTCACAAAGGCTTGAAGGCAAGTAAATGCGCAGCAGAGCTGAAAT 1560
DB 1501 TGAAGAGAAAGTCACAAAGGCTTGAAGGCAAGTAAATGCGCAGCAGAGCTGAAAT 1560
QY 1561 TTTATGCTTATGAGAGAAATGAAGAGCAAGAGTACATGAGGATTTCCAGAAAC 1620
DB 1561 TTTATGCTTATGAGAGAAATGAAGAGCAAGAGTACATGAGGATTTCCAGAAAC 1620
QY 1621 CTGACTTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAACAAGCTGAAAGCCAGCAATTTCTTGAAGTGAAGTGAAGTATCAAGTACGAA 1740
DB 1681 AGAACAAGCTGAAAGCCAGCAATTTCTTGAAGTGAAGTGAAGTATCAAGTACGAA 1740

Qy	1741	AAAAATGATCTCGAAGCACTTTTGTGAAGAACAAGAACTGGAAATTTACAGATGAG	1800
Db	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACAAGAACTGGAAATTTACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGCTTGAAAAAATGAATTCTGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGCTTGAAAAAATGAATTCTGAGCTTCT	1860
Qy	1861	CTTGAGTGTAGAAAGAAAGACATCTTGCATGATAATAGCTGCGGGAAGAAATT	1920
Db	1861	CTTGAGTGTAGAAAGAAAGACATCTTGCATGATAATAGCTGCGGGAAGAAATT	1920
Qy	1921	GCATGCTAAGACTGAGACTAGACACATGAAACATCAGAGCCAGCTTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGACTAGACACATGAAACATCAGAGCCAGCTTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

RESULT 5

ID AAH02780 standard; cDNA; 2000 BP.

AC AAH02780;

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen determined cDNA splice variant of B305D #9.

KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN W0200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US027464.

PR 04-OCT-1999; 99US-0157455P.

PA (CORI-) CORIXA CORP.

PI Xu J, Skeiky YAW, Reed SG, Cheever MA;

DR WPI; 2001-245062/25.

XX

PT treatment and diagnosis of prostate cancer.

PS Claim 50; Page 232; 276pp; English.

CC The present invention describes an isolated polypeptide (I) comprising at
CC least an immunogenic portion of a prostate tumour antigen protein or its
CC variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a polynucleotide
CC that encodes a prostate specific protein are useful for detecting the
CC presence or absence of a cancer or monitoring the progression the
CC progression of a cancer, especially prostate cancer. AAH02422 to AAH872,
CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC exemplification of the present invention

SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2000;	DB 4;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATGCGTGTGAAGTGAATTCATGCGGGCTGCCTCTCTGTGAAGAACATTTGGTCTC	60
Db	1	ATGGTGGTGAAGTGAATCCATGCCGGCTCTCTTCTGTGAAGAACCATTTGGTCTC	60
OY	61	AGAGCAAGATGAGCAAGTGGTGTGCTGCTTCTTCCCTGTGCAAGGAGAGCCGCAAG	120
Db	61	AGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGTGCAAGGAGAGCCGCAAG	120
OY	121	AGCAAGTGGGCACTTCTGGAGACCAAGACGACTCTGTATGAAGACATCTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGGAGACCAAGACGACTCTGTATGAAGACATCTCAGAGCAAG	180
OY	181	ATGGGCAAGTGGTGTGCGCCCACTGCTTCCCTGTGCAAGGGGAGTGGCAAGACAAAGTGTG	240
Db	181	ATGGGCAAGTGGTGTGCGCCCACTGCTTCCCTGTGCAAGGGGAGTGGCAAGACAAAGTGTG	240
OY	241	GGCGCTTCTGGAGACCAAGACGACTCTGTATGAAGACACTCAGAGAACAAATGGGCAAG	300
Db	241	GGCGCTTCTGGAGACCAAGACGACTCTGTATGAAGACACTCAGAGAACAAATGGGCAAG	300
OY	301	TGGTGTGCTGCCACTGTCTTCCCTGTGTGAAGGGGGAGCGGCAAGACAAAGTGGGCGTTGG	360
Db	301	TGGTGTGCTGCCACTGTCTTCCCTGTGTGAAGGGGGAGCGGCAAGACAAAGTGGGCGTTGG	360
OY	361	GGAGACTACGATGACATGTGCTTCAATGAGACCCAGGTACCAAGTCCGTGGAGAAAGTCTG	420
Db	361	GGAGACTACGATGACATGTGCTTCAATGAGACCCAGGTACCAAGTCCGTGGAGAAAGTCTG	420
OY	421	GACAAAGTCCACAGAGCTGCTGTGGGGGTAAAGTCCCAAGAAAGATCTTATCTGTATG	480
Db	421	GACAAAGTCCACAGAGCTGCTGTGGGGGTAAAGTCCCAAGAAAGATCTTATCTGTATG	480
OY	481	CTCAGGGACACTGACGTGAACAAGAACAGCAAGCAAAAGAGACTGCTTACATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGAACAAGAACAGCAAGCAAAAGAGACTGCTTACATCTGGCC	540
OY	541	TCTGCAATGGGAATTCAGAAAGTATGTAATACTCTGTGTGACAGACGATGTCACTTAAAT	600
Db	541	TCTGCAATGGGAATTCAGAAAGTATGTAATACTCTGTGTGACAGACGATGTCACTTAAAT	600
OY	601	GTCTTGAACAACAAAAGAGACAGCTCTGTATTAAGGCCGTACATTCGCAAGAAAGATGAA	660
Db	601	GTCTTGAACAACAAAAGAGAGCAGCTCTGTATTAAGGCCGTACATTCGCAAGAAAGATGAA	660
OY	661	TGTGCGTAAATGTTGTGTGGAACATGGACATGATCCAAATATTCCAGATGAGTATGAAAT	720
Db	661	TGTGCGTAAATGTTGTGTGGAACATGGACATGATCCAAATATTCCAGATGAGTATGAAAT	720
OY	721	ACCACTGTGACCTACGCTATCTAATATGAAGATTAATTAATGGCAAAAGACCTGCTTAA	780
Db	721	ACCACTGTGACCTACGCTATCTAATATGAAGATTAATTAATGGCAAAAGACCTGCTTAA	780
OY	781	TATGTGTCTGATATCCGAATCAAAAAACAAGCATGGCCCTCACACACCTGTTACTTGGTGTGA	840
Db	781	TATGTGTCTGATATCCGAATCAAAAAACAAGCATGGCCCTCACACACCTGTTACTTGGTGTGA	840
OY	841	CATGAGCAAAAAACGCAAGTCTGTAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACGCAAGTCTGTAAATTTTAAATCAAGAAAAAGGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGGACTGCTCTCATACTTGGTATGTTGTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCATACTTGGTATGTTGTGGATCAGCAAGTATA	960
OY	961	GTCAGCCCTTCACTTGAAGCAAAATATGAAGTATCTTCAAGAGTCTATCTGGACAAAGC	1020
Db	961	GTCAGCCCTTCACTTGAAGCAAAATATGAAGTATCTTCAAGAGTCTATCTGGACAAAGC	1020
OY	1021	GCCAGAGATATGCTGTCTTCTAGTCAATCATCATGTAATTTGCCAGTTACTTTCAGTAC	1080

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Db 1021 GCAGAGATATGCTTTTCTAGTCATCATGTATTTGGCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGTATGCTAAAAATCTCTTCTGAAAAACAGCAATCTAGAACACAGCTTAAAG 1140
Db 1081 AAAAGAAAAACAGTATGCTAAAAATCTCTTCTGAAAAACAGCAATCTAGAACACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATGTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATGTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGAATAATTAATGTGGGATTAATAAGAAACCTGACTAATGTGTCTGCTGCGC 1320
Db 1261 AAGCATGAAGAATAATTAATGTGGGATTAATAAGAAACCTGACTAATGTGTCTGCTGCGC 1320
QY 1321 AATGTGATTAATGATTTAATTTCTCTCAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTTAATTTCTCTCAAGAGAGAGCAACCTGAAAATCAGCAATTT 1380
QY 1381 CTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACAAACTTAAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACAAACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAGAAAGCTTGAAGGAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
Db 1501 TCAGAGAGAGAGTCAAGAAAGCTTGAAGGAGTGAATAATGGCCAGCAGAGCTAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAACCGAAGTATCTGATGTGGATTTCCAGAAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAACCGAAGTATCTGATGTGGATTTCCAGAAAAC 1620
QY 1621 CTGACATTAATGCTGCAATGCTGCGCAATGTGTAATGTGATTAATTTCTCCAGAGAGAGC 1680
Db 1621 CTGACATTAATGCTGCAATGCTGCGCAATGTGTAATGTGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAACAACCTGAAGAGCAGCAATTTCTGCACTAGAGATGAAGATATCACTAGTCGAA 1740
Db 1681 AGAACAACCTGAAGAGCAGCAATTTCTGCACTAGAGATGAAGATATCACTAGTCGAA 1740
QY 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACACAGATGAG 1800
Db 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAATAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAATAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGTGATGAATAATAGTACGTTGGCGGAAAGAAAT 1920
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGTGATGAATAATAGTACGTTGGCGGAAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACACATGAAACATTCAGAGCCAGCTAAAAAATGAAAT 1980
Db 1921 GCCATGCTAAGACTGAGAGCTAGACACATGAAACATTCAGAGCCAGCTAAAAAATGAAAT 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 6
AAH85029
ID AAH85029 standard; cDNA; 2000 BP.
XX
AC AAH85029;
```

```
XX
DT 25-SRP-2001 (first entry)
DE Human prostate-specific cDNA sequence B305D splice variant #9.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US030904.
XX
PR 12-NOV-1999; 99US-00439313.
XX
PR 18-NOV-1999; 99US-00443686.
XX
PA (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX
PS Claim 31; Page 247-248; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
Db 1 ATGTGTGTTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGTCTC 60
QY 61 AAGAGCAATGAGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AAGAGCAATGAGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 ACGCAAGTGGGCACTTCTGAGACAGACAGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 ACGCAAGTGGGCACTTCTGAGACAGACAGACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTG 240
QY 241 GCGCTTTCTGAGACACAGACAGACTTGTATGAAGACACTCAGAGAAAGATGGCAAG 300
Db 241 GCGCTTTCTGAGACACAGACAGACTTGTATGAAGACACTCAGAGAAAGATGGCAAG 300
QY 301 TGTGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGCAAGTGGCGCTTGG 360
```

Db 301 TGGTGTGCGCAGCTTCCCTCTGCGAGGGGAGCGGCAAGAGCGTGGCGCTTG 360
Qy 361 GGAGATACGATACAGTGTCTTCATGAGACCCAGGTACCACTCCGTGGAAGATCTG 420
Db 361 GGAGATACGATACAGTGTCTTCATGAGACCCAGGTACCACTCCGTGGAAGATCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAGAAAGATCATCGCATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAGAAAGATCATCGCATG 480
Qy 481 CTCAGGAGACGTGACGTGAAACAAGAGACAAAGAGAGAGCTCTTACATCTGGCC 540
Db 481 CTCAGGAGACGTGACGTGAAACAAGAGAGAGAGAGCTCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAGTATGTAATCTCTGTGGAACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTATGTAATCTCTGTGGAACAGAGATGCACTTAAT 600
Qy 601 GTGCTTGAACAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTGCTTGAACAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCGTTAATGTGTGCGAACAATGCACTGATCCAAATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTGTGCGAACAATGCACTGATCCAAATTTCCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACCTCTATCTAATGAAGATTAATTAAGGCAAGAGAGAGAGAG 780
Db 721 ACCACTCTGCACTACCTCTATCTAATGAAGATTAATTAAGGCAAGAGAGAGAGAG 780
Qy 781 TATGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 TATGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy 841 CATGAGCAAAAACAG 900
Db 841 CATGAGCAAAAACAG 900
Qy 901 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTTCTGACGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTTCTGACGAG 1020
Qy 1021 GGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1081 AAG 1140
Db 1081 AAG 1140
Qy 1141 CTGACATCAG 1200
Db 1141 CTGACATCAG 1200
Qy 1201 ATGCTCAAG 1260
Db 1201 ATGCTCAAG 1260
Qy 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Qy 1381 CCTGACAG 1440
Db 1381 CCTGACAG 1440

Db 1381 CCTGACAG 1440
Qy 1441 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1441 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Qy 1501 TCAG 1560
Db 1501 TCAG 1560
Qy 1561 TTTATGCTATGAG 1620
Db 1561 TTTATGCTATGAG 1620
Qy 1621 CTGACTAATGTGCGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CTGACTAATGTGCGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGAT 1680
Qy 1681 AGAAGACCTGAAAG 1740
Db 1681 AGAAGACCTGAAAG 1740
Qy 1741 CAAAATGATCTCAG 1800
Db 1741 CAAAATGATCTCAG 1800
Qy 1801 ATTCTGATTCATGAG 1860
Db 1801 ATTCTGATTCATGAG 1860
Qy 1861 CTTAGTTGTAAG 1920
Db 1861 CTTAGTTGTAAG 1920
Qy 1921 GCCATGCTAAGCTGAG 1980
Db 1921 GCCATGCTAAGCTGAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 7
ACAS9616
ID ACAS9616 standard; cDNA; 2000 BP.
XX
AC ACAS9616;
DT 10-JUN-2003 (first entry)
DE Prostate cancer therapy associated cDNA #359.
XX
KW Prostate cancer; vaccine; gene therapy; cytosolic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMa; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 98US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKI Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; ABU71669.
 XX
 PT Prostate specific protein and its encoding polymucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 XX
 PS Example 11; SEQ ID NO 374; 85bp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 3 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated cDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docid=US20020192763
 CC
 XX
 SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2000; DB 5; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 TGGTCTGCACTGCTCCCTGCTGACAGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
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 Db 301 TGGTCTGCACTGCTTCCCTGCTGACAGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
 QY 361 GGAAGCTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCGTGGAGAAAGTCTG 420
 |||||
 Db 361 GGAAGCTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCGTGGAGAAAGTCTG 420
 QY 421 GACAACTCCACAGAGCTGCGTGGTGGGTAAAGTCCCGAAGAAAGATCTACGTCATG 480
 |||||
 Db 421 GACAACTCCACAGAGCTGCGTGGTGGGTAAAGTCCCGAAGAAAGATCTACGTCATG 480
 QY 481 CTCAGGACACTGACGTGAACAAGAGACAAGCAAAAGAGACTGCTTACATCTGAGCC 540
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 Db 481 CTCAGGACACTGACGTGAACAAGAGACAAGCAAAAGAGACTGCTTACATCTGAGCC 540
 QY 541 TCTGCCAATGGGAATTGCAAGTATGTAATTAATCTCTGCTGACAGACGATGTCACTTAAT 600
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 Db 541 TCTGCCAATGGGAATTGCAAGTATGTAATTAATCTCTGCTGACAGACGATGTCACTTAAT 600
 QY 601 GTCCCTGCAACAAGAAAGAGACAGCTCTGATTAAGCCGTCATTCGCAAGAGATGAA 660
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 Db 601 GTCCCTGCAACAAGAAAGAGACAGCTCTGATTAAGCCGTCATTCGCAAGAGATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCCAGATGATGGAAAT 720
 |||||
 Db 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCCAGATGATGGAAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTATATATGAAAGATTAATTAAGCCAAAGCACTGCTTAA 780
 |||||
 Db 721 ACCACTCTGCACTACGCTATCTATATATGAAAGATTAATTAAGCCAAAGCACTGCTTAA 780
 QY 781 TATGTCGCTGATATGAAATCAAAAGCAAGCTGCTTCAACCACTGTTACTGGTGA 840
 |||||
 Db 781 TATGTCGCTGATATGAAATCAAAAGCAAGCTGCTTCAACCACTGTTACTGGTGA 840
 QY 841 CATGACAAAGAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
 |||||
 Db 841 CATGACAAAGAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
 QY 901 CTGATATGATATGAAAGAGCTGCTCATCTTCTGTATGTTGTGGATCAGCAAGTATA 960
 |||||
 Db 901 CTGATATGATATGAAAGAGCTGCTCATCTTCTGTATGTTGTGGATCAGCAAGTATA 960
 QY 961 GTGAGCTCTTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020
 |||||
 Db 961 GTGAGCTCTTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 |||||
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 QY 1081 AAAAGAAAAAGATGCTAAAAATCTTCTGAAAAAGCAATCCAGAACAGCTTTAAAG 1140
 |||||
 Db 1081 AAAAGAAAAAGATGCTAAAAATCTTCTGAAAAAGCAATCCAGAACAGCTTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGATCAAAAGCTTCAAAAGCATGAAATTAACCAAGCAAGAAA 1200
 |||||
 Db 1141 CTGACATCAGAGAAAGATCAAAAGCTTCAAAAGCATGAAATTAACCAAGCAAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATAGAGAGTTGAAGAAAGAAATGAAG 1260
 |||||
 Db 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATAGAGAGTTGAAGAAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAATTAATGGAATTAATGGAATTAATGGAATTAATGGAATTAATG 1320
 |||||
 Db 1261 AAGCATGAAAGTAATTAATGGAATTAATGGAATTAATGGAATTAATGGAATTAATG 1320
 QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACATCTGAAATTAATGCAATTT 1380
 |||||
 Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACATCTGAAATTAATGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAATTAATGTTCTGACTACAAAGAA 1440
 |||||

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Db 1381 CCGAGACAGCAAGTGAAGAGTATACAGAAATTTGCAATTTAGTTTGTGCTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAACAGCAACCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGATGACAAAGGCTTGAGGCGCATGAAAATGGCCAGGAGCTTGAATAAT 1560
Db 1501 TCAGAGAAAGATGACAAAGGCTTGAGGCGCATGAAAATGGCCAGGAGCTTGAATAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAAGACGAGAAAGTACTCATGTCGGAATCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAAGACGAGAAAGTACTCATGTCGGAATCCAGAAAC 1620
Qy 1621 CTGACTAATAGTGCACCTGCTGGCAATGTGATGATGATTAATTCCTCCAGAAAGAGC 1680
Db 1621 CTGACTAATAGTGCACCTGCTGGCAATGTGATGATGATTAATTCCTCCAGAAAGAGC 1680
Qy 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAGATTCACAGTGACGA 1740
Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAGATTCACAGTGACGA 1740
Qy 1741 CAAATATGATCTAGCAAGCAATTTGTGAGAAACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAATATGATCTAGCAAGCAATTTGTGAGAAACAGAACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGCAAGATGAAAGTGTGAAATAATGAATTCGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGCAAGATGAAAGTGTGAAATAATGAATTCGAGCTTCT 1860
Qy 1861 CTTAGTTGTAGAAAGAAAGACATTTTCATGAAATGTACGTTGCCGAAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAGAAAGACATTTTCATGAAATGTACGTTGCCGAAAGAAAT 1920
Qy 1921 GCCATGCTAGACTGAGAGTGAACAACAATGAAATCATGAGCCAGCTTAAATTAATTA 1980
Db 1921 GCCATGCTAGACTGAGAGTGAACAACAATGAAATCATGAGCCAGCTTAAATTAATTA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
ABL95179
ID ABL95179 standard; cDNA; 2000 BP.
AC ABL95179;
XX
XX 19-JUL-2002 (first entry)
DT
XX
XX Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
XX Human; Cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-00759143.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
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PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
XX (XUJ/) XU J.
XX (DIL/) DILLON D. C.
XX (MIT/) MITCHAM J. L.
XX (HAR/) HARLOCKER S. L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M. D.
XX (FANG/) FANGER G. R.
XX (RETT/) RETTER M. W.
XX (STOL/) STOLK J. A.
XX (DAYC/) DAY C. H.
XX (VEDV/) VEDVICK T. S.
XX (CART/) CARTER D.
XX (LISX/) LI S. X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y. A. W.
XX (HEPL/) HEPLER W. T.
XX (HEND/) HENDERSON R. A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedrick TS, Carter D;
XX Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer.
XX
XX Claim 1; SEQ ID NO 374; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX CC their encoded proteins. These can be used in the diagnosis and treatment
XX CC of cancers, particularly prostate cancer. The present sequence is a cDNA
XX CC described in the invention
XX
XX SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2000; DB 6; Length 2000;
XX Best Local Similarity 100.0%; Pred No. 0;
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGTGTGAGGATGATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGCTTC 60
Db 1 ATGGTGTGAGGATGATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGCTTC 60
Qy 61 AGAGCAAGATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACCGGCAAG 120
Db 61 AGAGCAAGATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGACATCAAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGACATCAAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240
Qy 241 GGGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGACATCAAGAGCAAGATGGGCAAG 300
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Db      241 GGGGCTTTGGAGACCAACGACGACTCTGATGAAAGCACTGAGAAACAAGATGGGCAAG 300
Qy      301 TGGTGTGCGCACTGCTTCCCTCTCTGCAAGGAGGAGCGGCAAGACAAAGTGGGCGCTTG 360
Db      301 TGGTGTGCGCACTGCTTCCCTCTCTGCAAGGAGGAGCGGCAAGACAAAGTGGGCGCTTG 360
Qy      361 GGAGACTAGTAGAGTGGCTTCATGAGGCCAGGATCAAGCTCCGTGGAGAAAGATCTG 420
Db      361 GGAGACTAGTAGAGTGGCTTCATGAGGCCAGGATCAAGCTCCGTGGAGAAAGATCTG 420
Qy      421 GACAACTCCACAGAGCTGCTGCTGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db      421 GACAACTCCACAGAGCTGCTGCTGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Qy      481 CTGAGGAGCACTGACGTGAACAAGAAAGACAAAGAAAGAGACTGCTCTACACTGCGCC 540
Db      481 CTGAGGAGCACTGACGTGAACAAGAAAGACAAAGAAAGAGACTGCTCTACACTGCGCC 540
Qy      541 TCTGCCAATGGGAATTGAGAAAGTAAATCTCTGCTGGAAGAGATGTCATCTTAAT 600
Db      541 TCTGCCAATGGGAATTGAGAAAGTAAATCTCTGCTGGAAGAGATGTCATCTTAAT 600
Qy      601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATAAAGGCGCTACAAATGCCAGAAAGATGA 660
Db      601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATAAAGGCGCTACAAATGCCAGAAAGATGA 660
Qy      661 TGTGCGCTTAAATGTTGCTGGAACATGCGCACTGATCCAAATTTCCAGATGATGGAAT 720
Db      661 TGTGCGCTTAAATGTTGCTGGAACATGCGCACTGATCCAAATTTCCAGATGATGGAAT 720
Qy      721 ACCACTGTGCACTACGCTATCTATTAATGAGATTAATTAATGAGCAAGCACTGCTT 780
Db      721 ACCACTGTGCACTACGCTATCTATTAATGAGATTAATTAATGAGCAAGCACTGCTT 780
Qy      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCAACACTGTTACTTGTGATGA 840
Db      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCAACACTGTTACTTGTGATGA 840
Qy      841 CATGACCAAAAAACAGACAGTCTGGAATTTTATCAAGAAAAAAGCAATTTAATGCA 900
Db      841 CATGACCAAAAAACAGACAGTCTGGAATTTTATCAAGAAAAAAGCAATTTAATGCA 900
Qy      901 CTGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTTGATGAGCAAGTATA 960
Db      901 CTGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTTGATGAGCAAGTATA 960
Qy      961 GTGAGCTTCTACTTGAACAAAAATTTGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Db      961 GTGAGCTTCTACTTGAACAAAAATTTGATGTAATCTTCTCAAGATCTATCTGACAGAG 1020
Qy      1021 GCCAGAGAGTATGCTGTTTCTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db      1021 GCCAGAGAGTATGCTGTTTCTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy      1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCATCAGAACCAAGCTTAAG 1140
Db      1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCATCAGAACCAAGCTTAAG 1140
Qy      1141 CTGACATCAGAGGAGAGTCAACAAAGTTCAAAAGGAGTGAATAATGAGCCAGAGAAAA 1200
Db      1141 CTGACATCAGAGGAGAGTCAACAAAGTTCAAAAGGAGTGAATAATGAGCCAGAGAAAA 1200
Qy      1201 ATGTCTCAAGAACCAAAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACCAAAAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy      1261 AAGCATGAAGATTAATTAATGAGATTACTAGAAAACTGACTAATGGTGCATCTGCTGGC 1320
Db      1261 AAGCATGAAGATTAATTAATGAGATTACTAGAAAACTGACTAATGGTGCATCTGCTGGC 1320
Qy      1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGAGCAACACTGAAAAATCGCAATTT 1380

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Db      1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGAGAGAACACTGAAAAATCAGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTTGGAATTGATTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTTGGAATTGATTCTGACTACAAAGAA 1440
Qy      1441 AAAAGATGCAAAATATCTCTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
Db      1441 AAAAGATGCAAAATATCTCTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCAAGTGAATAATGSCCAAGCAGAGCTAGAAAAAT 1560
Db      1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCAAGTGAATAATGSCCAAGCAGAGCTAGAAAAAT 1560
Qy      1561 TTTATGGCTATGGAAGAAATGAAAGAACCGGAAGTACTCATGTGGATTTCCAGAAAGC 1620
Db      1561 TTTATGGCTATGGAAGAAATGAAAGAACCGGAAGTACTCATGTGGATTTCCAGAAAGC 1620
Qy      1621 CTGACTAATGTGTGCCACTGCTGGCAATGATGATGATTAATTCCTCAAGAAAGAGC 1680
Db      1621 CTGACTAATGTGTGCCACTGCTGGCAATGATGATGATTAATTCCTCAAGAAAGAGC 1680
Qy      1681 AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTACGAA 1740
Db      1681 AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTACGAA 1740
Qy      1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Db      1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
Qy      1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATGAAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATGAAATCTGAGCTTTCT 1860
Qy      1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAATAATGATGCTGCGGAGAAATTT 1920
Db      1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAATAATGATGCTGCGGAGAAATTT 1920
Qy      1921 GCCATGCTTAAGCTGAGAGCTAAGACAAATGAAGACATCAGAGCAGCTTAAGAAAAA 1980
Db      1921 GCCATGCTTAAGCTGAGAGCTAAGACAAATGAAGACATCAGAGCAGCTTAAGAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 9
AAS99858
ID AAS99858 standard; cDNA; 2000 BP.
XX
AC AAS99858;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour--specific DNA B11g1 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN MO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-0069295.
PR 16-MAR-2001; 2001US-00810936.
XX

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Db 1681 AAGAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCACAGTGA CGAA 1740
Qy 1741 CAAAATGATACCTAGAGCAATTTTGTGAAGAA CAGAACACTGGAATTTTACACATGAG 1800
Db 1741 CAAAATGATACCTAGAGCAATTTTGTGAAGAA CAGAACACTGGAATTTTACACATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAAGCAGATGAGAGTGTTGAAAAAATGAAATTCGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAAGCAGATGAGAGTGTTGAAAAAATGAAATTCGAGCTTTCT 1860
Qy 1861 CTAGTGTGAAGAAAAGACATCTTGACATGAAATAGTACGTTGGCGGAGAAAGAAAT 1920
Db 1861 CTAGTGTGAAGAAAAGACATCTTGACATGAAATAGTACGTTGGCGGAGAAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACATGAAAACATCAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAAACATCAGAGCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
ACC95343
ID ACC95343 standard; cDNA; 2000 BP.
AC ACC95343;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 374.
XX
KM Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer; ss.
OS Homo sapiens.
XX
PN WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepier WT, Hurral J;
PI McNeill PD, Houghton RL, Vinals Y De BaeleisC, Foy TM, Watanabe Y;
PI Deng T;
XX
XX MPI; 2003-167130/16.
XX
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX Example 11; Page 415-416; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
XX and their coding sequences. The PSPs and their coding sequences are
XX useful for stimulating an immune response in a patient, or for treating
XX prostate cancer in a patient and for determining, detecting or diagnosing
XX the presence of a cancer in a patient. The present sequence was used to
XX illustrate the invention
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTGAGGTTGATTCATGCGGAGTCCCTCTTCTGTGAAGAACCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTTGATTCATGCGGAGTCCCTCTTCTGTGAAGAACCAATTTGGTCTC 60
Qy 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AAGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Qy 121 AAGCAAGTGGGCACTTTGTGAAGACACAGCACTCTGTATGAAGACACTCAGAGCAAG 180
Db 121 AAGCAAGTGGGCACTTTGTGAAGACACAGCACTCTGTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Qy 241 GGGCGTTCTGAGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGTTCTGAGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Qy 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Qy 361 GAGAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGTGGAGAGATCTG 420
Db 361 GAGAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGTGGAGAGATCTG 420
Qy 421 GACAAAGTCCCAAGAGAGTGGGCTGAGAGTAAAGTCCCAAGAAAGATTCATCCGTCAG 480
Db 421 GACAAAGTCCCAAGAGAGTGGGCTGAGAGTAAAGTCCCAAGAAAGATTCATCCGTCAG 480
Qy 481 CTCAGGAGACCTGAGAGTGGCTGAGAGTAAAGTCCCAAGAAAGATTCATCCGTCAG 540
Db 481 CTCAGGAGACCTGAGAGTGGCTGAGAGTAAAGTCCCAAGAAAGATTCATCCGTCAG 540
Qy 541 TCTGCCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGACAGATGTCATCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGACAGATGTCATCTTAAT 600
Qy 601 GTCTTGAACAAAG 660
Db 601 GTCTTGAACAAAG 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGATGGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATAATGAAGATTAATTAATGAGCCAGACCTGCTT 780
Db 721 ACCACTCTGCACTAGCTATCTATAATGAAGATTAATTAATGAGCCAGACCTGCTT 780
Qy 781 TATGTGCTGATATGATCAATCAAAAAAGAGATGGCTCAACACTGTTACTTGGTGT 840
Db 781 TATGTGCTGATATGATCAATCAAAAAAGAGATGGCTCAACACTGTTACTTGGTGT 840
Qy 841 CATGAGCAAAAAAGAGATGGCTGATTAATCAAAAAAGAGATTTAATGCA 900
Db 841 CATGAGCAAAAAAGAGATGGCTGATTAATCAAAAAAGAGATTTAATGCA 900
Qy 901 CTGAGATGATATGAG 960
Db 901 CTGAGATGATATGAG 960
Qy 961 GTGAGCTTCTACTTGAAG 1020
Db 961 GTGAGCTTCTACTTGAAG 1020

QY	1021	GCACAGAGTATGCTGTTTCTTAGTATCATCATGTAATTTGGCAATTACTTTGACATAC	1080
Db	1021	GCACAGAGTATGCTGTTTCTTAGTATCATCATGTAATTTGGCAATTACTTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCATTCACGAACAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCATTCACGAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGGAAGTGCACAAAGCTTCAAGAGCAGTGAATAATAGCCACAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTGCACAAAGCTTCAAGAGCAGTGAATAATAGCCACAGAGAA	1200
QY	1201	ATGTTCTCAAGAACCGAAATTAATTAAGATGGTGTATAGAGGCTTGAAGAAATGAAG	1260
Db	1201	ATGTTCTCAAGAACCGAAATTAATTAAGATGGTGTATAGAGGCTTGAAGAAATGAAG	1260
QY	1261	AAGCATGAAGTAATTAATGTGGGATTACTAGAAAACCTGATTAATGTGTCTGACTGGC	1320
Db	1261	AAGCATGAAGTAATTAATGTGGGATTACTAGAAAACCTGATTAATGTGTCTGACTGGC	1320
QY	1321	AATGTGTAAATGATTAATTCCTCAAGAGAGCAGAACACTGTAATAATCAGCAATTT	1380
Db	1321	AATGTGTAAATGATTAATTCCTCAAGAGAGCAGAACACTGTAATAATCAGCAATTT	1380
QY	1381	CCTGACAAACGAAAGTGAAGATATCACAAATTTGCGAATTAATTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGATATCACAAATTTGCGAATTAATTTCTGACTACAAAGAA	1440
QY	1441	AAACGAGATGCCAAAATCTCTTTCTGAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA	1500
Db	1441	AAACGAGATGCCAAAATCTCTTTCTGAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA	1500
QY	1501	TCAGAGAGAGTGCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTGAAAT	1560
Db	1501	TCAGAGAGAGTGCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTGAAAT	1560
QY	1561	TTTATGCTATCGAAGAAATGAAGAGCAGGAATGCTCATGTTCGATTTCCAGAAAAC	1620
Db	1561	TTTATGCTATCGAAGAAATGAAGAGCAGGAATGCTCATGTTCGATTTCCAGAAAAC	1620
QY	1621	CTGACTAATGCTGCCACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGC	1680
Db	1621	CTGACTAATGCTGCCACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGC	1680
QY	1681	AGAACACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGAGATACACAGTGAAGAA	1740
Db	1681	AGAACACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGAGATACACAGTGAAGAA	1740
QY	1741	CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACACTGGAATTAATTCACAGTAG	1800
Db	1741	CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACACTGGAATTAATTCACAGTAG	1800
QY	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAAGACACTTGTGATGAAAAATAGTAAGCTGGGGAAGAAAT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGACACTTGTGATGAAAAATAGTAAGCTGGGGAAGAAAT	1920
QY	1921	GCCATGCTAGACTGAGACTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAAA	1980
Db	1921	GCCATGCTAGACTGAGACTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 11			
ADAL1381 standard; cDNA; 2000 BP.			
XX			

AC ADA11381;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human breast cancer specific cDNA B1IC-8.
XX
KW ss; gene; human; breast cancer; cytostatic; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002165371-A1.
XX
PD 07-NOV-2002.
XX
PF 07-AUG-2001; 2001US-00924400.
XX
PR 11-JAN-1996; 96US-00585392.
XX
PR 10-JAN-1997; 97MO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00991789.
PR 17-APR-1998; 98US-0062451.
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
PR 24-MAY-2000; 2000US-00571505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX
PA (FRUD/) FRUDAKIS T N.
XX
PA (REED/) REED S G.
XX
PA (SMIT/) SMITH J M.
XX
PA (MISH/) MISHER L E.
XX
PA (DILL/) DILLON D C.
XX
PA (RETT/) RETTER M W.
XX
PA (WANG/) WANG A.
XX
PA (SKEI/) SKEIKY Y A W.
XX
PA (HARL/) HARLOCKER S L.
XX
PA (DAYC/) DAY C H.
XX
PA (LI SX/) LI S X.
XX
PA (DENG/) DENG T.
XX
PI Frudakis TN, Reed SG, Smith JM, Misner LE, Dillon DC, Retter MW,
PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
PI
DR MPI; 2003-247262/24.
XX
DX P-PSDB; ADA11384.
XX
PT New breast tumor proteins nucleic acids encoding such proteins, useful in
PT diagnosing, preventing and/or treating diseases such as cancer.
PT particularly breast cancer, and as markers for detecting the presence of
PT a cancer.
XX
PS Claim 1; Page 140; 190pp; English.
XX
XX The invention relates to a breast tumour polynucleotide selected from one
CC of the 275 fully defined nucleotide sequences (a) given in the
CC specification, including their complements, sequences consisting of at
CC least 20 contiguous residues of a sequence in (a), sequences that
CC hybridise to a sequence in (a) under moderately stringent conditions,
CC sequences having at least 75% or 90% identity to a sequence in (a), or
CC degenerate variants of a sequence in (a). Also included are an isolated
CC polypeptide (II) (comprising an amino acid sequence selected from
CC sequences encoded by (a), sequences having at least 70% or 90% identity
CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
CC sequences (c), and sequences having at least 70% or 90% identity to a
CC sequence in (c)), expression vectors comprising (a), a host cell
CC transformed or transfected with the expression vector, an isolated
CC antibody or its antigen-binding fragment that specifically binds to (II),
CC a method for detecting the presence of a cancer in a patient, a fusion
CC protein comprising at least one polypeptide (II), an oligonucleotide that
CC hybridises to (a), under moderately stringent conditions, a method for
CC stimulating and/or expanding T cells specific for a tumour protein (by

CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting T cells that express (ii), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGCAACCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGCAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTCCCTGCTGCAAGGAGACGGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTCCCTGCTGCAAGGAGACGGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTCCGCTCTCTCTGCTGCAAGGAGGAGTGGCAAGCAAGCGTG 240
DB 181 ATGGGCAAGTGGTGGTCCGCTCTCTCTGCTGCAAGGAGGAGTGGCAAGCAAGCGTG 240
QY 241 GGGGCTTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAAAGGAGTGGCAAG 300
DB 241 GGGGCTTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAAAGGAGTGGCAAG 300
QY 301 TGGTGGTCCACTGCTTCCCTGCTCTGCAAGGAGGAGGCAAGCAAGTGGGCTGG 360
DB 301 TGGTGGTCCACTGCTTCCCTGCTCTGCAAGGAGGAGGCAAGCAAGTGGGCTGG 360
QY 361 GGAAGCTAGATGACAGTGGCTTCTCATGAGCCCAAGGTACCACTCCGTGAGAAAGATCTG 420
DB 361 GGAAGCTAGATGACAGTGGCTTCTCATGAGCCCAAGGTACCACTCCGTGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTGATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTGATG 480
QY 481 CTCAGGAGACATGACGCTGAACAAGAAAGCAAGCAAAAGAGAGCTCTCTACATCTGGCC 540
DB 481 CTCAGGAGACATGACGCTGAACAAGAAAGCAAGCAAAAGAGAGCTCTCTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAAGTCTCTCTGCTGACAGACGATGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAAGTCTCTCTGCTGACAGACGATGTCAACTTAAT 600
QY 601 GTCCTTGAACAAGAAAGAGAGAGCTGATTAAGGCGGTAAAGTCCAGAGAAAGATGAA 660
DB 601 GTCCTTGAACAAGAAAGAGAGAGCTGATTAAGGCGGTAAAGTCCAGAGAAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGATGGAAT 720
QY 721 ACCACTCTGACATACGCTATCTATAATGAAGATAAATTAATGAGCAAGACCTGCTTAA 780
DB 721 ACCACTCTGACATACGCTATCTATAATGAAGATAAATTAATGAGCAAGACCTGCTTAA 780

QY 781 TATGGTGGTATGATGAATCAAAAAACAAGACATGGCTCACACCACTGTTACTGGTGA 840
DB 781 TATGGTGGTATGATGAATCAAAAAACAAGACATGGCTCACACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGACAGTCCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGACAGTCCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGATATGTTGGATCAGCAAGTAA 960
DB 901 CTGATATGATATGAAGAGCTGCTCATCTTCTGATATGTTGGATCAGCAAGTAA 960
QY 961 GTGAGCTTCTACTTGGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTACTTGGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGGAGTAAATAGCAGGCAAGAA 1200
DB 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGGAGTAAATAGCAGGCAAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGGTGTATGAGAGTTGAAGAAATGAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGGTGTATGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACTGACTAAATGTTCTACTGCTGGC 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACTGACTAAATGTTCTACTGCTGGC 1320
QY 1321 AATGGATATATGATTAATTTCTCAAGAGGAGAGAGAACCTGAAATATCAGCAATTT 1380
DB 1321 AATGGATATATGATTAATTTCTCAAGAGGAGAGAGAACCTGAAATATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACTTAAAGCTGACA 1500
DB 1441 AAAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATGACAAAGGCTTGGAGGCACTGAGAAATGGCCAGCAGAGCTAGAAAT 1560
DB 1501 TCAGAGAAAGATGACAAAGGCTTGGAGGCACTGAGAAATGGCCAGCAGAGCTAGAAAT 1560
QY 1561 TTTATGGCTATGGAAGAAATGAAGAGCAAGAAAGTATCATGTGCGAATTTCCAGAAAT 1620
DB 1561 TTTATGGCTATGGAAGAAATGAAGAGCAAGAAAGTATCATGTGCGAATTTCCAGAAAT 1620
QY 1621 CTGACTAATATGAGGCACTGCTGCAATGTTGATGATTAATTTCTCAAGAGAAAGAC 1680
DB 1621 CTGACTAATATGAGGCACTGCTGCAATGTTGATGATTAATTTCTCAAGAGAAAGAC 1680
QY 1681 AGAACAACCTGGAAGGAGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGCAGAA 1740
DB 1681 AGAACAACCTGGAAGGAGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGCAGAA 1740
QY 1741 CAAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTATTAAGATGAG 1800
DB 1741 CAAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTATTAAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATGAGAGTGGTTGAAAAATGAAATTTCTGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATGAGAGTGGTTGAAAAATGAAATTTCTGAGCTTTCT 1860

QY 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATAATAGTACGTTGGCGGAGAAAT 1920
DB 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATAATAGTACGTTGGCGGAGAAAT 1920
QY 1921 GCCATGCTAGACCTGAGCTGAGACACAAATGAAAATCATGAGAGCCAGCTAAAAA 1980
DB 1921 GCCATGCTAGACCTGAGCTGAGACACAAATGAAAATCATGAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 12
ADCI5354
ID ADCI5354 standard; DNA; 2000 BP.
XX
AC ADCI5354;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human breast tumour protein DNA, SEQ ID 302.
XX
KM Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KM de.
OS Homo sapiens.
XX
PN MO2003013431-A2.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002MO-US024917.
XX
PR 07-AUG-2001; 2001US-00924400.
PR 20-FEB-2002; 2002US-00079137.
PR 02-AUG-2002; 2002US-00212679.
XX
PA (CORI-) CORIXA CORP.
PI Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
PI Kalos MD;
XX
DR WPI; 2003-342398/32.
XX
PT New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
XX
PS Example 1; SEQ ID NO 302; 308bp; English.
XX
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best local Similarity 100.0%; Pred No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCAATTTGGTCTC 60
DB 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

DB 61 AGGAGCAAGATGGGCAAGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGACACAGACAGCTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
DB 241 GGGCTTCTGAGACACAGACAGCTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420
DB 361 GGAAGCTAGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420
QY 421 GACAAAGCTCAGAGAGCTGCTGCTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
DB 421 GACAAAGCTCAGAGAGCTGCTGCTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAG 480
QY 481 CTCAGGAGCACTGACGTGAAACAAAGAGCAAGCAAGAGCACTCTCTCACTCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAAACAAAGAGCAAGCAAGAGCACTCTCTCACTCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGACAGAGTCTCACTTAAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGACAGAGTCTCACTTAAAT 600
QY 601 GTCCCTTGAACAAAG 660
DB 601 GTCCCTTGAACAAAG 660
QY 661 TGTGCTTAAATGTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCTTAAATGTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTTGCACCTACGCTATCTAATAATGAAATTAATGAGCCAAAGCACTGCTTAA 780
DB 721 ACCACTTGCACCTACGCTATCTAATAATGAAATTAATGAGCCAAAGCACTGCTTAA 780
QY 781 TATGCTGATATGAAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGCTGATATGAAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGAGCAAAAG 900
DB 841 CATGAGCAAAAG 900
QY 901 CTGATATGATGAAAG 960
DB 901 CTGATATGATGAAAG 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATCATCATCATCATCATCATCATCATCATCAT 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATCATCATCATCATCATCATCATCATCATCAT 1080
QY 1081 AAG 1140
DB 1081 AAG 1140
QY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200

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Db      1141 CTGACATCAGAGGAGAGTCACAAAGTTCAAAGGAGTGAAATAGCCAGCCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACACAGAAATTAATAAGATGTGATAGAGAGGTGTAAGAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACACAGAAATTAATAAGATGTGATAGAGAGGTGTAAGAGAAATGAAG 1260
Qy      1261 AAGCATGAAAGTAAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCGC 1320
Db      1261 AAGCATGAAAGTAAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTGCTGCGC 1320
Qy      1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAAATAATCGCAATTT 1380
Db      1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAAATAATCGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTAAAGATGATCAAGAAATTTGGCAATTAATTTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTAAAGATGATCAAGAAATTTGGCAATTAATTTCTGACTACAAAGAA 1440
Qy      1441 AAACAGATGCGCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCGCAAAATACTCTTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAGAAAGATGACAAAGAGCTTTGAGGCGCATGTGAAAATGGCCAGCCAGCTAGAAAAT 1560
Db      1501 TCAGAGAGAAAGATGACAAAGAGCTTTGAGGCGCATGTGAAAATGGCCAGCTAGAAAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAAGAGCAGAAAGTACTCATGTGGATTTCCCGAAGAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAAGAGCAGAAAGTACTCATGTGGATTTCCCGAAGAAAC 1620
Qy      1621 CTGACTAATGTGTCGCACTGTGCGCAATGTGATGATGATTAATTTCTCCAGAGAAAGAC 1680
Db      1621 CTGACTAATGTGTCGCACTGTGCGCAATGTGATGATGATTAATTTCTCCAGAGAAAGAC 1680
Qy      1681 AGAACAACCTGAAAAGCCAGCAATTTCTGACACTGAAATGAGAGATATCACTAGTCGAA 1740
Db      1681 AGAACAACCTGAAAAGCCAGCAATTTCTGACACTGAAATGAGAGATATCACTAGTCGAA 1740
Qy      1741 CAAATATGATTAAGTAAAGCAATTTTGTGAAGACAGAAACCTGAAATTAATTAACGATGAG 1800
Db      1741 CAAATATGATTAAGTAAAGCAATTTTGTGAAGACAGAAACCTGAAATTAATTAACGATGAG 1800
Qy      1801 ATTCTGATTCATGAAAGAAAAGCAGATAGAAAGTGTGAAAATAATGTAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAAAGAAAAGCAGATAGAAAGTGTGAAAATAATGTAATCTGAGCTTTCT 1860
Qy      1861 CTTAGTTTGAAGAAAGAAAAGCATCTTGCATGAAAATAGTACGTTGCGGGAAGAAATTT 1920
Db      1861 CTTAGTTTGAAGAAAGAAAAGCATCTTGCATGAAAATAGTACGTTGCGGGAAGAAATTT 1920
Qy      1921 GCCATGCTTAAGACTGAGAGCTAGACATGAAATCATCAGAGCCAGCTAAATAAAAA 1980
Db      1921 GCCATGCTTAAGACTGAGAGCTAGACATGAAATCATCAGAGCCAGCTAAATAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 13
ADBI3824
ID      ADBI3824 standard; cDNA; 2000 BP.
XX
XX
AC      ADBI3824;
XX
XX      18-DEC-2003 (first entry)
XX
XX      Human prostate specific cDNA B305 splice variant #9.
DE
XX      Human prostate specific cDNA, cytosolic; immunostimulant;
XX      gene therapy; cell therapy; vaccine; T-cell epitope;
KM      class I major histocompatibility complex allele; MHC; prostate cancer;
KW      tumour; antigen presenting cell.

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XX      XX
OS      Homo sapiens.
XX      XX
PN      US2003185830-A1.
XX      XX
PD      02-OCT-2003.
XX      XX
PF      12-NOV-2002; 2002US-00294025.
XX      XX
PR      25-FEB-1997; 97US-00806099.
PR      01-AUG-1997; 97US-00904804.
PR      09-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.
PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00443686.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-005568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      09-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651235.
PR      06-SEP-2000; 2000US-00657279.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
PR      09-NOV-2000; 2000US-00709729.
PR      12-JAN-2001; 2001US-00759143.
PR      09-FEB-2001; 2001US-00780669.
PR      09-MAY-2001; 2001US-00852911.
PR      29-JUN-2001; 2001US-00895814.
PR      10-DEC-2001; 2001US-00012896.
PR      09-MAY-2002; 2002US-00144678.

(COR-) CORIXA CORP.
XX
XX      Xu J, Stolk JA, Kalos MD;
PI
XX
XX      WPI; 2003-756193/71.
DR
XX      P-PsDB; ADBI3829.
DR
XX
XX      New isolated polypeptide for use in a vaccine for stimulating an immune
PT      response, or for treating or diagnosis cancer, preferably prostate
PT      cancer.
XX
XX      Example 11; Page; 101pp; English.
PS
XX
XX      The invention relates to an isolated polypeptide comprising no more than
CC      11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC      peptides comprise a fragment ADBI3563 of that contain naturally processed
CC      T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC      alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC      cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC      encoding the proteins and peptides, expression vectors, a host cell
CC      transformed with the vector, an isolated antibody (or antigen binding
CC      fragment) that specifically binds to the protein or peptide, detecting
CC      the presence of a cancer in a patient (comprising contacting a patient
CC      sample with a binding agent that binds to the peptides or a polypeptide
CC      appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC      the agent and comparing the amount of polypeptide to a predetermined cut-
CC      off value to determine the presence of cancer), a fusion protein
CC      comprising the peptides or proteins, stimulating or expanding T cells
CC      specific for a tumour protein comprising contacting T cells with the
CC      peptides or the isolated T cell population, treating prostate cancer in a
CC      patient comprising administering a composition comprising the peptides,
CC      nucleic acids, antibodies or compounds, determining the presence of a
CC      cancer in a patient and treating prostate cancer in a patient comprising
CC      incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

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CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptide (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known CDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific CDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPO at
CC seqdata.uspro.gov/sequence.html?docid=20030185830.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 2000; Conservative 0; Indels 0; Caps 0;
QY 1 ATGAGTGGTGAAGTTCATGCGCGCTGCTCTTGTGGAAGACCATTTGTCTC 60
Db 1 ATGAGTGGTGAAGTTCATGCGCGCTGCTCTTGTGGAAGACCATTTGTCTC 60
QY 61 AGAGAGCAAGTGGGCAAGTGTGTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
Db 61 AGAGAGCAAGTGGGCAAGTGTGTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGCAACGACGCTGTGTAAGACATCAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTGTGAGCAACGACGCTGTGTAAGACATCAGAGAGAG 180
QY 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCGAGGAGTGGCAAGACGTG 240
Db 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGCGAGGAGTGGCAAGACGTG 240
QY 241 GGGGCTTGTGAGACCAACGACGCTGTGTAAGACATCAGAGAGAG 300
Db 241 GGGGCTTGTGAGACCAACGACGCTGTGTAAGACATCAGAGAGAG 300
QY 301 TGGTGTGCGACGCTTCCCTGCTGCGAGGAGGCGGCAAGAGTGGCGCTTGG 360
Db 301 TGGTGTGCGACGCTTCCCTGCTGCGAGGAGGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTAGAGTACAGTGTCTTCAATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
Db 361 GGAGACTAGAGTACAGTGTCTTCAATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
QY 421 GACACCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
Db 421 GACACCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGAGACATGACGTGTAACAGAGAGCAACAAAGAGAGCTGCTTCAATCTGGCC 540
Db 481 CTCAGGAGACATGACGTGTAACAGAGAGCAACAAAGAGAGCTGCTTCAATCTGGCC 540
QY 541 TCTGCAATGGAATTCAGAGTGTAAATCTCTGTGGAAGAGATGCAATCTTAAT 600
Db 541 TCTGCAATGGAATTCAGAGTGTAAATCTCTGTGGAAGAGATGCAATCTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGAGAGCTGTGATTAAGGCGCTACATGCGAGAGATGAA 660
Db 601 GTCTTGAACAACAAAGAGAGAGAGCTGTGATTAAGGCGCTACATGCGAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGCACTACGTATCTATTAATGAAGATAAATTAAGCCAAAGACATGCTCTTA 780
Db 721 ACCACTCTGCACTACGTATCTATTAATGAAGATAAATTAAGCCAAAGACATGCTCTTA 780

QY 781 TATGTCCTGATATGCAATTAACAAACAGATGCGCTCACACCATGTTACTTGTGCTA 840
Db 781 TATGTCCTGATATGCAATTAACAAACAGATGCGCTCACACCATGTTACTTGTGCTA 840
QY 841 CATGACCAAAAAACAGAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACCAAAAAACAGAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGTATATGTTGTGATCAGCAATATA 960
Db 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGTATATGTTGTGATCAGCAATATA 960
QY 961 GTACGCTTCTACTTGAACAAATATGATATCTTCTCAAGATCTATGTGACAGAGC 1020
Db 961 GTACGCTTCTACTTGAACAAATATGATATCTTCTCAAGATCTATGTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAATAATCTCTGTAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATAATCTCTGTAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTAATATGCCAGCAAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTAATATATGCCAGCAAGAGAA 1200
QY 1201 ATGTCTCAAGAAACCAAGATTAATAGATGTGATAGAGAGGTGAAGAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAAACCAAGATTAATAGATGTGATAGAGAGGTGAAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTGGATTAATCTAGAAAACTGATCTATGTGTGCTGCTGC 1320
Db 1261 AAGCATGAAGATTAATATGTGGATTAATCTAGAAAACTGATCTATGTGTGCTGCTGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAAATTTGTTCTGATCTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAAATTTGTTCTGATCTCAAGAA 1440
QY 1441 AAAAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAAAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
QY 1501 TCAAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTAAATGGCCAGAGCTAGAAAT 1560
Db 1501 TCAAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTAAATGGCCAGAGCTAGAAAT 1560
QY 1561 TTTATGCTATATGGAAGAAATGAAGAGCAAGAGATCTATGTCGATTTCCAGAAAC 1620
Db 1561 TTTATGCTATATGGAAGAAATGAAGAGCAAGAGATCTATGTCGATTTCCAGAAAC 1620
QY 1621 CTGACTTAATGTTGCACTGCTGCAATGTTGATGATTAATTTCTCCAGAGAAAGAGC 1680
Db 1621 CTGACTTAATGTTGCACTGCTGCAATGTTGATGATTAATTTCTCCAGAGAAAGAGC 1680
QY 1681 AGAACCTGGAAGCCAGAAATTTCTGCACTGAGATGAAGATGATCACTGAGCAAG 1740
Db 1681 AGAACCTGGAAGCCAGAAATTTCTGCACTGAGATGAAGATGATCACTGAGCAAG 1740
QY 1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACGAACTGGAATATTTACAGATGAG 1800
Db 1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACGAACTGGAATATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAAAGAGATAGAGTGTGTTGAAGAAATGAAATCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAAAGAGATAGAGTGTGTTGAAGAAATGAAATCTGAGCTTTCT 1860

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QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAAATGATGCTGGCGGAGAAATT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAAATGATGCTGGCGGAGAAATT 1920
QY 1921 GCCATGCTTAAGACTGGAAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 1980
DB 1921 GCCATGCTTAAGACTGGAAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 14
ADG26240
ID ADG26240 standard; cDNA; 2000 BP.
AC ADG26240;
DT 26-FEB-2004 (first entry)
XX
DE Human prostate-specific CDNA #359.
XX
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
XX cytoskeletal.
XX
OS Homo sapiens.
XX
PN US2003157089-A1.
XX
PD 21-AUG-2003.
XX
PF 09-MAY-2002; 2002US-00144678.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JT, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
PI Carier D, Li SX, Wang A, Skelky YAW, Hepner WT, Hurral J;
PI McNeill PD, Houghton RL, Vinals Y De Basolac, Roy TM, Matanabe Y;
PI Meagher MJ, Deng T;
XX
XX MPI; 2003-777973/73.
DR P-PSDB; ADG26245.
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```
XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
XX Example 11; SEQ ID NO 374; 99p; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2000 BP, 698 A, 388 C, 489 G, 425 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGGTGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCAATTGGTCTC 60
DB 1 ATGGTGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCAATTGGTCTC 60
QY 61 AAGAGCAAGATGGGCAAGTGGTGGCGGCTGCTCCCTGCTGCGAGGAGACGGCAAG 120
DB 61 AAGAGCAAGATGGGCAAGTGGTGGCGGCTGCTCCCTGCTGCGAGGAGACGGCAAG 120
QY 121 AAGCAAGTGGGCACTTCTGAGACCAAGCAAGCTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AAGCAAGTGGGCACTTCTGAGACCAAGCAAGCTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
QY 241 GGGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGCTGCACTGCTTCCCTGCTGCGAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGCTGCACTGCTTCCCTGCTGCGAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGAGAAAGATCTGG 420
DB 361 GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGAGAAAGATCTGG 420
QY 421 GAAAGCTCCAGAGAGCTGCTGGTGGGCTAAAGTCCCAAGAAAGGATCTCAATCGCATG 480
DB 421 GAAAGCTCCAGAGAGCTGCTGGTGGGCTAAAGTCCCAAGAAAGGATCTCAATCGCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGAAATTCAGAGTAAAGTCTCTGCTGGAACAGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGAAATTCAGAGTAAAGTCTCTGCTGGAACAGAGATGCACTTAAT 600
QY 601 GTCTTGAACAAGAAAGAGCAAGCTGTGATTAAGGCGGTCAATGCCAGGAAGATGAA 660
DB 601 GTCTTGAACAAGAAAGAGCAAGCTGTGATTAAGGCGGTCAATGCCAGGAAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGATGATGGAAT 720
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Db 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACCTGCACACCAACCTATCTTAATGAAATTAATGAGCCAAAGACCTGCTT 780
Db 721 ACCACCTGCACACCAACCTATCTTAATGAAATTAATGAGCCAAAGACCTGCTT 780
Qy 781 TATGCTGCTGATTCGAATCAAAAAAACAAGCATGGCTCACACAGCTTACTTGGT 840
Db 781 TATGCTGCTGATTCGAATCAAAAAAACAAGCATGGCTCACACAGCTTACTTGGT 840
Qy 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAAATG 900
Db 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAAATG 900
Qy 901 CTGATATGATATGGAAGGACCTGCTCATCTTCTGATATGTTGATGATCAGCAAT 960
Db 901 CTGATATGATATGGAAGGACCTGCTCATCTTCTGATATGTTGATGATCAGCAAT 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCCAAAGTCTATCTGACAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCCAAAGTCTATCTGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACT 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACT 1080
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Db 1081 AAAAGAAAAACAGTCTAAAAATCTTTCTGAAAAACGATCAGAACAGACTTAA 1140
Qy 1141 CTGACATCGAGGAAGATCAAAAGTTTCAAGGAGTAAATGTCAGCCAGAGAAA 1200
Db 1141 CTGACATCGAGGAAGATCAAAAGTTTCAAGGAGTAAATGTCAGCCAGAGAAA 1200
Qy 1201 ATGCTCAAGAAACAGAAATTAATAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAAACAGAAATTAATAAGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGAGGATTAATAAGAACTGATGATGATGATGATG 1320
Db 1261 AAGCATGAAAGTAAATATGAGGATTAATAAGAACTGATGATGATGATGATG 1320
Qy 1321 AATGATGATTAATGATTAATCTTCAAGGAGAGAGAAACCTGAAATTCGCAAT 1380
Db 1321 AATGATGATTAATGATTAATCTTCAAGGAGAGAGAAACCTGAAATTCGCAAT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGAATTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGAATTTCTGACTCAAGAA 1440
Qy 1441 AAAACAGATGCCAAATATCTTTCTGAAAAACAGAACCCAGAACAGATTAA 1500
Db 1441 AAAACAGATGCCAAATATCTTTCTGAAAAACAGAACCCAGAACAGATTAA 1500
Qy 1501 TCAAGGAGAGATCAAAAGGCTTGAAGGAGAGAAATGCGCAGAGCTGAGAAAT 1560
Db 1501 TCAAGGAGAGATCAAAAGGCTTGAAGGAGAGAAATGCGCAGAGCTGAGAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAAAGAGACGGAAGTACTCATGCGAATTTCCAG 1620
Db 1561 TTTATGCTATCGAAGAAATGAAAGAGACGGAAGTACTCATGCGAATTTCCAG 1620
Qy 1621 CTGACTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTCCAGAGAG 1680
Db 1621 CTGACTAATGCTGCACTGCTGCAATGATGATGATTAATTTCTCCAGAGAG 1680
Qy 1681 AGAAGACCTGGAAGCCAGCAATTTCTGACACTGAAATGAAGATATCACTG 1740
Db 1681 AGAAGACCTGGAAGCCAGCAATTTCTGACACTGAAATGAAGATATCACTG 1740
Qy 1741 CAAATATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAATATTTACGAT 1800
Db 1741 CAAATATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAATATTTACGAT 1800

Qy 1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGTTGAAAAATGAAATTTCTG 1860
Db 1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGTTGAAAAATGAAATTTCTG 1860
Qy 1861 CTGATGTTGAGAGAAAGAAAGCATCTTGCATGAAAAATGATGCTTGGCGGAGAAAT 1920
Db 1861 CTGATGTTGAGAGAAAGAAAGCATCTTGCATGAAAAATGATGCTTGGCGGAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACCAATGAAACATCAGAGCCAGCTTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACCAATGAAACATCAGAGCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 15
AAA06599
ID AAA06599 standard; cDNA; 2000 BP.
AC AAA06599;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
PN WO200004149-A2.
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 22-223; 263pp; English.
XX

The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumor protein (pTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and CC AA982000 to AA982020 represent sequences used in the exemplification of the present invention.

Sequence 2000 BP; 698 A; 387 C; 489 G; 426 T; 0 U; 0 Other;

Db 181 ATGGGCAAGTGTGCCGCCACTGCTTCCCTGTGCAAGGGGAGTGTGCAGACGAACTGTG 240
Qy 241 GGGCTTTCTGGAGACCAAGCACTGTCTATGAAGCACTCAAGAACTGAGGCAAG 300
Db 241 GGGCTTTCTGGAGACCAAGCACTGTCTATGAAGCACTCAAGAACTGAGGCAAG 300
Qy 301 TGGTGTGCGACCTGCTTCCCTGTGCAAGGGGAGTGTGCAGACGAACTGTG 360
Db 301 TGGTGTGCGACCTGCTTCCCTGTGCAAGGGGAGTGTGCAGACGAACTGTG 360
Qy 361 GGAAGCTACGATACAGTGTCTTCAAGAGCCCAAGTCAAGTCCCTGTGCAAGATCTG 420
Db 361 GGAAGCTACGATACAGTGTCTTCAAGAGCCCAAGTCAAGTCCCTGTGCAAGATCTG 420
Qy 421 GACAAGCTCCACAGAGTGTCTGTGGGATGAAGTCCCAAGAAAGATCTCATGTCTATG 480
Db 421 GACAAGCTCCACAGAGTGTCTGTGGGATGAAGTCCCAAGAAAGATCTCATGTCTATG 480
Qy 481 CTGAGGAGACCTGACGTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGACC 540
Db 481 CTGAGGAGACCTGACGTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGACC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGTGCAAGAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATACTCTGTGCAAGAGATGTCACTTAAT 600
Qy 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATGAAGGCGGTACATGCGAGAAAGATGA 660
Db 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATGAAGGCGGTACATGCGAGAAAGATGA 660
Qy 661 TGTGCTTAAATGTTGTGCAAGATGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTAAATGTTGTGCAAGATGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTGTGACCTACGTATCTATGAAGATTAATGAGCAAGATGCAAGATGCAAGAT 780
Db 721 ACCACTGTGACCTACGTATCTATGAAGATTAATGAGCAAGATGCAAGATGCAAGAT 780
Qy 781 TATGTGTCTGATATCGATCAAAAAACAAGATGAGCTGCAACCACTGTTACTGTGTA 840
Db 781 TATGTGTCTGATATCGATCAAAAAACAAGATGAGCTGCAACCACTGTTACTGTGTA 840
Qy 841 CATGAGCAAAAAAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTGATATGTTGTGATGAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTGATATGTTGTGATGAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGTGTCTAAAAATCTCTTCTGAAAAAGCAATCAAGACAAAGCTTAAAG 1140
Db 1081 AAAGAAAAACAGTGTCTAAAAATCTCTTCTGAAAAAGCAATCAAGACAAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAGAGTTCAAGAGGCTGAAATATGCGAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAGAGTTCAAGAGGCTGAAATATGCGAGAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATGTTGAGATTAAGAAAACTGACTATATGTGTCACTGTGCG 1320
Db 1261 AAGCATGAAGATTAATGTTGAGATTAAGAAAACTGACTATATGTGTCACTGTGCG 1320

Qy 1321 AATGGATATATGATTAATTCCTCAAGAGAGAGCAACCTGAAAAATGACAAATTT 1380
Db 1321 AATGGATATATGATTAATTCCTCAAGAGAGAGCAACCTGAAAAATGACAAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440
Qy 1441 AAAAGATGCGAAAAATCTCTTCTGAAAAACAGAACCCAGAACAGACTTTAAAGCTGAA 1500
Db 1441 AAAAGATGCGAAAAATCTCTTCTGAAAAACAGAACCCAGAACAGACTTTAAAGCTGAA 1500
Qy 1501 TCAGAGAGAGAGTCAAGAGCTTGAAGGCAAGTGAATAATGGCAGAGAGCTAGAAAT 1560
Db 1501 TCAGAGAGAGAGTCAAGAGCTTGAAGGCAAGTGAATAATGGCAGAGAGCTAGAAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGTGTGCACTGCTGCAATGTGATGATGATTAATTTCTCAAGAGAGAG 1680
Db 1621 CTGACTAATGTGTGCACTGCTGCAATGTGATGATGATTAATTTCTCAAGAGAGAG 1680
Qy 1681 AGAACACCTGAAAGCGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGAAG 1740
Db 1681 AGAACACCTGAAAGCGAGCAATTTCTGCACTGAGAAAGAAAGATGACAGTGAAG 1740
Qy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATTAACAGATGAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATTAACAGATGAG 1800
Qy 1801 ATTTGATTCAGAAAGAAAGCAAGATGAAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
Db 1801 ATTTGATTCAGAAAGAAAGCAAGATGAAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGCAATCTGATGAATATGATACGTGCGGAGAAATTT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGCAATCTGATGAATATGATACGTGCGGAGAAATTT 1920
Qy 1921 GCCATGCTAAGCTGAGAGCTAGACCAATGAACATCAGAGCAGCTAAAAATTT 1980
Db 1921 GCCATGCTAAGCTGAGAGCTAGACCAATGAACATCAGAGCAGCTAAAAATTT 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-352-616A-374
Sequence 374, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, David C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Wang, Yugu
APPLICANT: Xu, Jianshun
APPLICANT: Mitchem, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352, 616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTTGATTCATATGCGGCTGCTCTTCTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGTTGATTCATATGCGGCTGCTCTTCTGTGTGAAGAAGCCATTGGTCTC 60

QY 61 AGAGCAAAATGGGCAAGTGTGCTGCTGCTTCCCTGTGTGCAAGGAGGAGCGGCAAG 120
DB 61 AGAGCAAAATGGGCAAGTGTGCTGCTGCTTCCCTGTGTGCAAGGAGGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCTGTCTATGAAGACATCAGAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCTGTCTATGAAGACATCAGAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCTGCTGCTGCTTCCCTGTGTGCAAGGAGGAGGAGGAGGAGGAG 240
DB 181 ATGGGCAAGTGTGCTGCTGCTGCTTCCCTGTGTGCAAGGAGGAGGAGGAGGAGGAG 240

QY 241 GGGGCTTCTGTGAGACCAAGCAAGCTGTCTATGAAGACATCAGAGAAAGATGGGCAAG 300
DB 241 GGGGCTTCTGTGAGACCAAGCAAGCTGTCTATGAAGACATCAGAGAAAGATGGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 TGGTGTGCACTGCTTCCCTGTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360

QY 361 GGAAGCTAAGATGACAGTGTCTTCTATGAGGCCAGGATACAGCTCCGTGTGAGAAATCTG 420
DB 361 GGAAGCTAAGATGACAGTGTCTTCTATGAGGCCAGGATACAGCTCCGTGTGAGAAATCTG 420

QY 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAGTCCCAAGAAAGATCTCATGTCTATG 480
DB 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAGTCCCAAGAAAGATCTCATGTCTATG 480

QY 481 CTCAGGGAACATGACGTGAACAAGAAAGCAAGCAAAAGAGGAGCTGTCTATGATCTGGGC 540
DB 481 CTCAGGGAACATGACGTGAACAAGAAAGCAAGCAAAAGAGGAGCTGTCTATGATCTGGGC 540

QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGTGCAAGAGATGTCAATTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGTGCAAGAGATGTCAATTAAT 600

QY 601 GTCTTTGACAAACAAAAGAGGACAGCTGTATTAAGGCGTAAAGTCCAGAAAGATGA 660
DB 601 GTCTTTGACAAACAAAAGAGGACAGCTGTATTAAGGCGTAAAGTCCAGAAAGATGA 660

QY 661 TGTGGCTTAATGTGTGTGAACAATGGCACTGAATCCAAATATTCAGATGATGAAT 720
DB 661 TGTGGCTTAATGTGTGTGAACAATGGCACTGAATCCAAATATTCAGATGATGAAT 720

QY 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATGAAGCAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATGAAGCAAGCACTGCTCTTA 780

QY 781 TATGTGTGTATGCAATCAAAAACAAAGATGCGCTCAACACTGTTAATCTGTGTGA 840
DB 781 TATGTGTGTATGCAATCAAAAACAAAGATGCGCTCAACACTGTTAATCTGTGTGA 840

QY 841 CATGAGCAAAACAGCAAGTCCGGAATTTTAAATGAAGAAAGCAAGCAATTTAAATGA 900
DB 841 CATGAGCAAAACAGCAAGTCCGGAATTTTAAATGAAGAAAGCAAGCAATTTAAATGA 900

QY 901 CTGATAGATTAAGAGAGAGCTGCTCATATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB 901 CTGATAGATTAAGAGAGAGCTGCTCATATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 960

QY 961 GTGAGCTTCTTCTATGAGCAAAATTAATGATCTTCTCAAGATCTATCTGTGACAGAG 1020
DB 961 GTGAGCTTCTTCTATGAGCAAAATTAATGATCTTCTCAAGATCTATCTGTGACAGAG 1020

QY 1021 GCCAGAGATATGCTTTCTATGATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

DB 1021 GCCAGAGATATGCTTTCTATGATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

QY 1081 AAGAGAAACAGATGCTAAATCTCTGTGAAGACAGCAATCCAGAAAGCAAGCTTAAG 1140
DB 1081 AAGAGAAACAGATGCTAAATCTCTGTGAAGACAGCAATCCAGAAAGCAAGCTTAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAAGAGGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAGAGGTTCAAGGCAAGTGAATATGCCAGCCAGAGAA 1200

QY 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTTGAAGAAAGAAAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTTGAAGAAAGAAAG 1260

QY 1261 AAGCATGAAGATTAATATGAGATTAATAGAAACCTGATTAATGTGTCTATGCTGTGC 1320
DB 1261 AAGCATGAAGATTAATATGAGATTAATAGAAACCTGATTAATGTGTCTATGCTGTGC 1320

QY 1321 AATGTGTATTAATGATTAATTTCTCAAGAGAGCAAGACCTGAAATATGCAATTT 1380
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QY 1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGGAAATTAATTTCTGACTCAAGAA 1440
DB 1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGGAAATTAATTTCTGACTCAAGAA 1440

QY 1441 AAACAGATCCAAATATCTTTCTGAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
DB 1441 AAACAGATCCAAATATCTTTCTGAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500

QY 1501 TCAAGAGAGAGTCAAGAGGCTTGAAGGCAAGTGAATATGCGCAAGCAAGCTGAAT 1560
DB 1501 TCAAGAGAGAGTCAAGAGGCTTGAAGGCAAGTGAATATGCGCAAGCAAGCTGAAT 1560

QY 1561 TTTAATGGCTATGGAAGAAATGAAGAGCAAGGAGTCAATGTCGATTTCCAGAAAC 1620
DB 1561 TTTAATGGCTATGGAAGAAATGAAGAGCAAGGAGTCAATGTCGATTTCCAGAAAC 1620

QY 1621 CTGACTAATGATGCTGCTGCTGCAATGATGATGATTAATTTCTCAAGAGAGAGC 1680
DB 1621 CTGACTAATGATGCTGCTGCTGCAATGATGATGATTAATTTCTCAAGAGAGAGC 1680

QY 1681 ABAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGAA 1740
DB 1681 ABAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGAA 1740

QY 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAG 1800
DB 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGAG 1800

QY 1801 ATTCTGATTCATGAAGAAAGCAAGATAGAGTGTGAAGAAATGAATTTCTGAGCTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGCAAGATAGAGTGTGAAGAAATGAATTTCTGAGCTTCT 1860

QY 1861 CTTAGTTGTAAAGAAAGAAAGCAATCTTGTGCAATGAATGATGCTGGGGAAGAAAT 1920
DB 1861 CTTAGTTGTAAAGAAAGAAAGCAATCTTGTGCAATGAATGATGCTGGGGAAGAAAT 1920

QY 1921 GCCATGCTTAAGCTGAGAGTGAACAATGAAGCAATCAAGGCACTAATTAATTAATTA 1980
DB 1921 GCCATGCTTAAGCTGAGAGTGAACAATGAAGCAATCAAGGCACTAATTAATTAATTA 1980

QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3
US-09-289-198-302
; Sequence 302, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:


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Db 1681 AGAACCTGAAAGCAGCAATTTCTGACATGAGAAATGAGATATCACTAGTGCAG 1740
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Db 1741 CAATAATGATCTCAGAGCAATTTTGTGAAGAAACAGAACCTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAAGAAAGCAGATGAGATGAGTGTGAAAAATGAAATTTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAAGAAAGCAGATGAGATGAGTGTGAAAAATGAAATTTGAGCTTTCT 1860
Qy 1861 CTTAGTGTGAAGAAAGAAAGCAGATCTTGATGAAATAGTACGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGCAGATCTTGATGAAATAGTACGTTGCGGGAAGAAAT 1920
Qy 1921 GCCATCTTAAGACTGAGAGCTAGACAAATGAAACATCAAGAGCAGCTTAAAAA 1980
Db 1921 GCCATCTTAAGACTGAGAGCTAGACAAATGAAACATCAAGAGCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-636-215-374
/ Sequence 374, Application US/09636215
/ Patent No. 6620922
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqun
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Reiter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.42717C17
/ CURRENT APPLICATION NUMBER: US/09/636, 215
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGCTATGAGACACTCAGAGCAAG 180
Qy 181 ATGGCAAGTGTGCGCCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGCCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Qy 241 GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAGACACTCAGAGCAAGAGTGGCAAG 300
Db 241 GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAGACACTCAGAGCAAGAGTGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTCCCTTCAATGAGCCAGGTAACAGTCCGTGAGAGATCTG 420
Db 361 GGAAGCTACGATGACAGTCCCTTCAATGAGCCAGGTAACAGTCCGTGAGAGATCTG 420
Qy 421 GACAAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
Db 421 GACAAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
Qy 481 CTCAGGGAACATGACGCTGAAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGGAACATGACGCTGAAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Qy 541 TGTGCCAATGGGAATTCAGAAATGTAATAACTCTGCTGAGACAGAGATGTCATCTTAAT 600
Db 541 TGTGCCAATGGGAATTCAGAAATGTAATAACTCTGCTGAGACAGAGATGTCATCTTAAT 600
Qy 601 GTTCCTGACACAAAGAAAGAGCAGCTCTGATTAAGGCGGTACATGATCCAGAAAGTGA 660
Db 601 GTTCCTGACACAAAGAAAGAGCAGCTCTGATTAAGGCGGTACATGATCCAGAAAGTGA 660
Qy 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATAGTATGGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATAGTATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATGAAATGAAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAAATGAAATTAATGAGCCAAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGAAATCAAAAGAAAGAGATGCTCAACACTGTTACTTGTGATG 840
Db 781 TATGCTGCTGATATGAAATCAAAAGAAAGAGATGCTCAACACTGTTACTTGTGATG 840
Qy 841 CATGACAAAAACAGAAAGTGGAAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Db 841 CATGACAAAAACAGAAAGTGGAAATTTTAAATCAAGAAAAAGCAATTTAATGCA 900
Qy 901 CTGGATAGATATGAAAGACTGCTCTCATACTGCTGATGTTGTTGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGAAAGACTGCTCTCATACTGCTGATGTTGTTGATCAGCAAGTATA 960
Qy 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATTTATCTGACAGAG 1020
Db 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATTTATCTGACAGAG 1020
Qy 1021 GCCAGAGATAGCTGTTTCTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATAGCTGTTTCTAGTCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy 1081 AAGAGAAAAACAGATGTAATAAACTCTTCTGAAAAACAGCAATCCAGAACAGCTTTAAG 1140
Db 1081 AAGAGAAAAACAGATGTAATAAACTCTTCTGAAAAACAGCAATCCAGAACAGCTTTAAG 1140
Qy 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGGAAA 1200
Db 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGGAAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATAGAGGTTGAAGAAATGAAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATAGAGGTTGAAGAAATGAAAG 1260
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QY 1261 AAGCATGAAGTAAATATGTGGATTACTAGAAAACTGACTAATGTGTCCTGCTGAC 1320
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DB 1261 AAGCATGAAGTAAATATGTGGATTACTAGAAAACTGACTAATGTGTCCTGCTGAC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
| | | | |
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
| | | | |
DB 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAAAGATGCAAAATTAATCTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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DB 1441 AAAAGATGCAAAATTAATCTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
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DB 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TTTATGTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
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DB 1561 TTTATGTGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
| | | | |
DB 1621 CTGACTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 AGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
| | | | |
DB 1681 AGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAAAATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
| | | | |
DB 1741 CAAAATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 ATTCTGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
| | | | |
DB 1801 ATTCTGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 CTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
| | | | |
DB 1861 CTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
| | | | |
DB 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
| | | | |
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 5
US-09-685-166A-374
; Sequence 374, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguang
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
```

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; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yael A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGTGCTGATGAGTGAATTCATGCGCGCTGCTCTCTGTAAGAGCATTTGGTCTC 60
| | | | |
DB 1 AATGTGCTGATGAGTGAATTCATGCGCGCTGCTCTCTGTAAGAGCATTTGGTCTC 60
QY 61 AGAGCAAGATGGCAAGTGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
| | | | |
DB 61 AGAGCAAGATGGCAAGTGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AGCAACGTGGGCACTTCTGAGAGACGACGACGACGACGACGACGACGACGACGACGACG 180
| | | | |
DB 121 AGCAACGTGGGCACTTCTGAGAGACGACGACGACGACGACGACGACGACGACGACGACG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
| | | | |
DB 181 ATGGGCAAGTGTGCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCGGCTTCTGAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
| | | | |
DB 241 GCGGCTTCTGAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGGTGGCGCTTGG 360
| | | | |
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGGTGGCGCTTGG 360
QY 361 GAGACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
| | | | |
DB 361 GAGACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GACAAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
| | | | |
DB 421 GACAAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CTGAGGAGACCTGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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DB 481 CTGAGGAGACCTGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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DB 541 TCTGCAATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GTCTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
| | | | |
DB 601 GTCTTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCTTAATGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
| | | | |
DB 661 TGTGCTTAATGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACCACTCTGCACTAAGCTATCTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
| | | | |
DB 721 ACCACTCTGCACTAAGCTATCTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TATGTGCTGATGATGAATCAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
| | | | |
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Db	761	TATGTCGTGATATGGAATCAAAAACAGATGGCTTCAACCACTTAACTTGGTGA	840
Oy	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Oy	901	CTGATATGATATGGAAGACTGCTCTCAACTCTGCTGATGTTGTGATCAGCAATTA	960
Db	901	CTGATATGATATGGAAGACTGCTCTCAACTCTGCTGATGTTGTGATCAGCAATTA	960
Oy	961	GTGAGCCCTTACTTACCTGAGCAAAATATGATATGATCTTCAAGATCTATCTGCAAGC	1020
Db	961	GTGAGCCCTTACTTACCTGAGCAAAATATGATATGATCTTCAAGATCTATCTGCAAGC	1020
Oy	1021	GCCAGAGATATGCTGTTTCTAGTCATGATCATGTAATTTGCCAGTTACTTTCTGACATC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATGATCATGTAATTTGCCAGTTACTTTCTGACATC	1080
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Db	1081	AAAGAAAAACAGATCTAAAAATCTCTTGAAAAACAGCAATCCAGAAACAAGACTTAAG	1140
Oy	1141	CTGATATCAGAGAAAGATCACAAAAGTTCAAAAGCAGTGAATATGCAAGCAGAGAA	1200
Db	1141	CTGATATCAGAGAAAGATCACAAAAGTTCAAAAGCAGTGAATATGCAAGCAGAGAA	1200
Oy	1201	ATGTCTCAAGAAACAGAAATAAATTAAGAGTGGTGTAGAGAGTTGAAGAAGAAATAG	1260
Db	1201	ATGTCTCAAGAAACAGAAATAAATTAAGAGTGGTGTAGAGAGTTGAAGAAGAAATAG	1260
Oy	1261	AAGCATGAAGTAAATATATGTGGAGTTACTGAAAACTGACTAATGTGTCACTGTGC	1320
Db	1261	AAGCATGAAGTAAATATATGTGGAGTTACTGAAAACTGACTAATGTGTCACTGTGC	1320
Oy	1321	AATGTGTAATATGATTTAATCTTCAAGAAAGCAGACAACCTGAAAAATCAGCAATTT	1380
Db	1321	AATGTGTAATATGATTTAATCTTCAAGAAAGCAGACAACCTGAAAAATCAGCAATTT	1380
Oy	1381	CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTTCTGACTAAGAA	1440
Db	1381	CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTTCTGACTAAGAA	1440
Oy	1441	AAACAGATGCCAAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAACCTGACA	1500
Db	1441	AAACAGATGCCAAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAACCTGACA	1500
Oy	1501	TCAAGAGAAAGTCACAAAAGCTTGAGGGCACTGAAAAATGGCCAGCCAGACTTGAAAT	1560
Db	1501	TCAAGAGAAAGTCACAAAAGCTTGAGGGCACTGAAAAATGGCCAGCCAGACTTGAAAT	1560
Oy	1561	TTTATGGCTATCGAAGAAATGAAGAAGACGGAAGTCTCATGTGCGAATTTCCAGAAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGACGGAAGTCTCATGTGCGAATTTCCAGAAAAC	1620
Oy	1621	CTGACTAATGATGTCACCTGCTGCGCAATGATGATGATTAATTTCTCCAAAGAAAGC	1680
Db	1621	CTGACTAATGATGTCACCTGCTGCGCAATGATGATGATTAATTTCTCCAAAGAAAGC	1680
Oy	1681	AGAACACTTGAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATCAGATGACGAA	1740
Db	1681	AGAACACTTGAAGCCAGCAATTTCTTGACACTGAGAAATGAAGATATCAGATGACGAA	1740
Oy	1741	CAAAATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATGAG	1800
Oy	1801	ATTCTGATTCAGAGAAAGCAGATGAGTGTGTAAGAAAAATTCAGACTTTCT	1860
Db	1801	ATTCTGATTCAGAGAAAGCAGATGAGTGTGTAAGAAAAATTCAGACTTTCT	1860
Oy	1861	CTTAGTTGAAGAAAGAAAGACATCTTGCAATGAATTAAGCTTGGGGAAGAAAT	1920
Db	1861	CTTAGTTGAAGAAAGAAAGACATCTTGCAATGAATTAAGCTTGGGGAAGAAAT	1920

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Db      1861  CTTAGTTTAAGAAAGAAAAAGACATCTTGTCATGAAAAATAGTACGTTGGGGAAGAAATT 1920
OY      1921  GCCATGCTAATACCTCGAGCTAGACACATGAAACATGACGACCACTTAAAAAATAAAAA 1980
Db      1921  GCCATGCTAATACCTCGAGCTAGACACATGAAACATGACGACCACTTAAAAAATAAAAA 1980
OY      1981  AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981  AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 6
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Prudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PaetsEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  ATGTGTGTGAGGTGAATTCATATGCGGCGGCTCCCTTCTGTGAAAGCAATTTGGTCTC 60
Db      1  ATGTGTGTGAGGTGAATTCATATGCGGCGGCTCCCTTCTGTGAAAGCAATTTGGTCTC 60
OY      61  AGAGCAAGATGAGCAAGTGGTGTGCTGCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
Db      61  AGAGCAAGATGAGCAAGTGGTGTGCTGCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
OY      121  AGCAACGTGGCACTTCTTGAGACACGACGACTCTGCTATGAACACTCAGAGCAAG 180
Db      121  AGCAACGTGGCACTTCTTGAGACACGACGACTCTGCTATGAACACTCAGAGCAAG 180
OY      181  ATGGGCAAGTGTGTCGCCCACTGTTCCCTGCTGACGGGGAGTGGCAAGCAAGTGTG 240
Db      181  ATGGGCAAGTGTGTCGCCCACTGTTCCCTGCTGACGGGGAGTGGCAAGCAAGTGTG 240
OY      241  GGCCCTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGAGAACAAATGGGCAAG 300
Db      241  GGCCCTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGAGAACAAATGGGCAAG 300
OY      301  TGTGTCTGCCACTGCTTTCCTCTGCTGACGGGGAGCGGCAAGCAAGATGGCGCTTGG 360
Db      301  TGTGTCTGCCACTGCTTTCCTCTGCTGACGGGGAGCGGCAAGCAAGATGGCGCTTGG 360
OY      361  GGAACACTACATGACATGTGCTTCATATGAGCCCAAGATACCAACGTCCTGGAGAAATCTG 420
Db      361  GGAACACTACATGACATGTGCTTCATATGAGCCCAAGATACCAACGTCCTGGAGAAATCTG 420
OY      421  GACAAAGCTCCACAGAGCTGCTGTGTGGGTAAATGCCCAAGAAAGATCTCATCTGTATG 480
Db      421  GACAAAGCTCCACAGAGCTGCTGTGTGGGTAAATGCCCAAGAAAGATCTCATCTGTATG 480
OY      481  CTCAGGACACTGACGTGAACAGAGGACCAAGCAAAAGAGACTGCTTACATCTTGCC 540
Db      481  CTCAGGACACTGACGTGAACAGAGGACCAAGCAAAAGAGACTGCTTACATCTTGCC 540

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Db 481 CTCAGGAGCACTGACCTGAAACAAGAGACAAGCAAAAGAGACTGCTCTACCTGACC 540
Qy 541 TCTGCCAATGGGAAATTCAGAGATGTAATAATCTCTGCTGGAACAGAGATGTAATTAAT 600
Db 541 TCTGCCAATGGGAAATTCAGAGATGTAATAATCTCTGCTGGAACAGAGATGTAATTAAT 600
Qy 601 GTCTTTGACCAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGAA 660
Db 601 GTCTTTGACCAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGAA 660
Qy 661 TGTGCTTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGATGGAAT 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGATGGAAT 720
Qy 721 ACCACTCTGCACTACCTATCTATTAAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTACCTATCTATTAAGATTAATTAATGAGCCAAAGCACTGCTCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTGACACCACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTGACACCACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGAACTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAACTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
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Db 901 CTGATATGATATGGAAGAGACTGCTCATATCTGTATGTTGTTGATCAGCAATGATA 960
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Db 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAAGGAGTGAATTAAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAAGGAGTGAATTAAGCCAGCAGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
Qy 1261 AAGCATGAAAGTAAATATATGTTGGGATTAATAGAAAACTGATATATGTTGCTGCTGAC 1320
Db 1261 AAGCATGAAAGTAAATATATGTTGGGATTAATAGAAAACTGATATATGTTGCTGCTGAC 1320
Qy 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGAACCTGTAATTAATGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGAACCTGTAATTAATGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGCAATTTGTTCTGATCAAAAGAA 1440
Qy 1441 AAAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCAAGAACCAAGCTTAAGCTGACA 1500
Qy 1501 TCAGAGAGAAAGTCAAAAAGCTTGAAGGCAAGTGAATTTGCGCAGCAGAGCTAGAAAAAT 1560
Db 1501 TCAGAGAGAAAGTCAAAAAGCTTGAAGGCAAGTGAATTTGCGCAGCAGAGCTAGAAAAAT 1560
Qy 1561 TTTATGCTATGAGAGAAATGAAAGACAGCAAGATATCTATGCTGGAATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATGAGAGAAATGAAAGACAGCAAGATATCTATGCTGGAATTTCCAGAAAAAC 1620

Qy 1621 CTGACTAATGATGACCACTGCTGGAATGATGATTAATTTCTTCAAGAGAGAGC 1680
Db 1621 CTGACTAATGATGACCACTGCTGGAATGATGATTAATTTCTTCAAGAGAGAGC 1680
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Db 1681 AGAACACCTGAAAGCAGCAATTTCTCTGACATGAAATGAAGATATCAAGTACGAA 1740
Qy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAAAGCAGATAGAAAGTGTGAAAAAATGAAATCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAAAGCAGATAGAAAGTGTGAAAAAATGAAATCTGAGCTTCT 1860
Qy 1861 CTTAGTTGTAGAAAAAGAACATCTTGCAATGAAATATGATACGTTGGGAGAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAAAGAACATCTTGCAATGAAATATGATACGTTGGGAGAGAAAT 1920
Qy 1921 GCCATGCTTAAGCTGAGAGTACACATGAAACATCAGAGCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTTAAGCTGAGAGTACACATGAAACATCAGAGCAGCTAAAAAAGAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-679-426-374
Sequence 374, Application US/09679426
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yael A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGCTTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGCTTC 60

APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yaelir A.W.
APPLICANT: Hedler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGGCTCTTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGGGCTCTTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCGTTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGGAAGGAGGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGGAAGGAGGAGTGGCAAGCAAGTGG 240
QY 241 GGGGCTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGGAGCAAGTGGGCAAG 300
DB 241 GGGGCTTCTGGAACAAGACGACTCTGTATGAAGACACTCAGGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGCGCAAGGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGCGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGAGTGGCTTCTGAGAGCCCAAGGATCCAGTCCGTGGAGAAATCTG 420
DB 361 GGAGACTAGATGAGTGGCTTCTGAGAGCCCAAGGATCCAGTCCGTGGAGAAATCTG 420
QY 421 GACAGACTCCAGAGCTGCTGAGTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
DB 421 GACAGACTCCAGAGCTGCTGAGTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
QY 481 CTGAGGAGCACTGAGTGAACAAAGAGCAACAAAGAGAGCTCTCTCAATCTGGCC 540
DB 481 CTGAGGAGCACTGAGTGAACAAAGAGCAACAAAGAGAGCTCTCTCAATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAAGAGATGTCAACTTAAT 600
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QY 601 GTCTTGAACAACAAAAAGAGAGCAGCTGTATAAAGCCGTACATGCGAAGATGAA 660
DB 601 GTCTTGAACAACAAAAAGAGAGCAGCTGTATAAAGCCGTACATGCGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720

QY 721 ACCAGCTGCACTAGCTATCTATATGAAGATAATTAATGGCCAAAGCACTGCTCTTA 780
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DB 841 CATGAGCAAAAAACAGAGTGTGAATTTTATTCAGAAAAAAGCCAAATTTAATGCA 900
QY 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
DB 901 CTGGATATGATGAAGAGCTGCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
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DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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DB 1081 AAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGATCCAGAACTTAAAG 1140
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DB 1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCATGAAATAGCCAGCAAGAAA 1200
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DB 1201 ATGCTCAAGAAACAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAA 1260
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DB 1621 CTGACATTAATGATGCACTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAC 1680
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DB 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800

OY		1801	ATTCGATCTCATAAGAAAGAAGCATAPACGTCTTGAAAAAATGAATTTCGACTTCT	1867
Dd		1801	ATTCGATCTCATAAGAAAGAAGCATAPACGTCTTGAAAAAATGAATTTCGACTTCT	1866
OY		1861	CTTAGGTTTAAGAAAAGAAAAGACAATCTTGCAATGAAAATATGACGTGGGAGAAAT	1920
Dd		1861	CTTAGGTTTAAGAAAAGAAAAGACAATCTTGCAATGAAAATATGACGTGGGAGAAAT	1922
OY		1921	GCCATGCTPAAGCTCGAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAAAAAA	1980
Dd		1921	GCCATGCTPAAGCTCGAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAAAAAA	1980
OY		1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Dd		1981	AAAAAAAAAAAAAAAAAAAAA 2000	


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RESULT 9
US-09-651-236-374
; Sequence 374, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651.236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-374
Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dd		1	ATGGGTGTTGAGGTGATTTCCATGCGCGGTGCCTTCTGTAAGAGAAGCCATTGGTCTC	60
OY		61	AGAGCAAGATGAGCGCAAGTGCTGCTGCCGTTGCTTCCCCTGCTGACGAGAGCGCCAAAG	120
Dd		61	AGAGCAAGATGAGCGCAAGTGCTGCTGCCGTTGCTTCCCCTGCTGACGAGAGCGCCAAAG	120
OY		121	AGCAACGTGGGCACTTCTTGAGAACACAGACCACTCTGCTATGAAACACTCAGAGGCAAG	180
Dd		121	AGCAACGTGGGCACTTCTTGAGAACACAGACCACTCTGCTATGAAACACTCAGAGGCAAG	180
OY		181	ATGGGCAAGTGTGTCGCGCACACTGCTTCCCTGCTGSCAGGGGAGTGGCAAGCAACGTG	240
Dd		181	ATGGGCAAGTGTGTCGCGCACACTGCTTCCCTGCTGSCAGGGGAGTGGCAAGCAACGTG	240
OY		241	GAGCGCTTGGAGACCACAGACGACTCTGCTATGAAGACACTTCAGAACCAAGTGGCAAG	300

Db	241	GGCGCTTTGGAGACCACGACGACTCTGTATGAAACATCTCAGGAAACAAGTGGCAG	300
QY	301	TGTTGTCCCACTGCTTCCCTCGTCGACGGGGAGCGGCAAGACAAAGTGGCGCTTGG	360
Db	301	TGTTGTCTGCCACTGCTTCCCTCGTCGACGGGGAGCGGCAAGACAAAGTGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTGTCGTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTGTCGTGAGAAAGATCTG	420
QY	421	GACCAAGCTTCCACAGAGCTGCTGGTGGGGTTAAATGCCACGAAAGATCTCATGTCAATG	480
Db	421	GACCAAGCTTCCACAGAGCTGCTGGTGGGGTTAAATGCCACGAAAGATCTCATGTCAATG	480
QY	481	CTCAGGGGACATGACGTGACCAAGAGGACAAAGGAAAGAGACTGCTCTCATCTGACC	540
Db	481	CTCAGGGGACATGACGTGACCAAGAGGACAAAGGAAAGAGACTGCTCTCATCTGACC	540
QY	541	TCTGCGCATGGGAATTCCAGAGTAGTAAATCTCTGCTGACAGACGATGTCACTTAAT	600
Db	541	TCTGCGCATGGGAATTCCAGAGTAGTAAATCTCTGCTGACAGACGATGTCACTTAAT	600
QY	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGGAAGATGA	660
Db	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGGAAGATGA	660
QY	661	TGTGGGTTAAGTTGCTGGGAACTAGGGCACTGATCCAAATATTCAGATGAGTATGGAAAT	720
Db	661	TGTGGGTTAAGTTGCTGGGAACTAGGGCACTGATCCAAATATTCAGATGAGTATGGAAAT	720
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Db	721	ACCACTCTGCACTACGCTATCTATATAGAGATTAATTAATGSCCAAGCACTGCTCTTA	780
QY	781	TATGTGTGTGATATTCGAATCAAAAAACAAGATGGCTCACACCACTGTACTTGGTGTGA	840
Db	781	TATGTGTGTGATATTCGAATCAAAAAACAAGATGGCTCACACCACTGTACTTGGTGTGA	840
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Db	901	CTGATATGATATGGAAGGACTGCTCTCACTCTGCTGATGTGTGATCAGCAAGTATA	960
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Db	961	GTCAGCCTTCTACTTGAACAAAATATTGATGATCTTCTCAAGATCTATCTGACACAGCG	1020
QY	1021	GCCGAGAGATATGCTGTTTCTAGTCATCACTCATCTGATGTGTGATCAGCAAGTATA	1080
Db	1021	GCCGAGAGATATGCTGTTTCTAGTCATCACTCATCTGATGTGTGATCAGCAAGTATA	1080
QY	1081	AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAAAGCTTAAG	1140
QY	1141	CTGACATCAGAGGAAAGTCACAAAGGTTCAAGGCAAGTGAATAATGACCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAAGTCACAAAGGTTCAAGGCAAGTGAATAATGACCCAGAGAAA	1200
QY	1201	ATGTCTCAAGAACCAAGAAATTAATPAGAGTGTATAGAGGTTGAAGGAAGAAATGAG	1260
Db	1201	ATGTCTCAAGAACCAAGAAATTAATPAGAGTGTATAGAGGTTGAAGGAAGAAATGAG	1260
QY	1261	AAGCATGAAGTAAATATGTTGGGATTTCTAGAAAACTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGTAAATATGTTGGGATTTCTAGAAAACTGACTAATGTGTCACTGTGGC	1320
QY	1321	AATGTGTATATGATTTATTTCTTCMAAGGACGAGACACTGAAATCAGCAATTT	1380

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Db      1381 CCTGCAACGAAAGATGAGAGATACACAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440
Qy      1441 AAACAGATGCCAAATTAATCTTTCTGAAAAACAGAACCCAGAACCAAGACTTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATTAATCTTTCTGAAAAACAGAACCCAGAACCAAGACTTTAAAGCTGACA 1500
Qy      1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGACAGCTAGTAAAT 1560
Db      1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGACAGCTAGTAAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAGAGACAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAGAGACAGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Qy      1621 CTGACTTAATGTGTGCCACTGCTGGCAAATGTTGATGATGATTAATTCCTCAAGAGAGAGC 1680
Db      1621 CTGACTTAATGTGTGCCACTGCTGGCAAATGTTGATGATGATTAATTCCTCAAGAGAGAGC 1680
Qy      1681 AGAAGCCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACAGTGCAGAA 1740
Db      1681 AGAAGCCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACAGTGCAGAA 1740
Qy      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAACAGAACCTGGAATTAATTAACAGATGAG 1800
Db      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAACAGAACCTGGAATTAATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAGAGAGAGAGATGAGTGTGTAATAATTAATTCAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAGAGAGAGAGATGAGTGTGTAATAATTAATTCAGCTTTCT 1860
Qy      1861 CTTAGCTTTGAAGAAAGAAAGACATCTTGATGAAATTAATTAATTCAGCTTTCT 1920
Db      1861 CTTAGCTTTGAAGAAAGAAAGACATCTTGATGAAATTAATTAATTCAGCTTTCT 1920
Qy      1921 GCCATGCTAGAGCTGAGCTGAGACACATGAAATCATCAGAGCAGCTTAATAAAAAA 1980
Db      1921 GCCATGCTAGAGCTGAGCTGAGACACATGAAATCATCAGAGCAGCTTAATAAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-699-295-302
; Sequence 302, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Prudakie, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelley, Yaelir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; CURRENT FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-302
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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGTGTGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCAATTTGCTCTC 60
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Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTGCTCCCTGCTGAGAGGAGCGGCAAG 120
Qy      121 AGCAAGTGTGGCACTTCTGAGAGACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
Db      121 AGCAAGTGTGGCACTTCTGAGAGACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
Qy      181 ATGGCAAGTGTGCTGCGGCACTGCTTCCCTGTCTGCAAGGAGAGTGGCAAGCAAG 240
Db      181 ATGGCAAGTGTGCTGCGGCACTGCTTCCCTGTCTGCAAGGAGAGTGGCAAGCAAG 240
Qy      241 GGGCGCTTCTGAGACCAAGACGACTGTGTAAGACACTCAGAGCAAGTGGCAAG 300
Db      241 GGGCGCTTCTGAGACCAAGACGACTGTGTAAGACACTCAGAGCAAGTGGCAAG 300
Qy      301 TGGTCTGCACTGCTTCCCTGTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db      301 TGGTCTGCACTGCTTCCCTGTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Qy      361 GGAGACTAGATGACAGTGCCTTCATGAGAGCCAGAGTACACAGCTCCGTGAGAGATCTG 420
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Qy      421 GACAGCTCCACAGAGCTGCGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db      421 GACAGCTCCACAGAGCTGCGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
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Db      481 CTCAGAGCACTGAGCTGAGACAAAGAGACAAAGCAAGAGAGAGCTCTACATCTGCGC 540
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Db      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGAGACAGATGTCACATTAAT 600
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Db      601 GTTCCTGACAAAGAAAGAGGACAGCTCTGATTAAGCCGCTCAATGCCAGAGATGAA 660
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Db      721 ACCACTCTGACACTAGCTATCTATATGAGATTAATTAAGCCAAAGCACTGCTCTTA 780
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Db      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
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Db	1201	ATGTCCTCAAGAACCGAAATTAATAAGATGGTGTATAGAGGCTTGAAGAAATGAG	1266
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Db	1501	TCAGAGGAAGTCCAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
OY	1561	TTTATGCTATGCAAGAAATGAAAGACACGGAAGTCTCATGTGCGATTTCCAGAAAAC	1620
Db	1561	TTTATGCTATGCAAGAAATGAAAGACACGGAAGTCTCATGTGCGATTTCCAGAAAAC	1620
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Db	1621	CTGACTAATGTTGGTCCACTGCTGGCAATGGTATGATGATTAATTCCTCCAGAAAGAGC	1680
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Db	1681	AGAACCTGTAAGAGCCAGACAAATTTCTGACACTGAGATGAAGATACACAGTGAACAA	1740
OY	1741	CAAAATGATCTCAGAACCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAACCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG	1800
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Db	1801	ATTCTGATTCATGAAAGAAAGCAGATGAAGTGTGAAAAATGAATTCCTGAGCTTTCT	1866
OY	1861	CTTAGTTGTAAGAAAGAAAGACATCTTTCGATGAAATATAGTACGTTGCGGAGAAATTT	1920
Db	1861	CTTAGTTGTAAGAAAGAAAGACATCTTTCGATGAAATATAGTACGTTGCGGAGAAATTT	1920
OY	1921	GCCATGCTAAGACTGAGACTAGACACATATGAAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGACTAGACACATATGAAACATCAGAGCCAGCTAAAAA	1980
OY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

[illegible]

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Db 781 TATGCTGCTGATATCGATATCAAAAAAAMAGATGCGCTCACACCTGTTACTTGGTGA 840
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Db 961 GTGAGCTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACGAGC 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAGAACAGCAATCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAGAACAGCAATCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATTCAGAGAAAGTCACAAAAGTTCAAGGCGAGTAAATAGCCACGAGAAA 1200
Db 1141 CTGACATTCAGAGAAAGTCACAAAAGTTCAAGGCGAGTAAATAGCCACGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGTTGAGTAACTAGAAAACCTGACTAATGCTGCTGAC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGAGTAACTAGAAAACCTGACTAATGCTGCTGAC 1320
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Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGAATTTAGTTCTGACTGCAAGAA 1440
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Db 1441 AAAAGATGCAAAATATCTCTTGAAGAACAGCAACCCAGAACAGACTTAAAGTGA 1500
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Db 1621 CTGACTAATGCTGCACTGCTGCAATGATGATGATGATTTTCTCCAGAGAAAG 1680
Qy 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATCACTGAGCAA 1740
Db 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATCACTGAGCAA 1740
Qy 1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGACAGAACCTGGAATATTAACGATGAG 1800
Db 1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGACAGAACCTGGAATATTAACGATGAG 1800
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Db 1801 ATTCTGATTCATGAGAAAGAGATGAAAGTGTGAAATTTGAATTTCTGAGCTTCT 1860
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Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCAATGAAATATGTAAGTTGCGGAGAAAT 1920
Qy 1921 GCCATGCTAGACTGAGAGTACACAAATGAACATCAGAGCAGCTAATAAAAA 1980
Db 1921 GCCATGCTAGACTGAGAGTACACAAATGAACATCAGAGCAGCTAATAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 12
US-09-657-279-374
; Sequence 374, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kales, Gary R.
; APPLICANT: Rafter, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT FILING DATE: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-657-279-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGATGAGAGTATTCATGCGAGCTGCTCTTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGCTGATGAGAGTATTCATGCGAGCTGCTCTTGTGAAGAGCAATTTGGTCTC 60
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Db 61 AGAAGCAAGATGAGAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
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Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGT 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGT 240
Qy 241 GCGGCTTCTGAGAGCAAGCACTTGTGTAAGAGCACTGAGAACTGAGAACTGAGCAAG 300
Db 241 GCGGCTTCTGAGAGCAAGCACTTGTGTAAGAGCACTGAGAACTGAGCAAG 300
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DB 361 GGAAGCTACGATGACAGTGGCTTTCATGAGAGCCAGGATCCAGCTCCGTGGAGAGATCTG 420
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DB 481 CTCAGGGAGCACTGACGCTGAACAAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
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QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATATGATCGTTGCGGAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATATGATCGTTGCGGAGAAATTT 1920
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DB 1921 GCCATGCTAGAGCTGAGCTAGACAAATGAACATCAGAGCAGCTAATAAAAAA 1980
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DB 1981 AAAAAAAAAAAAAAAAAA 2000
RESULT 13
US-10-012-896-374
; Sequence 374, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Basols, Carlot
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanebe, Yoshihiro

```
/ APPLICANT: Meagher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012,896
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: PaSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-012-896-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAAAGCCATTGGTCTC 60
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DB      61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
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DB      121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
QY      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
DB      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
QY      241 GGGGCTTCTGAGAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB      241 GGGGCTTCTGAGAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
DB      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGGAGTGGGCGCTTGG 360
QY      361 GGAAGCTACAGATGAGAGTGTGCTTCCCTGCTGCAAGGAGGAGTGGGCGCTTGG 420
DB      361 GGAAGCTACAGATGAGAGTGTGCTTCCCTGCTGCAAGGAGGAGTGGGCGCTTGG 420
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DB      421 GACAGCTTCAAGAGTGTGCTGCTTCCCTGCTGCAAGGAGGAGTGGGCGCTTGG 480
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DB      481 CTCAGGAGCACTGAGCGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY      541 TCTGCAATGAGGAATTCAGAGTGTGCTTCCCTGCTGCAAGGAGGAGTGGGCGCTTGG 600
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DB      661 TGTGGCTTATGTTGTGGAAGCACTGCACTGAATTCCTCAATGATGATGAAT 720
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DB      721 ACCACTCTGCACTACCTATCTATTAATGAATTAATTAATGAGCAAGCACTGCTTGA 780
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QY      1561 TTTATGGCTATGGAAGAAATGAAGAAAGCAAGAGTACTATGCGAATTCAGAAAGAA 1620
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QY      1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAAAGCAAGCACTGGAATTAATTAACGATGAG 1800
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QY      1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGTAAGAAATTAATTAATGAGCTTTCT 1860
DB      1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGTAAGAAATTAATTAATGAGCTTTCT 1860
QY      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAATATGTAAGTGTGCGGAGAGAAAT 1920
DB      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAATATGTAAGTGTGCGGAGAGAAAT 1920
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RESULT 14
US-09-439-313-375

; Sequence 375, Application US/09439313

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: DILLON, Davin C.

APPLICANT: Harlocker, Susan Lou

APPLICANT: Jlang Yuqul

APPLICANT: Kaled, Steven G.

APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark

APPLICANT: SOLK, John
APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITION

TITLE OF INVENTION: DIAGNOSIS OF

FILE REFERENCE: 210121.427C

CURRENT FILING DATE: 1999-11-12

! NUMBER OF SEQ ID NOS: 575

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; SOFTWARE: FastSeq for Windows
; SEQ ID NO 37E

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; SEQ ID NO 3/3
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: LENGTH: 2040

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TYPE: DNA

ORGANISM: Homo sapien

05-09-439-313-31

Query Match

Best Local

Matches 1551; Conserva

QY 1 ATG

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Query Match      77.5%; Score 1551; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY	121	AGCAAAGTGGGCACTTTCTGAGAACCAACAACAAGACTCTGCTATGAACAACA CTGAGAGCAAG	180
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Dd	181	ATGGGCAAGTGTGGCGGCACCTGCTTCCCCCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG	240
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OY	301	TGGTGTCTGCCA CTGCTTCCCCTGCTGCAAGGGGAGCGGC AAGGCAAGTGGGCGCTTGG	360
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QY	481	CTCAGGGCACTGACGTGAAACAGAGAGACAGCAAAAGAGACTGCTTACATCTGGCC	540
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 21:07:27 ; Search time 1627.72 Seconds
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10160.671 Million cell updates/sec

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 413468905 residues

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Minimum DB seq length: 10
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Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

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2	2000	100.0	2000	US-09-759-143-374	Sequence 374, App
3	2000	100.0	2000	US-09-780-669-374	Sequence 374, App
4	2000	100.0	2000	US-09-810-936-302	Sequence 302, App
5	2000	100.0	2000	US-09-822-827-374	Sequence 374, App
6	2000	100.0	2000	US-09-429-755-302	Sequence 302, App
7	2000	100.0	2000	US-09-924-400-302	Sequence 302, App
8	2000	100.0	2000	US-09-895-793-374	Sequence 374, App
9	2000	100.0	2000	US-09-895-814-374	Sequence 374, App
10	2000	100.0	2000	US-10-012-896-374	Sequence 374, App
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12	2000	100.0	2000	US-10-212-679-302	Sequence 302, App
13	2000	100.0	2000	US-10-144-678A-374	Sequence 374, App
14	2000	100.0	2000	US-10-033-527-6	Sequence 6, App1
15	2000	100.0	2000	US-10-294-025-374	Sequence 374, App
16	2000	100.0	2000	US-10-079-137B-302	Sequence 302, App
17	1551	77.5	2040	US-09-825-301-7	Sequence 7, App1
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36	1128	56.4	1155	3	US-09-810-936-301	Sequence 301, App
37	1128	56.4	1155	3	US-09-822-827-373	Sequence 373, App
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44	1128	56.4	1155	6	US-10-212-679-301	Sequence 301, App
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ALIGNMENTS

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RESULT 1
US-09-825-301-6
Sequence 6, Application US/09825301
Patent No. US2002009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jiangchun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPR: DNA
ORGANISM: Homo sapien
US-09-825-301-6

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61 AGGAGCAAGATGGGCAAGTGTCGCTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120

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DB      121 AGCAACGTGGGCACTTCTGGAGACGACGACTGTGCTATGAAGACATCTCAGAGCAAG 180

QY      181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGACGCTG 240
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RESULT 2
US-09-759-143-374
Sequence 374, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiaqichun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

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; NUMBER OF SEQ ID NOS: 934
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US-09-759-143-374

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Best Local Similarity 100.0%; Pred. No. 0;
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QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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Db	1561	TTTATGGCTATCGAAGAAATGAGAGACGGAAGTACTCATGTGCGATTTCCAGAAAC	1620
QY	1621	CTGACTAATGGTGGCAGCTGGGCAATGGTGATGATGGAATTAAATTCTCCAGAAGAGAGC	1680
Db	1621	CTGACTAATGGTGGCAGCTGGGCAATGGTGATGATGGAATTAAATTCTCCAGAAGAGC	1680
QY	1661	AGAACACCTGAAGGCAAGCAATTTCTTGACACTGAGATGAAGAGTATCACAGTGACGA	1740
Db	1661	AGAACACCTGAAGGCAAGCAATTTCTTGACACTGAGATGAAGAGTATCACAGTGACGA	1740
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QY	1921	GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGACCAGCTAAAAAAAAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGACCAGCTAAAAAAAAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	

RESULT 4

US-09-810-936-302

/ Sequence 302, Application US/09810936

/ Patent No. US20020068285A1

/ GENERAL INFORMATION:

/ APPLICANT: Prudakis, Tony N.

/ APPLICANT: Reed, Steven G.

/ APPLICANT: Smith, John M.

/ APPLICANT: Misher, David E.

/ APPLICANT: Dillon, David C.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Wang, Aijun

/ APPLICANT: Skeiky, Yasir A.W.

/ APPLICANT: Harlocker, Susan L.

/ APPLICANT: Day, Craig H.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

/ FILE REFERENCE: 210121.419C11

/ CURRENT FILING DATE: 2001-03-16

/ NUMBER OF SEQ ID NOS: 334

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 302

/ LENGTH: 2000

/ TYPE: DNA

/ ORGANISM: Homo sapien

US-09-810-936-302

Dp	61	AGGAGCAAGATGGGCAATGGTGTCTGCCCTTGCTTCCCTGCTGCAAGGAGACGGCAAG	120
Qy	121	AGCAACGTGGCACTTCTGAGACACGACGACTCTGCTATGAAGACATCAGAGCAAG	180
Dp	121	AGCAACGTGGCACTTCTGAGAGACCAAGACACTCTGCTATGAAGACACTCAGAGCAAG	180
Qy	181	ATGGGCAAGTGGTCCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG	240
Dp	181	ATGGGCAAGTGGTCCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG	240
Qy	241	GGCGCTTCTGAGACCAACGACGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG	300
Dp	241	GGCGCTTCTGAGACCAAGACGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG	300
Qy	301	TGTTGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360
Dp	301	TGTTGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG	360
Qy	361	GGAGACTACGATGACAGTGTCTTATGAGGCCAGGTACCACTGTCGGAGAAAGATCTG	420
Dp	361	GGAGACTACGATGACAGTGTCTTATGAGGCCAGGTACCACTGTCGGAGAAAGATCTG	420
Qy	421	GACAAGCTCCACAGAGCTGCTGGTGGGGGTAAATGCCCAGAAAGGATCTATGTCATG	480
Dp	421	GACAAGCTCCACAGAGCTGCTGGTGGGGGTAAATGCCCAGAAAGGATCTATGTCATG	480
Qy	481	CTCAGGGACACTGACGTGACCAAGAAAGGACAAAGCAAGCACTGCTTACATCTGGCC	540
Dp	481	CTCAGGGACACTGACGTGACCAAGAAAGGACAAAGCAAGCACTGCTTACATCTGGCC	540
Qy	541	TCTGCGAATGGGAATTCAGAGTATGAATACTCTGCTGCAAGAGCATGTCAAATTAT	600
Dp	541	TCTGCGAATGGGAATTCAGAGTATGAATACTCTGCTGCAAGAGCATGTCAAATTAT	600
Qy	601	GTCCTTGAACAATAAAGAGGACAGCTCTGATAAGGCCGTACAAATGCCAGGAAGTCAA	660
Dp	601	GTCCTTGAACAATAAAGAGGACAGCTCTGATAAGGCCGTACAAATGCCAGGAAGTCAA	660
Qy	661	TGTGCGTAAATGTTGCTGGAACATGCGCACTGATCCAATATTCAGATGATATGAAT	720
Dp	661	TGTGCGTAAATGTTGCTGGAACATGCGCACTGATCCAATATTCAGATGATATGAAT	720
Qy	721	ACCACTGTGACCTACGCTATCTATATGAAGATAAATTAATGAAGCCACTGCTCTTA	780
Dp	721	ACCACTGTGACCTACGCTATCTATATGAAGATAAATTAATGAAGCCACTGCTCTTA	780
Qy	781	TATGTGTGTAATTCGAATCAAAAAACAAGATGGCTCACACCACTGTAATCTTGGTGA	840
Dp	781	TATGTGTGTAATTCGAATCAAAAAACAAGATGGCTCACACCACTGTAATCTTGGTGA	840
Qy	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTTAATGCA	900
Dp	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTAATCAAGAAAAAGCAATTTTAATGCA	900
Qy	901	CTGATATGATATGAAAGGACTGCTCTCAATACCTTGCTGATGTTGATTCAGCAATATA	960
Dp	901	CTGATATGATATGAAAGGACTGCTCTCAATACCTTGCTGATGTTGATTCAGCAATATA	960
Qy	961	GTCAGCTTCTACCTTGAACAAAATATGATATCTTCTCAAGATCTATCTGACAGACG	1020
Dp	961	GTCAGCTTCTACCTTGAACAAAATATGATATCTTCTCAAGATCTATCTGACAGACG	1020
Qy	1021	GCAGAGAGTATGCTGTTCTAGTCATCATGTAATTTGCGAGTAACTTCTGACCTAC	1080
Dp	1021	GCAGAGAGTATGCTGTTCTAGTCATCATGTAATTTGCGAGTAACTTCTGACCTAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
Dp	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
Qy	1141	CTGACATTCAGAGAAAGTCAAAAAGTTCAAAGCAGTGAATAATGCCACCCAGAGAA	1200

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Db      1141 CTGACATCAGAGAGAGATGCACAAAGTTCAAAAGCATGTAATATGACCGACGAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACCCAGAAATTAATAAGATGTGATAGAGGTTGAAGAATAAGAAAG 1260
Db      1201 ATGTCTCAAGAACCCAGAAATTAATAAGATGTGATAGAGGTTGAAGAATAAGAAAG 1260
Qy      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTATATGCTGCTGAC 1320
Db      1261 AAGCATGAAAGTAATAATGTGGATTACTAGAAAACCTGACTATATGCTGCTGAC 1320
Qy      1321 AATGTGATATATGATTAATCTCTCAAGAGAGACAAACCTGATAATGCTGCTGAC 1380
Db      1321 AATGTGATATATGATTAATCTCTCAAGAGAGACAAACCTGATAATGCTGCTGAC 1380
Qy      1381 CCTGACAAAGAGAGAGATGATCAAGAAATTTGGAAATTAATGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAGAGATGATGATCAAGAAATTTGGAAATTAATGTTCTGATCAAGAA 1440
Qy      1441 AAACAGATGCGCAAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCGCAAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAGAGAGATCAAGAGGCTTGAAGGCAATGAAAATGGCCAGCCAGCTAGAAAT 1560
Db      1501 TCAGAGAGAGAGATCAAGAGGCTTGAAGGCAATGAAAATGGCCAGCCAGCTAGAAAT 1560
Qy      1561 TTTATGCTATCGAAGAAATGAAGAAAGCACGAAAGTACTATGTGGGATTTCCAGAAAC 1620
Db      1561 TTTATGCTATCGAAGAAATGAAGAAAGCACGAAAGTACTATGTGGGATTTCCAGAAAC 1620
Qy      1621 CTGACTAATGTGTCACATGCTGCGCAATGTGATGATGATTAATCTCCAGAGAAAGAC 1680
Db      1621 CTGACTAATGTGTCACATGCTGCGCAATGTGATGATGATTAATCTCCAGAGAAAGAC 1680
Qy      1681 AGAAGACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGAGATCACTAGTCGAA 1740
Db      1681 AGAAGACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGAGATCACTAGTCGAA 1740
Qy      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGACAGAACTGGAAATATTAACGATGAG 1800
Db      1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGACAGAACTGGAAATATTAACGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAATTAATGATTCGAGCTTTC 1860
Db      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAATTAATGATTCGAGCTTTC 1860
Qy      1861 CTTAGTTGTAGAGAGAGAAAGCATCTTGCATGAAATATGATCGTTGCGGAGAAAT 1920
Db      1861 CTTAGTTGTAGAGAGAGAAAGCATCTTGCATGAAATATGATCGTTGCGGAGAAAT 1920
Qy      1921 GCCATGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db      1921 GCCATGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 5
US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374

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; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGTGTGTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGTCTC 60
Qy      61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGGAGACGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGGAGACGGCAAG 120
Qy      121 AGCAACGTGGGCACTTTGTGAGACCAAGCAAGCTGTCTATGAGAGCACTCAGAGCAG 180
Db      121 AGCAACGTGGGCACTTTGTGAGACCAAGCAAGCTGTCTATGAGAGCACTCAGAGCAG 180
Qy      181 ATGGGCAAGTGTGCTGCCGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGCTG 240
Db      181 ATGGGCAAGTGTGCTGCCGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGCTG 240
Qy      241 GGCCTTCTGAGAGACCAAGCAAGCTGTCTATGAGAGCACTCAGAGCAAGATGGCAAG 300
Db      241 GGCCTTCTGAGAGACCAAGCAAGCTGTCTATGAGAGCACTCAGAGCAAGATGGCAAG 300
Qy      301 TGTGTCTGCACTGCTTCCCTGCTGCAAGGGAGACGGCAAGCAAGTGGGCGCTTGG 360
Db      301 TGTGTCTGCACTGCTTCCCTGCTGCAAGGGAGACGGCAAGCAAGTGGGCGCTTGG 360
Qy      361 GGAAGACTAGATGAGACAGTGTCTTCAATGAGGCCAGGTACAGTCCGTGGAAGATCTG 420
Db      361 GGAAGACTAGATGAGACAGTGTCTTCAATGAGGCCAGGTACAGTCCGTGGAAGATCTG 420
Qy      421 GACCAAGCTCAGAGAGCTGCTGTGTGGGTAAGTCCCGAGAAAGGATCTACGTCATG 480
Db      421 GACCAAGCTCAGAGAGCTGCTGTGTGGGTAAGTCCCGAGAAAGGATCTACGTCATG 480
Qy      481 CTCAAGGACACTGAGCGTGAACAAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
Db      481 CTCAAGGACACTGAGCGTGAACAAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTCTGTCGACAGAGATGTCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTCTGTCGACAGAGATGTCACTTAAT 600
Qy      601 GTCCCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGGCGCTCAATGGCCAGGAAGTGA 660
Db      601 GTCCCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGGCGCTCAATGGCCAGGAAGTGA 660
Qy      661 TGTGCTTAATGTGCTGAGACATGCACTGATTAAGTAATTAATGAGAGAGAGAGAG 720
Db      661 TGTGCTTAATGTGCTGAGACATGCACTGATTAAGTAATTAATGAGAGAGAGAGAG 720
Qy      721 ACCACTCTGCACTAGCGCTATCTTAATGAGAGTAATTAATGAGAGAGAGAGAGAG 780
Db      721 ACCACTCTGCACTAGCGCTATCTTAATGAGAGTAATTAATGAGAGAGAGAGAGAG 780
Qy      781 TATGGTGTGATGATGAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db      781 TATGGTGTGATGATGAGAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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Db      841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAACGAAATTTAATGCA 900
Qy      901 CTGATAGATATGAGAGAGCTGCTCATATCTTGTCTGATGTGTGAGATCAGCAAGTATA 960
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QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCTGTAATAATACCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCTGTAATAATACCCAGAGAGAA 1200
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DB 1741 CAAAATGATCTAGAGAGCAATTTTGTGAAGAACAGAACTGGAATTAATTAACGATGAG 1800
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DB 1861 CTTAGTTGTAAGAAAGAAAGCATTTCTGATGAATAATGTAATTTCTGAGCTTTCT 1920
QY 1921 GCCATGCTAGAGCTGAGCTAGACCAATGAATCATGAGAGCAGCTTAAGAAAGAGAG 1980
DB 1921 GCCATGCTAGAGCTGAGAGCTAGACCAATGAATCATGAGAGCAGCTTAAGAAAGAGAG 1980
QY 1981 AAAAGAAAACAGATGCTAAAATCTCTTCTGAAAACGCAATCCAGAACAGACTTAAG 2000
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RESULT 6
US-09-429-755-302
/ Sequence 302, Application US/09429755A
/ Patent No. US20020111467A1
/ GENERAL INFORMATION:
/ APPLICANT: Prudakis, Tony N.
/ APPLICANT: Smith, John M.
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Misher, Lynda
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Dillon, Davin C.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ TITRE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.419C6
/ CURRENT APPLICATION NUMBER: US/09/429, 755A
/ CURRENT FILING DATE: 1999-10-28
/ NUMBER OF SEQ ID NOS: 315
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 302
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-429-755-302
Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGTGAGAGTATTCATTCAGAGGCTGCTCTTCTGTAAGAGAGCATTTGCTC 60
DB 1 ATGAGGTGAGAGTATTCATTCAGAGGCTGCTCTTCTGTAAGAGAGCATTTGCTC 60
QY 61 AGGAGCAAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGACGAGAGAGCGCAAG 120
DB 61 AGGAGCAAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGACGAGAGAGCGCAAG 120
QY 121 AGCAAGTGTGAGCACTTCTGAGACCAAGAGACTCTGCTATGAAGACCTCAGAGCAAG 180
DB 121 AGCAAGTGTGAGCACTTCTGAGACCAAGAGACTCTGCTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAATGAGGCGGCACTGCTTCCCTGCTGACGAGGAGAGGAGTGGCAAGCGTG 240
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DB 241 GGGCTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
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DB 301 TGGTCTGCACTGCTTCCCTGCTGACGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGAGAGACAGTCTTCAATGAGAGCCAGGTATCAAGTCCGTGGAAGAGATCTG 420
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QY 661 TGTGCTTAATGTTGCTGAGACATGCACTGATCCAAATATTCTCAGATGATGAAAT 720

DB 661 TGGCGTATATGTTGTCGAAACATGACATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACACGCTCTATCTATATGAAAGTAATTAATGAGCCACACCTGCTT 780
DB 721 ACCACTCTGCACACGCTCTATCTATATGAAAGTAATTAATGAGCCACACCTGCTT 780
QY 781 TATGCTGATATTCGATCAAAACAAAGCATGCTCAGACACCTGTTACTTGATG 840
DB 781 TATGCTGATATTCGATCAAAACAAAGCATGCTCAGACACCTGTTACTTGATG 840
QY 841 CATGACCAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAACGAAATTTAAATGA 900
DB 841 CATGACCAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAACGAAATTTAAATGA 900
QY 901 CTGATATGATATGGAAGACCTGCTCATATCTGCTATGTTGTTGATGATCAGACATTA 960
DB 901 CTGATATGATATGGAAGACCTGCTCATATCTGCTATGTTGTTGATGATCAGACATTA 960
QY 961 GTGAGCTTCTACTTGTAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGTAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGATC 1080
DB 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGATC 1080
QY 1081 AAAAGAAAAACAGTGTCTTAAATCTCTTCTGAAAAACAGCATCTGAAACAGCTTAA 1140
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QY 1141 CTGACATCAGAGAGATGACAAAGGTTCAAGGAGTGAATAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAGATGACAAAGGTTCAAGGAGTGAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7

US-09-924-400-302
Sequence 302, Application US/09924400
Patent No. US20020165371A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misner, Lynda B.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A. W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel X.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C12
CURRENT APPLICATION NUMBER: US/09/924,400
NUMBER OF SEQ ID NOS: 340
CURRENT FILING DATE: 2001-08-07
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-924-400-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
DB 1 ATGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
QY 61 AAGAGCAGATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
DB 61 AAGAGCAGATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 121 AAGAGCAGATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
DB 121 AAGAGCAGATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 181 ATGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 ATGGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 241 GGGGCTTCTGAGAGCAGACAGATCTGCTATGAAAGACATGAGGAAACAAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGAGCAGACAGATCTGCTATGAAAGACATGAGGAAACAAGATGGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGGAGGCAAGGATGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGGGAGGCAAGGATGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGGAGAAAGATCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCTGGAGAAAGATCTG 420
QY 421 GACAGCTCACAAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAGCTCACAAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCATGCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTCATGCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTCTGAGACAGAGATGCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTCTGAGACAGAGATGCACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGAGAGCTGATTAAGGCGTACATGCAAGAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGAGAGAGCTGATTAAGGCGTACATGCAAGAGATGA 660
QY 661 TGTGCGTTAATGTTGTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTGACGTATCTTAATGAAGATTAATGAGCCAAAGACCTGCTTA 780
DB 721 ACCACTGTGCACTGACGTATCTTAATGAAGATTAATGAGCCAAAGACCTGCTTA 780
QY 781 TATGTGTGATATTCGAATCAAAAAACAAGCATGGCTCAGACACTGTTACTGGTGA 840
DB 781 TATGTGTGATATTCGAATCAAAAAACAAGCATGGCTCAGACACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGAGTCTGGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGAGTCTGGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGAGCTGCTCATGCTGATGATGTTGAGATCAGCAATATA 960
DB 901 CTGATATGATATGAGAGAGCTGCTCATGCTGATGATGTTGAGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAAGTCTAAAAATCTCTGAAAAACAAGATCAAAACAAGCTTAAAG 1140
DB 1081 AAAAGAAAAACAAGTCTAAAAATCTCTGAAAAACAAGATCAAAACAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTAAATAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGAGTAAATAGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGAGGATTAATAGAAACCTGATTAATGATGATGATGATG 1320
DB 1261 AAGCATGAAGATTAATGAGGATTAATAGAAACCTGATTAATGATGATGATGATG 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACTGAAATCAAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGCAACTGAAATCAAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCAATTAATGTTCTGATCAAAAGAA 1440

DB 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCAATTAATGTTCTGATCAAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATCAACAAAGCTTGAAGGCACTGAAATATGCGCAGCAGAGCTAGAAAT 1560
DB 1501 TCAGAGAAAGATCAACAAAGCTTGAAGGCACTGAAATATGCGCAGCAGAGCTAGAAAT 1560
QY 1561 TTTATGGCTATGAAAGAAATGAAGAGACAGGAATGATCATGCGGATTTCCAGAAAGAC 1620
DB 1561 TTTATGGCTATGAAAGAAATGAAGAGACAGGAATGATCATGCGGATTTCCAGAAAGAC 1620
QY 1621 CTGACTAATGATGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 CTGACTAATGATGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 AGAACACTGAAAGGAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
DB 1681 AGAACACTGAAAGGAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
QY 1741 CAAAATGATCTCAGAGAGCAATTTGTGAAGACAGAACCTGGAATTTACAGCATGAG 1800
DB 1741 CAAAATGATCTCAGAGAGCAATTTGTGAAGACAGAACCTGGAATTTACAGCATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGAGATGAGATGATGATGATGATGATGATGATGATG 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGAGATGAGATGATGATGATGATGATGATGATGATG 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGTGATGAAATATGATGATGATGATGATG 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGTGATGAAATATGATGATGATGATGATG 1920
QY 1921 GCCATGCTTAAGCTGAGAGTACACAAATGAAACATCAAGAGCCAGCTTAAATTAAT 1980
DB 1921 GCCATGCTTAAGCTGAGAGTACACAAATGAAACATCAAGAGCCAGCTTAAATTAAT 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
US-09-895-793-374
Sequence 374, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carleca
APPLICANT: Foy, Teresa
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF PROSTATE CANCER

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FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGATTGATTCATGCGCGTCTCTTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGGTGTTGAGATTGATTCATGCGCGTCTCTTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAGGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAGGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCCACTGCTTCCCTGCTGCAGGGAGAGTGGCAAGAGCAAG 240
DB 181 ATGGGCAAGTGTGCGGCCCACTGCTTCCCTGCTGCAGGGAGAGTGGCAAGAGCAAG 240
QY 241 GCGGCTTCTGAGAGACCAAGCAAGCTCTGCTATGAAGCACTCAAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGAGACCAAGCAAGCTCTGCTATGAAGCACTCAAGAAAGATGGGCAAG 300
QY 301 TGGTGCTGCACCTGCTTCCCTGCTGCAGGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGCTGCACCTGCTTCCCTGCTGCAGGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTAGAGTGAAGTGTCTTCAATGAGCCCAAGTACCAAGTCCGTGGAAGAGTCTG 420
DB 361 GGAAGACTAGAGTGAAGTGTCTTCAATGAGCCCAAGTACCAAGTCCGTGGAAGAGTCTG 420
QY 421 GACAAGCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAAGCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGCACTGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTGCTGCTGCTGCTG 540
DB 481 CTCAGGAGCACTGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTGCTGCTGCTGCTG 540
QY 541 TCTGCCAATAGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGAGTCACTTAAT 600
DB 541 TCTGCCAATAGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGAGTCACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 601 GTCTTGAACAACAAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TGTGCTTATGTTGCTGGAACATGAGCACTGATCCAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTATGTTGCTGGAACATGAGCACTGATCCAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTTGA 780
DB 721 ACCACTCTGCACTACCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTTGA 780
QY 781 TATGCTGCTGATATGATCAATCAAAAAGAGAGTGGCTGCACTGCTGCTGCTGCTG 840
DB 781 TATGCTGCTGATATGATCAATCAAAAAGAGAGTGGCTGCACTGCTGCTGCTGCTG 840
QY 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAACGATTTAAATGCA 900
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DB 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAACGATTTAAATGCA 900
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DB 901 CTGGATATGATGGAAGAGCTGCTCTCATCTTGTGCTGATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGAAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGAAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGAAATCCGAACAAACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGAAATCCGAACAAACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAAGTAATTAAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAAGTAATTAAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAAACAGAAATTAATAGATGATGATGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAAACAGAAATTAATAGATGATGATGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTTACTGAAAACTGACATTAATGTTGCTGCTGGC 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTTACTGAAAACTGACATTAATGTTGCTGCTGGC 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACACTGAAAAATCAGCAATT 1380
DB 1321 AATGCTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACACTGAAAAATCAGCAATT 1380
QY 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTTGATTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTTGATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
DB 1441 AAAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGCTAGAAAAAT 1560
DB 1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGCTAGAAAAAT 1560
QY 1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGTACTCATGTGCGAATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATGCTGCACTGCTGCAATGCTGATGATTAATTTCTTCCAGAGAAAGAC 1680
DB 1621 CTGACTAATGCTGCACTGCTGCAATGCTGATGATTAATTTCTTCCAGAGAAAGAC 1680
QY 1681 AGAACACCTGAAAGCAGAGATTTTCTGCACTGGAATGAAGAGATCAGAGTGCAGAA 1740
DB 1681 AGAACACCTGAAAGCAGAGATTTTCTGCACTGGAATGAAGAGATCAGAGTGCAGAA 1740
QY 1741 CAAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
DB 1741 CAAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATGAGAGTGTGAAAAATGAATCTCAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATGAGAGTGTGAAAAATGAATCTCAGCTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGAACATCTTGCATGAAATATGATGCTGCGGAGAGAAATTT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGAACATCTTGCATGAAATATGATGCTGCGGAGAGAAATTT 1920
QY 1921 GCCATGCTAAGAGCTGAGCTAGACACAATGAAGACATCAGAGCCAGCTAAAAAAGAAAA 1980
DB 1921 GCCATGCTAAGAGCTGAGCTAGACACAATGAAGACATCAGAGCCAGCTAAAAAAGAAAA 1980
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QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9
US-09-895-814-374
Sequence 374, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGGAAGCCATTGGTCTC 60
Db 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGGAAGCCATTGGTCTC 60

QY 61 AGAGCAAGTGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGGAGCGGCAAG 120
Db 61 AGAGCAAGTGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCTGTGTAAGACACTCAGAGGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCTGTGTAAGACACTCAGAGGCAAG 180

QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240

QY 241 GGGGCTTTGAGACCAAGCAAGCTGTGTAAGACACTCAGAACTCAGAACTGAGGCAAG 300
Db 241 GGGGCTTTGAGACCAAGCAAGCTGTGTAAGACACTCAGAACTCAGAACTGAGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

QY 361 GGAGACTAGATGACGTGCTTCATGAGCCCAAGTACCAGTCCGTGGAAGACATCTG 420
Db 361 GGAGACTAGATGACGTGCTTCATGAGCCCAAGTACCAGTCCGTGGAAGACATCTG 420

QY 421 GACCAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAGAAAGGATCTCATGTCATG 480
Db 421 GACCAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAGAAAGGATCTCATGTCATG 480

QY 481 CTCAGGAGACATGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTCTACATCTGGCC 540
Db 481 CTCAGGAGACATGACCTGGAACAAGAGCAAGCAAAAGAGAGTCTCTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAGTGAATACTCTCTGTCGACAGAGATCTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTGAATACTCTCTGTCGACAGAGATCTCACTTAAT 600

QY 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGCCGTACAAATGCGAGAAAGTGA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGCCGTACAAATGCGAGAAAGTGA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720

QY 721 ACCACTCTGACTACGCTATCTAATAAGATTAATTAAGGCAAGCACTGCTCTTA 780
Db 721 ACCACTCTGACTACGCTATCTAATAAGATTAATTAAGGCAAGCACTGCTCTTA 780

QY 781 TATGTCGTGATATGCAATCAAAAACAGCATGCGCTCACACACTGTTACTGGTGA 840
Db 781 TATGTCGTGATATGCAATCAAAAACAGCATGCGCTCACACACTGTTACTGGTGA 840

QY 841 CATGACAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAACGAATTTAATGCA 900
Db 841 CATGACAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAACGAATTTAATGCA 900

QY 901 CTGATATGATATGGAAGACTGCTCTCATACTTCTGTATGTTGTGATCAGCAATGA 960
Db 901 CTGATATGATATGGAAGACTGCTCTCATACTTCTGTATGTTGTGATCAGCAATGA 960

QY 961 GTACGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020
Db 961 GTACGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020

QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGATTTGCAATCTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGATTTGCAATCTTCTGACTAC 1080

QY 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCTCAGAACAGCTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCTCAGAACAGCTTAAG 1140

QY 1141 CTGACATCAGAGGAAGTCAAAAAGTTCAAAAGGAGTGAATAATGCGCAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGTCAAAAAGTTCAAAAGGAGTGAATAATGCGCAGAGAAA 1200

QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAGATTAATATGAGGATTAAGAAAACTGACTAATATGATGCTGCTG 1320
Db 1261 AAGCATGAAGATTAATATGAGGATTAAGAAAACTGACTAATATGATGCTGCTG 1320

QY 1321 AATGATGAATATGATTAATTTCTCAAGAGGAAGCAAGCACTGGAATAATGCAATTT 1380
Db 1321 AATGATGAATATGATTAATTTCTCAAGAGGAAGCAAGCACTGGAATAATGCAATTT 1380

QY 1381 CTTGACAAAGAAAGTATCAAGAAATTTGGAATTTGATTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAAGTATCAAGAAATTTGGAATTTGATTTCTGACTACAAAGAA 1440

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Qy 1441 AAACAGATGCCAAATATCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGTGACA 1500
Qy 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCACTGAAAATGCGCAGCAAGCTAGAAAAT 1560
Db 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGCACTGAAAATGCGCAGCAAGCTAGAAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAAAGAGCAGCAAGTACTATGATTTCCAGAAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAAGAGCAGCAAGTACTATGATTTCCAGAAAAC 1620
Qy 1621 CTGACTAATGTCGCCACTGTCGCAATGATGATGATTAATTCCTCCAGAAAGAC 1680
Db 1621 CTGACTAATGTCGCCACTGTCGCAATGATGATGATTAATTCCTCCAGAAAGAC 1680
Qy 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGAGTATCAAGTGAAGAA 1740
Db 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGATGAGAGTATCAAGTGAAGAA 1740
Qy 1741 CAAAAATGATCTGAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Db 1741 CAAAAATGATCTGAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGCAAGATGAGAGTGTGAAAAATGAAATTCGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGCAAGATGAGAGTGTGAAAAATGAAATTCGAGCTTTCT 1860
Qy 1861 CTTAGTTGTGAGAAAGAAAGACATCTTGCATGAAATGTAGCTTGGCGGAAAGAAAT 1920
Db 1861 CTTAGTTGTGAGAAAGAAAGACATCTTGCATGAAATGTAGCTTGGCGGAAAGAAAT 1920
Qy 1921 GCCATGCTAAGAGCTGAGAGTACAGACATGAAATCATCAGAGCCGCTAAAAAAA 1980
Db 1921 GCCATGCTAAGAGCTGAGAGTACAGACATGAAATCATCAGAGCCGCTAAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-10-012-896-374
; Sequence 374, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27

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; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-374

Query Match      100.0%; Score 2000; DB 5; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Db 1 ATGGGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTCTCCCTGCTGCAGGAGAGCGCAAG 120
Qy 121 AGCAACGTGGGCACTTTCTGAGACCAAGCACTCTGTATGAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTTCTGAGACCAAGCACTCTGTATGAGACACTCAGAGCAAG 180
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Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGCACTG 240
Qy 241 GCGGCTTCTGAGACCAAGCAAGCTCTGTATGAGACACTCAGAGCAAGTGGCAAG 300
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Qy 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
Qy 361 GGAAGACTAGAGACAGAGCTTCAATGAGCCCAAGTACCAAGTCCGTGGAATAATCTG 420
Db 361 GGAAGACTAGAGACAGAGCTTCAATGAGCCCAAGTACCAAGTCCGTGGAATAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTG 480
Db 421 GACAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTG 480
Qy 481 CTCAGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTG 540
Db 481 CTCAGGACACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTG 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGTCAATCTTAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGTCAATCTTAT 600
Qy 601 GTCTTTGACAAACAAGAGAGCAGCTGTATTAAGGCGCTCAATGCCAGAAAGATGAA 660
Db 601 GTCTTTGACAAACAAGAGAGCAGCTGTATTAAGGCGCTCAATGCCAGAAAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGACACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGACACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTAGGCTATCTATAAGATTAATTAATGGCCAAAGCACTGCTT 780
Db 721 ACCACTCTGCACTAGGCTATCTATAAGATTAATTAATGGCCAAAGCACTGCTT 780
Qy 781 TATGGTGTGATGATGAAATCAAAAAAGAGATGAGCTCAAGCACTGTTAGTGTGTA 840
Db 781 TATGGTGTGATGATGAAATCAAAAAAGAGATGAGCTCAAGCACTGTTAGTGTGTA 840
Qy 841 CATGAGCAAAAAAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900

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QY 901 CTGGATAGATATGGAAGGAGTCTGCTCATCTTCTGTATGTTGTGATTCAGCAAGATATA 960
DB 901 CTGGATAGATATGGAAGGAGTCTGCTCATCTTCTGTATGTTGTGATTCAGCAAGATATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAATCTATCTTGACAGAGC 1020
DB 961 GTGAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAATCTATCTTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTTCCAGTTACTTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTTCCAGTTACTTTCTGATAC 1080
QY 1081 AAGAAAAAAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACCAAGCTTAAAG 1140
DB 1081 AAGAAAAAAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAAGGTTCAAAAGGAGTAAATAGCCAGCAAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAAAGGTTCAAAAGGAGTAAATAGCCAGCAAGAGAA 1200
QY 1201 ATGCTTCAGAACCCAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
DB 1201 ATGCTTCAGAACCCAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTACTTGAAAACTGACTATGCTGCTGCTGCTG 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTACTTGAAAACTGACTATGCTGCTGCTGCTG 1320
QY 1321 AATGTGATTAATGATTAATTTCTTCAAAAGAGAGCAACCTGAAATAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTTCAAAAGAGAGCAACCTGAAATAGCAATTT 1380
QY 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTAAGAA 1440
DB 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTTCTGACTAAGAA 1440
QY 1441 AAAACATGCTCAAAATCTTTCTGAAAAACGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
DB 1441 AAAACATGCTCAAAATCTTTCTGAAAAACGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATCACAAGGCTTGAAGGAGTGAATGGCCAGCCAGAGCTAAGAAAT 1560
DB 1501 TCAGAGGAAGATCACAAGGCTTGAAGGAGTGAATGGCCAGCCAGAGCTAAGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAACGAGAACTCATGTCGATTCGCCAGAAAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAGAACGAGAACTCATGTCGATTCGCCAGAAAC 1620
QY 1621 CTGACTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 CTGACTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAAGCCTGAAAGGCAAGGAAATTTCTGACATGAGAAATGAAGATGACATGACGAA 1740
DB 1681 AGAAGCCTGAAAGGCAAGGAAATTTCTGACATGAGAAATGAAGATGACATGACGAA 1740
QY 1741 CAAATGATATCTGAGAAAGCAATTTTGTGAAGAACAGAACTGAAATATTAACAGTAGAG 1800
DB 1741 CAAATGATATCTGAGAAAGCAATTTTGTGAAGAACAGAACTGAAATATTAACAGTAGAG 1800
QY 1801 ATTCTGATTAAGAAAGCAAGATGAAAGTGGTTGAAAAATGAATTTCTGAGCTTCT 1860
DB 1801 ATTCTGATTAAGAAAGCAAGATGAAAGTGGTTGAAAAATGAATTTCTGAGCTTCT 1860
QY 1861 CTTAGTTTGAAGAAAGCAATTTTCTGAGAAATTTCTGAGCTTCTGAGCTTCTGAGCTT 1920
DB 1861 CTTAGTTTGAAGAAAGCAATTTTCTGAGAAATTTCTGAGCTTCTGAGCTTCTGAGCTT 1920
QY 1921 GCCATGCTAAGCTGAGCTGAGCACAATGAAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
DB 1921 GCCATGCTAAGCTGAGCTGAGCACAATGAAACATCAGAGCCAGCTAAAAAAGAAAAA 1980

QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 11
US-10-010-940-374
Sequence 374, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalo, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-10-010-940-374

Query Match 100.0%; Score 2000; DB 5; Length 2000;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTTCTGTGAAAGCAATTTGCTTC 60
DB 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTTCTGTGAAAGCAATTTGCTTC 60
QY 61 AGAGCAATATGGGCAAGTGTGCTGCTGCTTCTGCTGCAAGGAGGCAAG 120
DB 61 AGAGCAATATGGGCAAGTGTGCTGCTGCTTCTGCTGCAAGGAGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 ATGGGCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGGCTTCTGAGCAAGCAAGCACTTCTGATGAAGCACTCAGAAAGATGGCAAG 300
DB 241 GGGCTTCTGAGCAAGCAAGCACTTCTGATGAAGCACTCAGAAAGATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGGAGGAGGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGGAGGAGGCTTGG 360
QY 361 GGAAGCTAAGATGAGTCTTCTGAGAGCCAGGTAACAGTCCGAGAGAGATCTG 420
DB 361 GGAAGCTAAGATGAGTCTTCTGAGAGCCAGGTAACAGTCCGAGAGAGATCTG 420
QY 421 GACAACTTCAAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTTCAAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGGAACCTGAGCTGAGCAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAGGGAACCTGAGCTGAGCAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540

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QY 541 TCTGCAATGGGAATT CAGAAAGTAAAACTCTGCTGGACAGAGATGCACTTAAT 600
DB 541 TCTGCAATGGGAATT CAGAAAGTAAAACTCTGCTGGACAGAGATGCACTTAAT 600
QY 601 GTCTTGAACAACAAAAAGAGACAGCTCTGATTAAGCCGTCAATGCGAGAAATGAA 660
DB 601 GTCTTGAACAACAAAAAGAGACAGCTCTGATTAAGCCGTCAATGCGAGAAATGAA 660
QY 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTTCCAAATGAGTATGAAAT 720
DB 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTTCCAAATGAGTATGAAAT 720
QY 721 ACCACTCTGCACTACCTATCTATTAATGAAGATAATTAATGSCCAAGACCTGCTCTTA 780
DB 721 ACCACTCTGCACTACCTATCTATTAATGAAGATAATTAATGSCCAAGACCTGCTCTTA 780
QY 781 TATGTGCTGATATTCGAATCAAAAAACAAGCATGGCCTCAACACACTGTTACTTGTGTA 840
DB 781 TATGTGCTGATATTCGAATCAAAAAACAAGCATGGCCTCAACACACTGTTACTTGTGTA 840
QY 841 CATGACCAAAAAACAGAAAGTCGTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGCA 900
DB 841 CATGACCAAAAAACAGAAAGTCGTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGACCTGCTCATATCTGCTGATATGTTGAGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGACCTGCTCATATCTGCTGATATGTTGAGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTTACTTGAGCAAAATATTTGATATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTGAGCCTTCTTACTTGAGCAAAATATTTGATATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGAGTAATGCTTTTCTACTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGAGTAATGCTTTTCTACTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAAACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGATCACAAGAGTTCAAAAGGAGTGAATAATGACCCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGATCACAAGAGTTCAAAAGGAGTGAATAATGACCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTATATATGATGAGATTACTAGAAAACTGACTAATGATGCTGCTGGC 1320
DB 1261 AAGCATGAAAGTATATATGATGAGATTACTAGAAAACTGACTAATGATGCTGCTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGAGCAACACTGAAATTCAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCTCAAGAGAGAGCAACACTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGCAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
DB 1441 AAACAGATGCAAAATCTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTACAAAAGCTTGAAGGCAAGTGAATGAGCCAGCCAGAGCTTGAAGAA 1560
DB 1501 TCAGAGAAAGAGTACAAAAGCTTGAAGGCAAGTGAATGAGCCAGCCAGAGCTTGAAGAA 1560
QY 1561 TTTATGGCTATTCGAAGAAATGAAGAGCAGAAAGTATCTATGTCGATTTCCAGAAAC 1620
DB 1561 TTTATGGCTATTCGAAGAAATGAAGAGCAGAAAGTATCTATGTCGATTTCCAGAAAC 1620

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QY 1621 CTGACTAATGTCGCACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTCGCACTGCTGGCAATGGTATGATGATTAATTTCTCAAGAAAGAC 1680
QY 1681 AGAACAACCTGAAAGCCAGCAATTTCTTGACACTGAGATGAAGATATCACAGTACGAA 1740
DB 1681 AGAACAACCTGAAAGCCAGCAATTTCTTGACACTGAGATGAAGATATCACAGTACGAA 1740
QY 1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACGAACACTGGAATATTAACAATGAG 1800
DB 1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACGAACACTGGAATATTAACAATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGAGACATAGAAAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAGAAAGAGACATAGAAAGTGTGAAAAATGAAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATATGATACGTTGCGGAAAGAAAT 1920
DB 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATATGATACGTTGCGGAAAGAAAT 1920
QY 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAAGAAAA 1980
DB 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 12
US-10-212-679-302
; Sequence 302, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hixel, Shannon Kathleen
; APPLICANT: Dillon, Davin
; APPLICANT: Roy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Pehring, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSB for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302

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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGAATTCATGCGCGCTGCTCTTCTGTAAGAACCAATTTGCTTC 60
DB 1 ATGTGTTGAGTGAATTCATGCGCGCTGCTCTTCTGTAAGAACCAATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACATCTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACATCTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240
DB 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGCAAGCTG 240

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QY 241 GGGCTTTGGAGACGACGACGACTCTGATGAAAGCACTCAGAAACAAGATGGGCAAG 300
 Db 241 GGGCTTTGGAGACGACGACGACTCTGATGAAAGCACTCAGAAACAAGATGGGCAAG 300
 QY 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
 Db 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
 QY 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCGAGGTACCACTCCGTGAGAAAGATCTG 420
 Db 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCGAGGTACCACTCCGTGAGAAAGATCTG 420
 QY 421 GACAAGCTCCAGAGAGTGTCTGAGGGGATTAAGTCCCGCAAAAGATCTCATGCTCATG 480
 Db 421 GACAAGCTCCAGAGAGTGTCTGAGGGGATTAAGTCCCGCAAAAGATCTCATGCTCATG 480
 QY 481 CTCAGGGACACTGACGCTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTTCACTCTGGCC 540
 Db 481 CTCAGGGACACTGACGCTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTTCACTCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGAGACAGACGATGCACTTAAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAATGATAAACTCTGCTGAGACAGACGATGCACTTAAAT 600
 QY 601 GTCTCTGACAAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGCTACATTCGCAAGAAATGAA 660
 Db 601 GTCTCTGACAAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGCTACATTCGCAAGAAATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATTTTCAGATGAGTATGGAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATTTTCAGATGAGTATGGAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTATAATGAAATTAATTAATGCAAGCAAGCTCTTAA 780
 Db 721 ACCACTCTGCACTACGCTATCTATAATGAAATTAATTAATGCAAGCAAGCTCTTAA 780
 QY 781 TATGCTGCTGATATTCGAATTAACAAAACAAGCATGGGCTCACACGCTTAACTTGGTGA 840
 Db 781 TATGCTGCTGATATTCGAATTAACAAAACAAGCATGGGCTCACACGCTTAACTTGGTGA 840
 QY 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGGAAATTTAAATGCA 900
 Db 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGGAAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGCTGCTCTCATCTTCTGATATGTTGGATCAGCAAGATTA 960
 Db 901 CTGGATAGATATGGAAGAGCTGCTCTCATCTTCTGATATGTTGGATCAGCAAGATTA 960
 QY 961 GTGAGCCTTCTACTTGAAGCAAAATTTATGATTAATCTTTCAGATCTATCTGACAGAG 1020
 Db 961 GTGAGCCTTCTACTTGAAGCAAAATTTATGATTAATCTTTCAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTCTAGCATCATCATGTAATTTGCAAGTAACTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTCTAGCATCATCATGTAATTTGCAAGTAACTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGCAAAATCTCTTCTGAAACACAGATCAGAACAGACTTAAAG 1140
 Db 1081 AAAAGAAAAACAGATGCAAAATCTCTTCTGAAACACAGATCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGCAAGTAAATGCGCAGAGAGAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGCAAGTAAATGCGCAGAGAGAA 1200
 QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
 Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAGTAAATTAATGTTGAGATTAATAAGAAACCTGACTAATGCTGCTGGC 1320
 Db 1261 AAGCATGAAGTAAATTAATGTTGAGATTAATAAGAAACCTGACTAATGCTGCTGGC 1320

QY 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 Db 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTTGGATTTAGTTCTGACTCAAGAA 1440
 Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTTGGATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAAAGATCCAAATTAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 Db 1441 AAAAGATCCAAATTAATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 Db 1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 Db 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 QY 1621 CTGACTAATGATGTCACCTGCGCAATGATGATGATTAATTCCTCAAGAGAGAGAG 1680
 Db 1621 CTGACTAATGATGTCACCTGCGCAATGATGATGATTAATTCCTCAAGAGAGAGAG 1680
 QY 1681 AGAAGACCTGAAAG 1740
 Db 1681 AGAAGACCTGAAAG 1740
 QY 1741 CAAATGATATCTAG 1800
 Db 1741 CAAATGATATCTAG 1800
 QY 1801 ATTCTGATTCATGAG 1860
 Db 1801 ATTCTGATTCATGAG 1860
 QY 1861 CTTAGTTTGAAG 1920
 Db 1861 CTTAGTTTGAAG 1920
 QY 1921 GCCATGCTAAG 1980
 Db 1921 GCCATGCTAAG 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 RESULT 13
 US-10-144-678A-374
 / Sequence 374, Application US/10144678A
 / Publication No. US20030157089A1
 GENERAL INFORMATION:
 / APPLICANT: Xu, Jiangchun
 / APPLICANT: Dillon, Devin C.
 / APPLICANT: Mitcham, Jennifer L.
 / APPLICANT: Harlocker, Susan L.
 / APPLICANT: Jiang, Yugu
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Fanger, Gary R.
 / APPLICANT: Retter, Marc W.
 / APPLICANT: Stolk, John A.
 / APPLICANT: Day, Craig H.
 / APPLICANT: Vedvick, Thomas S.
 / APPLICANT: Carter, Derrick
 / APPLICANT: Li, Samuel X.
 / APPLICANT: Wang, Aijun
 / APPLICANT: Skeiky, Yasir A. W.
 / APPLICANT: Hepler, William T.
 / APPLICANT: Hural, John
 / APPLICANT: McNeill, Patricia D.

```
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Bassols, Carlota
/ APPLICANT: Roy, Teresa M.
/ APPLICANT: Metanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ CURRENT FILING DATE: 2002-08-12
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-374

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGCTGTTGAGGTTGATTCATGCGCGCTCTCTTCTGTGAAGACCATTTGGTCTC 60
DB      1 ATGCTGTTGAGGTTGATTCATGCGCGCTCTCTTCTGTGAAGACCATTTGGTCTC 60

QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120

QY      121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180

QY      181 ATGAGGCAAGTGTGCGCGCCACTCTCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTTG 240
DB      181 ATGAGGCAAGTGTGCGCGCCACTCTCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTTG 240

QY      241 GGGCGTTCTGGAGACCAAGCAAGCACTGAGTGAAGACACTGAGAAACAAGATGGGCAAG 300
DB      241 GGGCGTTCTGGAGACCAAGCAAGCACTGAGTGAAGACACTGAGAAACAAGATGGGCAAG 300

QY      301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGACAGTGGCGCTTGG 360
DB      301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGACAGTGGCGCTTGG 360

QY      361 GGAAGACTAGCAATGACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGAGAAAGATCTG 420
DB      361 GGAAGACTAGCAATGACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGAGAAAGATCTG 420

QY      421 GACAACTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGCTAG 480
DB      421 GACAACTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGCTAG 480

QY      481 CTGAGGAGCACTGACGTGAAACAAGAAAGACAAGCAAAAGAGAGACTCTCTTCAATCTGGCC 540
DB      481 CTGAGGAGCACTGACGTGAAACAAGAAAGACAAGCAAAAGAGAGACTCTCTTCAATCTGGCC 540

QY      541 TCTGCGCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGAGACAGAGTCAACTTAAT 600
DB      541 TCTGCGCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGAGACAGAGTCAACTTAAT 600

QY      601 GTCTTGAACAACAAAAGAGGACAGCTCTGATAAAGCGGTAAATGGCCAGAAAGATGA 660
DB      601 GTCTTGAACAACAAAAGAGGACAGCTCTGATAAAGCGGTAAATGGCCAGAAAGATGA 660

QY      661 TGTGCGTATATGTTGTGCAATGACACTGATCCAAATATTCAGATGAGTATGA 720
DB      661 TGTGCGTATATGTTGTGCAATGACACTGATCCAAATATTCAGATGAGTATGA 720

QY      721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780
DB      721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780
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QY      781 TATGTCGTGATATGGAATCAAAAAACAAGCATGGCTCACACACTGTACTTGGTGA 840
DB      781 TATGTCGTGATATGGAATCAAAAAACAAGCATGGCTCACACACTGTACTTGGTGA 840

QY      841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900
DB      841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900

QY      901 CTGATATGATATGGAAGAGCTGCTCATCTTGTGTATGTTGTGATACACCAAGTAT 960
DB      901 CTGATATGATATGGAAGAGCTGCTCATCTTGTGTATGTTGTGATACACCAAGTAT 960

QY      961 GTCAAGCTTCTACTGAGCAAAATATATGATCTTCTCAAGATCTATCTGGAACAGAG 1020
DB      961 GTCAAGCTTCTACTGAGCAAAATATATGATCTTCTCAAGATCTATCTGGAACAGAG 1020

QY      1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

QY      1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGAAATCCAGAAACAAACTTAAG 1140
DB      1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGAAATCCAGAAACAAACTTAAG 1140

QY      1141 CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCAGAGAA 1200
DB      1141 CTGACATCAGAGAAAGAGTCAAAAAGTTCAAAAGCAAGTAAATAGCCAGCAGAGAA 1200

QY      1201 ATGTCTCAAGAAACAGAAATAAATAGATAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAAACAGAAATAAATAGATAGTGTGATAGAGAGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAGATATATATGAGGATTAATGAGAAAACTGATCTAATGTGTGCTGCTGTCG 1320
DB      1261 AAGCATGAAGATATATATGAGGATTAATGAGAAAACTGATCTAATGTGTGCTGCTGTCG 1320

QY      1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGAGAGAAACCTGAATAATCAGCAATTT 1380
DB      1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGAGAGAAACCTGAATAATCAGCAATTT 1380

QY      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
DB      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440

QY      1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAGCTGACA 1500
DB      1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAGCTGACA 1500

QY      1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCAAGTGAATAAGCCAGACAGAGCTAAGAAAT 1560
DB      1501 TCAGAGAAAGAGTCAAAAAGCTTGAAGGCAAGTGAATAAGCCAGACAGAGCTAAGAAAT 1560

QY      1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1620
DB      1561 TTTATGCTATGAAAGAAATGAAGAGCAAGAGATCTCATGTGGAATTTCCAGAAAAAC 1620

QY      1621 CTGACTAATGTGTGCCACTGCTGCAATGTGATGATTAATTTCTTCCAAAGAAAGAGC 1680
DB      1621 CTGACTAATGTGTGCCACTGCTGCAATGTGATGATTAATTTCTTCCAAAGAAAGAGC 1680

QY      1681 AGAACACCTGAAAGCAGAGCAATTTCTCTGCACTGAGAAATGAAGAGATCAGAGTGCAG 1740
DB      1681 AGAACACCTGAAAGCAGAGCAATTTCTCTGCACTGAGAAATGAAGAGATCAGAGTGCAG 1740

QY      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAAACAGAACTGGAATATTAACAGATGAG 1800
DB      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAAACAGAACTGGAATATTAACAGATGAG 1800

QY      1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTTGAAAAAATGAATTTCTGAGCTTTCT 1860
DB      1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTTGAAAAAATGAATTTCTGAGCTTTCT 1860
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|||||
Db 1561 TTATGGCTATCGAATAAATGAAGAAGCAGAAAGTACTGATGCGATTCCAGAAAC 1620
QY 1621 CTGACTTAATGGTCCCTGCTGGCAATGGATGATGATTAATCTCTCCAGAAAGAC 1680
Db 1621 CTGACTTAATGGTCCCTGCTGGCAATGGATGATGATTAATCTCTCCAGAAAGAC 1680
QY 1681 AGAACAACCTGAAGCCAGCAATTTCTGCACTGAGATGAAGAATGATCAAGTGCAGAA 1740
Db 1681 AGAACAACCTGAAGCCAGCAATTTCTGCACTGAGATGAAGAATGATCAAGTGCAGAA 1740
QY 1741 CAAAATGATACTCAGAAAGCAATTTTGTAAAGACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAAATGATACTCAGAAAGCAATTTTGTAAAGACAGAACTGGAATATTACAGATGAG 1800
QY 1801 ATTCTGATTCAATGAAGAAAGCAGATGAGATGGTTGAAATTAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCAATGAAGAAAGCAGATGAGATGGTTGAAATTAATTTCTGAGCTTTCT 1860
QY 1861 CTGAGTTGTAAGAAAGAAAGACATCTTGCAATGAATATGATGCTGGCGGAAAGAAAT 1920
Db 1861 CTGAGTTGTAAGAAAGAAAGACATCTTGCAATGAATATGATGCTGGCGGAAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGGCTAGACAAATGAATCATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGGCTAGACAAATGAATCATCAGAGCCAGCTAAAAA 1980
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Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 15
US-10-294-025-374
; Sequence 374, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Skolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-374

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTAAGAACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTAAGAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTC 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACGTC 240

QY 241 GCGGCTTCTGAGACCAAGCACTCTGCTATGAAGACATCAGGAACAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGACCAAGCACTCTGCTATGAAGACATCAGGAACAGATGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGCGGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGCTGAGTGAAGAGGCTTCAATGAGGCCAGGTACAGGTCGTGGAAGATCTG 420
Db 361 GGAAGCTGAGTGAAGAGGCTTCAATGAGGCCAGGTACAGGTCGTGGAAGATCTG 420
QY 421 GACAAGCTCAAGAGCTGCTGCTGGGTAAGTCCCGAGAAAGATCTCATCTCATG 480
Db 421 GACAAGCTCAAGAGCTGCTGCTGGGTAAGTCCCGAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGAACCTGACGTGAACAAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGC 540
Db 481 CTCAGGGAACCTGACGTGAACAAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATTAATTAATCTCTGCTGCAAGACATGCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATTAATTAATCTCTGCTGCAAGACATGCTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGGACAGCTCTGATTAAGCCGTACAAATGCGAGAGATGA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTCTGATTAAGCCGTACAAATGCGAGAGATGA 660
QY 661 TGTGGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCACTAGGCTATCTATATGAAGTAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTGCACTAGGCTATCTATATGAAGTAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGTTGCTGATATGAAATCAAAAAAAGAGCTGCTCACCACTGTTACTGGTGA 840
Db 781 TATGTTGCTGATATGAAATCAAAAAAAGAGCTGCTCACCACTGTTACTGGTGA 840
QY 841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATGAAGAGCTGCTCAATCTTCTGATATGTTGGATGACCAAGTAA 960
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QY 961 GTACGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
Db 961 GTACGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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QY 1141 CTGACATCAGAGGAAGTCAAAAGGTTCAAGGCAAGTGAATAGCCAGCAAGAAA 1200
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QY 1201 ATGTCTCAAGAACAGAAATTAATGAATGATGATAGAGGTTGAAGAAATGAAG 1260
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Db 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCAGAACAGAATTAAAGCTGACA 1500
QY 1501 TCAGAGGAAAGATCAAGAGGCTTTGAGGAGGAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
Db 1501 TCAGAGGAAAGATCAAGAGGCTTTGAGGAGGAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTCCCGAAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGGATTCCCGAAGAAAC 1620
QY 1621 CTGACTAATGTGTCCTGCTGCGCATGTGTATGATGATTAATTCCTCCAGAGAAAGGC 1680
Db 1621 CTGACTAATGTGTCCTGCTGCGCATGTGTATGATGATTAATTCCTCCAGAGAAAGGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGACGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGACGAA 1740
QY 1741 CAAATATGATACTGAGAAAGCAATTTTGTGAGAAACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAATATGATACTGAGAAAGCAATTTTGTGAGAAACAGAACTGGAATATTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGCAGATGAGAGTGTGTAATAATGAATTCGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGCAGATGAGAGTGTGTAATAATGAATTCGAGCTTTCT 1860
QY 1861 CTTAGTTGTAGAAAGAAAGAAAGACATCTTGATGAAATATGTACGTTGCCGGAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAAGAAAGAAAGACATCTTGATGAAATATGTACGTTGCCGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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Job time : 1633.72 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 01:38:47 ; Search time 243.564 Seconds
(without alignments)
4025.047 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atgctgctgctgctgctgctc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 4161431 seqs, 245089505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8322154

Minimum DB seq length: 10

Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database : Published Applications NA.New.*

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5: /cgn2_6/prodata/1/pubpna/PCR_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	37	1.8	201	6	US-10-995-561-30293
C 2	37	1.8	201	6	US-10-995-561-30293
C 3	37	1.8	201	6	US-10-995-561-30411
C 4	37	1.8	201	6	US-10-995-561-30414
C 5	37	1.8	148320	7	US-11-121-086-90
C 6	35	1.8	187986	6	US-10-995-561-13252
C 7	35	1.8	201	6	US-10-995-561-26191
C 8	35	1.8	201	6	US-10-995-561-46434
C 9	35	1.8	600	7	US-10-995-561-73430
C 10	35	1.8	722	6	US-11-123-896-256
C 11	35	1.8	1279	7	US-10-689-742-79
C 12	35	1.8	1279	7	US-11-179-411-31
C 13	35	1.8	1478	6	US-11-175-766-31
C 14	35	1.8	1968	6	US-10-909-125-1744
C 15	35	1.8	2036	6	US-10-131-826A-163
C 16	35	1.8	2120	6	US-10-996-217A-8
C 17	35	1.8	3001	7	US-11-167-856-29
C 18	35	1.8	3001	7	US-11-145-703-153
C 19	35	1.8	14082	6	US-11-145-703-187
C 20	35	1.8	153376	7	US-10-995-561-13445
C 21	35	1.8	171732	7	US-11-121-086-5
C 22	35	1.8	172543	7	US-11-121-086-98
C 23	35	1.8	181172	7	US-11-121-086-6

24	35	1.8	186442	7	US-11-121-086-104	Sequence 104, App
25	35	1.8	191684	7	US-11-121-086-2	Sequence 2, Appl1
C 26	35	1.8	200628	7	US-11-121-086-62	Sequence 62, Appl1
C 27	35	1.8	305312	6	US-10-995-561-13236	Sequence 13236, A
C 28	35	1.8	645179	6	US-10-995-561-13293	Sequence 13293, A
C 29	34	1.7	201	6	US-10-995-561-24366	Sequence 24366, A
C 30	34	1.7	201	6	US-10-995-561-24433	Sequence 24433, A
C 31	34	1.7	201	6	US-10-995-561-24470	Sequence 24470, A
C 32	34	1.7	201	6	US-10-995-561-50304	Sequence 50304, A
C 33	34	1.7	201	6	US-10-995-561-50702	Sequence 50702, A
C 34	34	1.7	201	6	US-10-995-561-50702	Sequence 50702, A
C 35	34	1.7	201	6	US-10-995-561-50871	Sequence 50871, A
C 36	34	1.7	201	6	US-10-995-561-55517	Sequence 55517, A
C 37	34	1.7	398	7	US-11-123-896-262	Sequence 262, App
C 38	34	1.7	470	7	US-11-123-896-88	Sequence 88, Appl1
C 39	34	1.7	517	7	US-11-123-896-467	Sequence 467, App
C 40	34	1.7	551	7	US-11-123-896-358	Sequence 358, App
C 41	34	1.7	602	7	US-11-077-386-7	Sequence 7, Appl1
C 42	34	1.7	778	6	US-10-986-501-38	Sequence 38, Appl1
C 43	34	1.7	958	7	US-11-179-411-5	Sequence 5, Appl1
C 44	34	1.7	958	7	US-11-175-766-5	Sequence 549, App
C 45	34	1.7	1088	6	US-10-131-826A-549	

ALIGNMENTS

RESULT 1
US-10-995-561-30293/c
; Sequence 30293, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30293
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-30293

Query Match
Best Local Similarity 1.8%, Score 37, DB 6, Length 201;
Matches 37, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
Oy 1964 ACCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 145 ACCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 109

RESULT 2
US-10-995-561-30411/c
; Sequence 30411, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30411
; LENGTH: 201
; TYPE: DNA

/ ORGANISM: Homo sapiens
US-10-995-561-30411

Query Match 1.8%; Score 37; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 148 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 112

RESULT 3
US-10-995-561-30414/C
Sequence 30414, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30414
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-30414

Query Match 1.8%; Score 37; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 98 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 62

RESULT 4
US-11-121-086-90
Sequence 90, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:

APPLICANT: POUlsen, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 90
LENGTH: 148220
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-90

Query Match 1.8%; Score 37; DB 7; Length 148220;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 144334 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 144370

RESULT 5
US-10-995-561-13252/C

Sequence 13252, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13252
LENGTH: 187986
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(187986)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13252

Query Match 1.8%; Score 37; DB 6; Length 187986;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 139832 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 139796

RESULT 6
US-10-995-561-26191/C

Sequence 26191, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26191
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-26191

Query Match 1.8%; Score 35; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 152 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 118

RESULT 7
US-10-995-561-46434

Sequence 46434, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702

APPLICANT:	Baker, Kevin P.
APPLICANT:	Berselli, Maureen
APPLICANT:	DeForge, Laura
APPLICANT:	Desnoyers, Luc
APPLICANT:	Filavotti, Ellen
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerisleen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Shemwood, Steven
APPLICANT:	Smith, Victoria
APPLICANT:	Stewart, Timothy A
APPLICANT:	Tunas, Daniel
APPLICANT:	Watnambe, Colin K

Db 603 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 569

Search completed: December 19, 2005, 09:12:35
Job time : 246.564 secs

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APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-163
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Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred.No. 0.00013;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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RESULT 15
US-10-996-217A-8/C
Sequence 8, Application US/10996217A
Publication No. US20050266561A1
GENERAL INFORMATION:
APPLICANT: Revivicor, Inc.
APPLICANT: Wells, Kevin
TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
FILE REFERENCE: 10785.105070 REV 1015 US
CURRENT APPLICATION NUMBER: US/10/996,217A
CURRENT FILING DATE: 2004-11-22
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR FILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 2036
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-996-217A-8
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Query Match 1.8%; Score 35; DB 6; Length 2036;
Best Local Similarity 100.0%; Pred.No. 0.00013;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:08:19 ; Search time 8061.39 Seconds
(without alignment)
11607.702 Million cell updates/sec

Title: US-09-924-400-302

Sequence: 1 atggtggttgaggtggtcattc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82154912

Minimum DB seq length: 10
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_esc11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	24.6	729	5	BU930826 AGENCOURT
2	184	-9.2	521	9	AO204617 HS 3229 B
3	141	7.0	865	2	BF676987 602084215
4	140	7.0	451	1	AI804773
5	137	6.9	289	1	AA53501
6	129	6.5	531	9	AO615477 HS 5144 B
7	117	5.9	621	3	BM763942 K-EST0045
8	117	5.9	633	3	BM763453 K-EST0044
9	117	5.9	817	5	BQ441373 AGENCOURT
10	90	4.5	263	10	AG192933
11	89	4.5	400	9	AO124119 HS 3122 A
12	87	4.3	399	9	AO030111 RPI11-39
13	87	4.3	544	1	AL703938 DKF20686E
14	79	4.0	279	3	BI461255 603206584
15	76	3.8	6098	4	BSM809370
16	74	3.7	505	5	BX492731 Homo sapi
17	73	3.6	385	5	AO63365 CIT-HSP-2
18	73	3.2	282	5	BU584009 2275475H1
19	64	3.2	381	7	CR747857 CR747857
20	59	2.9	707	10	AG045796 Pan trogl
21	57	2.9	607	9	B48260 RPI11-6K4
22	52	2.6	380	2	BF329652 RC6-BN027

23	50	2.5	592	9	AQ372700 RPI11-14
24	49	2.5	493	10	AG193231
25	49	2.5	495	9	AO469831 CITBI-E1-
26	49	2.5	557	9	AO469663 CITBI-E1-
27	49	2.5	667	10	AG156382
28	49	2.5	697	9	AO030113 RPI11-39
29	47	2.4	187	2	BE069869 CM1-RN039
30	46	2.3	351	7	CV383025 QV0-FN018
31	46	2.3	400	9	AO057106 CIT-HSP-2
32	45	2.2	218	5	BU584404 3967290H1
33	45	2.2	259	5	BU584020 4133307H1
34	45	2.2	338	5	BU584405 3967290F6
35	45	2.2	423	5	BU584403 3967290F6
36	45	2.2	874	6	CD358418 AGENCOURT
37	45	2.2	894	2	BF675049 602136643
38	45	2.2	5483	4	BC063888 Homo sapi
39	44	2.2	460	9	AO360298 HS 5035 A
40	41	2.1	476	9	AO392059 CITBI-E1-
41	41	2.1	710	10	AG165908 Pan trogl
42	41	2.1	770	5	BU611819 UI-M-F10-
43	40	2.0	184	1	AW302924 XR8607.x
44	40	2.0	199	1	AW302925 XR8608.x
45	40	2.0	224	1	AI344928 TB01604.x

ALIGNMENTS

RESULT 1
BU930826
LOCUS
DEFINITION
AGENCOURT_10425351 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:668956
5', mRNA sequence.
ACCESSION
BU930826.1 GI:24119645
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 729)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: BLCM2943 row: 0 column: 04
High quality sequence stop: 555.
Location/Qualifiers
1. 729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:668956"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccgcggcc); Site 2: SfiI
(ggccatcagcc); 5' and 3' adaptor were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

ORIGIN and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 24.6%; Score 492; DB 5; Length 729;
Best Local Similarity 100.0%; Pred. No. 4,2e-229;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 635 AGGCGGTACAAATCCAGGAAGATGATGCGGTATGTCGGAACATGGCAGTATC 694
DB 89 AGGCGGTACAAATCCAGGAAGATGATGCGGTATGTCGGAACATGGCAGTATC 148
QY 695 CAAATATCCAGATGATGATGAAATACCACTGCTGCACTATCTATTAAGAGATA 754
DB 149 CAAATATCCAGATGATGATGAAATACCACTGCTGCACTATCTATTAAGAGATA 208
QY 755 AATTATGCGCAAGACCTGCTCTTATATGTCGTATGATCGAATCAAAAACAGCATG 814
DB 209 AATTATGCGCAAGACCTGCTCTTATATGTCGTATGATCGAATCAAAAACAGCATG 268
QY 815 GCCTCACACACTGTTACTGTTGATGATGAGCAAAAACAGCAAGTCGTAATTTTAA 874
DB 269 GCCTCACACACTGTTACTGTTGATGATGAGCAAAAACAGCAAGTCGTAATTTTAA 328
QY 875 TCAAGAAAAAGCAATTTAATGCACTGATGATGAGAGACCTGCTCATCTTG 934
DB 329 TCAAGAAAAAGCAATTTAATGCACTGATGATGAGAGACCTGCTCATCTTG 388
QY 935 CTGTATGTTGATGATGAGCAAGTATGTCAGCTTCTTACTTGAGCAAAATTTGATGAT 994
DB 389 CTGTATGTTGATGATGAGCAAGTATGTCAGCTTCTTACTTGAGCAAAATTTGATGAT 448
QY 995 CTCTCAAGATCTATCTGAGCAGACGCGCAGAGATGTCGTTTCTAGCATCATCATG 1054
DB 449 CTCTCAAGATCTATCTGAGCAGACGCGCAGAGATGTCGTTTCTAGCATCATCATG 508
QY 1055 TAATTGCGAGTACTTCTGACTACAAAGAAAAAGATGCTAAATCTCTTGAAA 1114
DB 509 TAATTGCGAGTACTTCTGACTACAAAGAAAAAGATGCTAAATCTCTTGAAA 568
QY 1115 ACAGCATTCAG 1126
DB 569 ACAGCATTCAG 580

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RESULT 2
LOCUS AQ024617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS 3229, B1 G12, T7 CIT Approved Human Genomic Sperm Library D Homo

sapiens genomic clone Plate=3229 Col=23 Row=N, genomic survey
sequence.
ACCESSION AQ024617
VERSION AQ024617.1 GI:3615187
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 Row: N Column: 23
Class: BAC ends
High quality sequence stop: 521.
Location/Qualifiers
1..521
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3229 Col=23 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match 9.2%; Score 184; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 3e-78;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1550 AGCTGAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTATGTCGAT 1609
DB 231 AGCTGAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTATGTCGAT 290
QY 1610 TCCGAAAACTGACTATGTTGTCGACCTGCGCAATGTCGATGATTAATTCCTC 1669
DB 291 TCCGAAAACTGACTATGTTGTCGACCTGCGCAATGTCGATGATTAATTCCTC 350
QY 1670 CAAGAAAGCAGAAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAAGATATC 1729
DB 351 CAAGAAAGCAGAAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAAGATATC 410
QY 1730 ACAG 1733
DB 411 ACAG 414

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RESULT 3
LOCUS BF676987 865 bp mRNA linear EST 21-DEC-2000
DEFINITION 602084215P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',

mRNA sequence.
ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers
1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"

FEATURES

source

/clone lib="NIH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccgcccgc); Site_2: SfiI
(ggccatcagccc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTGAGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCGCCGACGANG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Query Match 7.0%; Score 141; DB 2; Length 865;
Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 ACTGCTCATCTTCTGCTATGTTGTGATCAGCAAGATAGTACCTTCTACTTGG 978
DB 353 ACTGCTCATCTTCTGCTATGTTGTGATCAGCAAGATAGTACCTTCTACTTGG 412
QY 979 CAAATATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCCAGAGATGCTTT 1038
DB 413 CAAATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCCAGAGATGCTTT 472
QY 1039 TCTAGTCATCATCATTAATT 1059
DB 473 TCTAGTCATCATCATTAATT 493

RESULT 4
A1804733 451 bp mRNA linear EST 07-MAR-2000
LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
DEFINITION mRNA sequence.

ACCESSION A1804733
VERSION A1804733.1 GI:5370205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 451)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
www-bio.lnlnl.gov/bbrp/image/image.html
Insert length: 543 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
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1..451
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2253677"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone lib="NCI CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and as
circles were used in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 7.0%; Score 140; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 AGACTGCTCATCTTCTGCTATGTTGTGATCAGCAAGATAGTACCTTCTACTT 975
DB 47 AGACTGCTCATCTTCTGCTATGTTGTGATCAGCAAGATAGTACCTTCTACTT 106
QY 976 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCCAGAGATGCT 1035
DB 107 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCCAGAGATGCT 166
QY 1036 GTTCTAGTCATCATCATGT 1055
DB 167 GTTCTAGTCATCATCATGT 186

RESULT 5
AA533501 289 bp mRNA linear EST 21-AUG-1997
LOCUS nj96a04.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000302,
DEFINITION mRNA sequence.

ACCESSION AA533501
VERSION AA533501.1 GI:2277597
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 289)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.,
Chunhui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
www-bio.lnlnl.gov/bbrp/image/image.html
Insert length: 217 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham.

FEATURES
source
1..289
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1000302"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/clone lib="NCI CGAP_Pr11"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."

ORIGIN

Query Match 6.9%; Score 137; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 3.1e-55;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1743 AATGATCTCAGAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAGAT 1802
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 DB 9 AATGATCTCAGAGCAATTTTGTGAAGACAGAACTGTGAATTTACAGATGAGAT 68
 |||||

QY 1803 TCTGATTCATGAGAAAGAGATAGAGTGTGTAAGAAATGAATTCGAGCTTCTCT 1862
 |||||
 DB 69 TCTGATTCATGAGAAAGAGATAGAGTGTGTAAGAAATGAATTCGAGCTTCTCT 128
 |||||

QY 1863 TAGTGTGAAGAAAGAAA 1879
 |||||
 DB 129 TAGTGTGAAGAAAGAAA 145
 |||||

RESULT 6
 A0615477 531 bp DNA linear GSS 15-JUN-1999
 LOCUS HS_5144.B1.G01.T7A.RPCI-11.Human Male BAC library Homo sapiens
 DEFINITION genomic clone Plate=720 Col=1 Row=N, genomic survey sequence.
 ACCESSION A0615477 GI:5076753
 VERSION A0615477.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS Mahitras,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahitras GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pletcher de Jong
 (pletched@u.washington.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.u.washington.edu/ordering/bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htec.washington.edu
 Plate: 720 row: N column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 531.

FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=720 Col=1 Row=N"
 /sex="male"
 /clone_1lb="RPCI-11 Human Male BAC library"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

ORIGIN
 Query Match 6.5%; Score 129; DB 9; Length 531;
 Best Local Similarity 100.0%; Pred. No. 2.6e-51;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CATGCACTGATCCAAATTTCCAGATGATGAAATACCACTTCGACTACGCTATC 741
 |||||
 DB 117 CATGCACTGATCCAAATTTCCAGATGATGAAATACCACTTCGACTACGCTATC 176
 |||||

QY 742 TATATGAAGATTAATTAATGCGCAAGCACTGCTTATATGATGCTGATATCA 801
 |||||
 DB 177 TATATGAAGATTAATTAATGCGCAAGCACTGCTTATATGATGCTGATATCA 236
 |||||

QY 802 AAAAACAG 810
 |||||
 DB 237 AAAAACAG 245
 |||||

RESULT 7
 BM763942 621 bp mRNA linear EST 04-MAR-2002
 LOCUS K-EST0045367.S13KMS5.Homo sapiens cDNA clone S13KMS5-25-A11.5',
 DEFINITION mRNA sequence.
 ACCESSION BM763942 GI:19093557
 VERSION BM763942.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 621)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsun@mail.kribb.re.kr
 High quality sequence stop: 621.

FEATURES
 source
 1..621
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-25-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_1lb="S13KMS5"
 /note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI. The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoRI site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dT-tailed vector. The dT-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10P by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN
 Query Match 5.9%; Score 117; DB 3; Length 621;
 Best Local Similarity 99.1%; Pred. No. 2e-45;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 CAGCAAAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAA 569
Db 1 CAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAA 60
QY 570 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAGAGACACTCT 629
Db 61 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAGAGACACTCT 120
QY 630 GATTAAGCCCGTACAAATGCCAGAGATGAATGCGTTAATGTTCTGGACATGCGAC 689
Db 121 GACAAAGCCGTCATATGCGAGAAATGATGCGTTAATGTTCTGGACATGCGAC 180
QY 690 TGATCCAAATATTCAGATGATGAAATACACTCT 728
Db 181 TGATCCAAATATTCAGATGATGAAATACACTCT 219

RESULT 8
BM763453 633 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM763453
VERSION BM763453.1 GI:19093068
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 633)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
High quality sequence stop: 633.
Location/Qualifiers
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-16-A11"
/issue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deapped with tobacco acid
pyrophosphatase (TAP). The deapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

ORIGIN

Query Match 5.9%; Score 117; DB 3; Length 633;
Best Local Similarity 99.1%; Pred. No. 2e-45;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 510 CAGCAAAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAA 569
Db 1 CAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTCAGAACTAGTAA 60
QY 570 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAGAGACACTCT 629
Db 61 ACTCGTGTGACAGACGATGTCACTTAATGTCTTGAACAACAAAGAGACACTCT 120
QY 630 GATTAAGCCCGTACAAATGCCAGAGATGAATGCGTTAATGTTCTGGACATGCGAC 689
Db 121 GACAAAGCCGTCATATGCGAGAAATGATGCGTTAATGTTCTGGACATGCGAC 180
QY 690 TGATCCAAATATTCAGATGATGAAATACACTCT 728
Db 181 TGATCCAAATATTCAGATGATGAAATACACTCT 219

RESULT 9
BQ441373 817 bp mRNA linear EST 24-MAY-2002
LOCUS AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
DEFINITION 5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA library Preparation: CLONTECH Laboratories, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1CM2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6103855"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccctcgagc); Site 2: SfiI (ggccatcatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATGTGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCGCCACATG-dT (30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN
Query Match 5.9%; Score 117; DB 5; Length 817;
Best Local Similarity 100.0%; Pred. No. 2e-45;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1408 AGAATTGGCAATTAAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTCTGAA 1467
    |||||
Db 319 AGAATTGGCAATTAAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTCTGAA 378
    |||||
Oy 1468 AACAGCAACCCGAAACAGACTTAAAGCTGACATCAGAGAAAGTCCAGAAAGGCTT 1524
    |||||
Db 379 AACAGCAACCCGAAACAGACTTAAAGCTGACATCAGAGAAAGTCCAGAAAGGCTT 435
    |||||

RESULT 10
AG192933 263 bp DNA linear GSS 06-MAR-2004
LOCUS AG192933
DEFINITION Pan troglodytes DNA, clone: RP43-069L23.TU, genomic survey
sequence.
ACCESSION AG192933
VERSION AG192933.1 GI:45225109
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.U.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 263)
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.U.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seo Park, Korea Research Institute of
BioScience and Biotechnology (KRIBS), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 263
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-069L23.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match 4.5%; Score 90; DB 10; Length 263;
Best Local Similarity 100.0%; Pred.No.3.2e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1739 AACCAATGATGATCTGAGAGCAATTTTGGAGAGACAGAACTGGAATATTACAGATG 1798
    |||||
Db 90 AACCAATGATGATCTGAGAGCAATTTTGGAGAGACAGAACTGGAATATTACAGATG 31
    |||||
Oy 1799 AGATTCTGATTCAATGAAGAAAGACAGATAG 1828
    |||||
Db 30 AGATTCTGATTCAATGAAGAAAGACAGATAG 1
    |||||

RESULT 11
AO124119 400 bp DNA linear GSS 22-SEP-1998
LOCUS AO124119

```

```

DEFINITION HS 3122 A1 C07 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey
sequence.
ACCESSION AO124119
VERSION AO124119.1 GI:3501285
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 Row: E Column: 13
Classes: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3122 Col=13 Row=E"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/cnote="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
R-Col1 DH10B"

ORIGIN
Query Match 4.5%; Score 89; DB 9; Length 400;
Best Local Similarity 100.0%; Pred.No.1e-31;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 635 AGCGGTACATGCCAGAGAGATGATGCGTTATGTTGCTGGAACATGCACATGATC 694
    |||||
Db 237 AGCGGTACATGCCAGAGAGATGATGCGTTATGTTGCTGGAACATGCACATGATC 296
    |||||
Oy 695 CAATATTCAGATGATGATGGAATATAC 723
    |||||
Db 297 CAATATTCAGATGATGGAATATAC 325
    |||||

RESULT 12
AO030111 399 bp DNA linear GSS 14-APR-1999
LOCUS AO030111
DEFINITION RPTC11-39K18.TP RPTC-11 Homo sapiens genomic clone RPTC-11-39K18,
genomic survey sequence.
ACCESSION AO030111
VERSION AO030111.1 GI:3274075
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
AUTHORS Adams,M.D., Rounisley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)

```

JOURNAL COMMENT

Unpublished (1998)
Other GSSs: RPC111-39K18.TV
Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: madam@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (inforesgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Sp6
Clase: BAC ends.

FEATURES

Location/Qualifiers

1..399

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7514849"

/db_xref="taxon:9606"

/clone="RPC1-11-39K18"

/sex="Male"

/cell_type="Lymphocytes"

/clone_11b="RPC1-11"

/note="Vector: pBACE3.6; Site 1: EcoRI; site_2: EcoRI; PC111 Human Male BAC Library"

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 9.6e-31;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGTGAAGCAACAAATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTA 1791

DB 102 AGTGAAGCAACAAATGATCTCAGAGCAATTTTGTGAAGACAGAACTGGAATATTA 43

QY 1792 CACGATGAGATTTCTGATTGATGAGAA 1818

DB 42 CACGATGAGATTTCTGATTGATGAGAA 16

RESULT 13

LOCUS

AL703938 544 bp mRNA linear EST 04-SEP-2003

DEFINITION DKF2p686E1728_r1.686 (synonym: h1cc3) Homo sapiens cDNA clone

AL703938 DKF2p686E1728_5', mRNA sequence.

AL703938 AL703938.1 GI:19687293

EST.

KEYWORDS

SOURCE

ORGANISM

EST.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: MIPS

MIPS

Ingsrieder Landstr.1, D-85764 Neuberg, Germany

This is the 5' sequence of the clone insert.

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

sequenced by MedGenomix (Martinsried/Germany) within the cDNA

sequencing consortium of the German Genome Project. No 31 sequence

available.

FEATURES

source

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..544

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKF2p686E1728"

/dev_stage="adult"

/lab_host="DH10B"

/clone_11b="686 (synonym: h1cc3)"

/note="Vector: pTriblax2; Site_1: SfiI; Site_2: SfiIb;

cDNA-collection"

ORIGIN

Query Match 4.3%; Score 87; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 9.8e-31;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAAGAAAACAGATGCTAAATCTTCTGAAAACAGCAATCCAGACAGCTTAAG 1140

DB 432 AAAGAAAACAGATGCTAAATCTTCTGAAAACAGCAATCCAGACAGCTTAAG 491

QY 1141 CTGACATCAGAGAAAGTCACAAAG 1167

DB 492 CTGACATCAGAGAAAGTCACAAAG 518

RESULT 14

LOCUS

BI461255 279 bp mRNA linear EST 21-ANG-2001

DEFINITION 603206584P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364_5',

BI461255 mRNA sequence.

BI461255 BI461255.1 GI:15251911

EST.

KEYWORDS

SOURCE

ORGANISM

EST.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palokvits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki

Toshinuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L14M11687 row: 9 column: 21

High quality sequence stop: 236.

FEATURES

source

1..279

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5272364"

/lab_host="DH10B"

/clone_11b="NIH MGC 97"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average

insert size 2.2 kb and normalized to RGT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

ORIGIN (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

Search completed: December 19, 2005, 20:05:01
Job time : 8066.39 secs

Query Match 4.0%; Score 79; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 7.8e-27;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGGTTCATGATTCATGCGGCGCTCTTCGTGAAGAGCCATTGGCTTC 60
|||||
DB 84 ATGGTGGTTCATGATTCATGCGGCGCTCTTCGTGAAGAGCCATTGGCTTC 25
|||||

OY 61 AGGAGCAAGATGGGCAAGT 79
|||||
DB 24 AGGAGCAAGATGGGCAAGT 6
|||||

RESULT 15 HSM809270 6098 bp mRNA linear HTC 20-JAN-2005

LOCUS Homo sapiens mRNA; cDNA DKFZp686J0529 (from clone DKFZp686J0529).
DEFINITION BX649118

ACCESSION BX649118.1 GI:34368290
VERSION
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM

REFERENCE 1 (bases 1 to 6098)
AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Well, B., Amid, C., Oeanger, A.,
Fobo, G., Han, M., and Wiemann, S.

CONSRMT The German cDNA Consortium
TITLE Direct Submission

JOURNAL Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.

This clone (DKFZp686J0529) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686J0529

Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers
1..6098

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp686J0529Q"
/db_xref="taxon:9606"
/clone="DKFZp686J0529"
/issue_type="testis"
/clone_lib="686 (synonym: hlc03). Vector pSport1_Sfi; host
DH10B; sites SfiI + SfiI"
/dev_stage="adult"
/note="putative transcript"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 986 TTGATGTATCTTCTCAAGATCTATCTGACAGCGGCCAGAGATGCTGTTCTAGTC 1045
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DB 1426 TTGATGTATCTTCTCAAGATCTATCTGACAGCGGCCAGAGATGCTGTTCTAGTC 1485
|||||

OY 1046 ATCATCATGTAATTG 1061
|||||
DB 1486 ATCATCATGTAATTG 1501
|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:28:25 ; Search time 10112.4 Seconds
(without alignments)
11242.353 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atggtgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sbs: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_hcg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	100.0	2000	6	BD242272 Compounds
2	2000	100.0	2000	6	AR278479 Sequence
3	2000	100.0	2000	6	AR350943 Sequence
4	2000	100.0	2000	6	AR367175 Sequence
5	2000	100.0	2000	6	AR371071 Sequence
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ALIGNMENTS

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DEFINITION	BD242272				
ACCESSION	BD242272.1	GI:33052042			
VERSION	JP 2002520054-A/359.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumalia; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 2000)				
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2002520054-A 359 09-JUL-2002;				
COMMENT	CORIXA CORP				
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15-JAN-1999 US	09/232880,15-JAN-1999 US 09/232149 PR				
09-APR-1999 US	09/288946				
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JIANGCHUN XU,	PI				
PI	JENNIFER LYNN MITCHAM				
PC	C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,				
PC	C12N5/10,				
PC	C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,				
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CC	and methods				
CC	for their use				
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RESULT 2
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LOCUS AR278479 2000 bp DNA linear PAT 10-Apr-2003
DEFINITION Sequence 374 from patent US 6512094.
ACCESSION AR278479
VERSION AR278479.1 GI:29712725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, O.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 374 28-JAN-2003;
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LOCUS AR350943 2000 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 302 from patent US 6586570.
ACCESSION AR350943
VERSION AR350943.1 GI:33752583
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M. and Misher,L.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6586570-A 302 01-JUL-2003;
Corixa Corporation; Seattle, WA
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AR367175 2000 bp DNA linear PAT 12-SEP-2003
LOCUS AR367175 Sequence 374 from patent US 6329505.
DEFINITION AR367175
ACCESSION AR367175 GI:34600150
VERSION AR367175.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugi,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 374 11-DEC-2001;
FEATURES Corixa Corporation; Seattle, WA
source 1..2000
location/Qualifiers
/organism="unknown"
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RESULT 5
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 DEFINITION AR371071
 ACCESSION AR371071
 VERSION AR371071.1 GI:34607964
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 UNCLASSIFIED.
 1 (bases 1 to 2000)
 REFERENCES
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocke,S.L. and Yugi,J.
 TITLE Prostate specific fusion protein compositions
 JOURNAL Patent: US 6395278-A 374 28-MAY-2002;
 Corixa Corporation; Seattle, WA

FEATURES
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 6
AR400211 2000 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 374 from patent US 6620922.
DEFINITION AR400211
ACCESSION AR400211
VERSION AR400211.1 GI:40143375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kalos M.D., Fanger G.R., Retter M.W., Stolk J.A., Day C.H.,
Vedrick T.S., Carter D., Li S.X., Wang A., Skelley Y.A.W.,
Hepler W.T. and Henderson R.A.
TITLES Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 374 16-SEP-2003;
FEATURES
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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AR405478
LOCUS AR405478 2000 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 374 from patent US 6630305.
ACCESSION AR405478
VERSION AR405478.1 GI:40154315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y., Kadosh M.D., Fanger G.R., Retter M.W., Stolk J.A., Day C.H., Vedrick T.S., Carter D., Li S.X., Wang A., Skeiky Y.A.W., Hepler W.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 374 07-OCT-2003;
CORIXA Corporation; Seattle, WA;
WOX;
FEATURES
source location/Qualifiers
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/organism="unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
AR433319 2000 bp DNA linear PAT 18-DEC-2003
LOCUS AR433319
DEFINITION Sequence 302 from patent US 6656480.
ACCESSION AR433319
VERSION AR433319.1 GI:40196101
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Rether, M.W. and Dillon, D.C.
TITLES Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6656480-A 302 02-DEC-2003;
Corixa Corporation; Seattle, WA
FEATURES
source 1..2000
/organism="unknown"
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR563858 2000 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 374 from patent US 6759515.
ACCESSION AR563858
VERSION AR563858.1 GI:53978909
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,

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DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
ARS88844
LOCUS ARS88844
DEFINITION Sequence 374 from patent US 6800746.
ACCESSION ARS88844
VERSION ARS88844.1 GI:56635741
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 Unclassified.
AUTHORS Xu, D., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kales, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Veddyck, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6800746-A 374 05-OCT-2004;
FEATURES Corixa Corporation; Seattle, WA
source 1. .2000
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Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
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ACCESSION	AR605664					
VERSION	AR605664.1		GI:56657328			
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2000)					
AUTHORS	Xu J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Reiter, M.W., Stolik, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, W.T. and Henderson, R.A.					
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer					
JOURNAL	Patent: US 6818751-A 374.16-NOV-2004;					
FEATURES	Corixa Corporation; Seattle, WA					
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 DEFINITION Sequence 302 from patent US 6828431.
 ACCESSION AR615063
 VERSION AR615063.1 GI:56671467
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2000)
 AUTHORS Prudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
 Reiter,M.W., Wang,A., Skeiky,Y.A.W. and Harlocke,S.L.
 TITLE Compositions and methods for the therapy and diagnosis of breast
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 JOURNAL Patent: US 6828431-A 302 07-DEC-2004;
 Corixa Corporation; Seattle, WA
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ACCESSION AR642105
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ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2000)
AUTHORS  Frudakis,T.N., Smith,J.M., Reed,S.G., Misner,L.E., Retter,M.W. and
          Dillon,D.C.
TITLE     Compositions and methods for the treatment and diagnosis of breast
          cancer
JOURNAL   Patent: US 6861506-A 302 01-MAR-2005;
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 ACCESSION AR657003
 VERSION AR657003.1 GI:67590123
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2000)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kados,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Veddy,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepier,M.T. and Henderson,R.A.
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
 AUTHORS Compositions and methods for therapy and diagnosis of prostate
 TITLE Cancer
 JOURNAL Patent: WO 0125272-A 374 12-APR-2001;
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GenCore version 5.1.6
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Post-processing: Minimum Match 0%

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KW Human; breast tumour-specific antigen; cytostatic; vaccine;
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PN WO200061753-A2.
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XX PR
XX 23-MAR-2000; 2000US-00534825.
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XX WPI; 2000-628403/60.
XX F-PSDB; AAB28629.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
XX tumor protein used for inhibiting the development of cancer, especially
XX breast cancer, and monitoring cancer progression in a patient.
XX
XX Claim 4; Page 177-178; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
XX and methods for the treatment and diagnosis of breast cancer. Nucleotide
XX sequences that are preferentially expressed in breast tumor tissue, and
XX the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTTGAGTTTATTCATGCGGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
DB 1 ATGTGGTTGAGTTTATTCATGCGGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAACAACAAGACTCTGTATGAAGACCTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAACAACAAGACTCTGTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGGAAGTGGGCGGCACTGCTCCCTGCTGAGAGGAGAGTGGCAAGCAACGTC 240
DB 181 ATGGGGAAGTGGGCGGCACTGCTCCCTGCTGAGAGGAGAGTGGCAAGCAACGTC 240
QY 241 GGGGCTTCTGAGAACCAACAAGACTCTGTATGAAGACCTCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGAACCAACAAGACTCTGTATGAAGACCTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGCCTTCAATGAGGCCAAGTACACGTCGCTGAGAAAGTCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTCAATGAGGCCAAGTACACGTCGCTGAGAAAGTCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATCGCATG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATCGCATG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGCAGAGATGTCATTAT 600
DB 541 TCTGCAATGGGAATTCAGAGTAAAGTCTCTGCTGAGCAGAGATGTCATTAT 600
QY 601 GTCTTGAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGGTACATGCCAGAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGCAAGCTCTGATTAAGGCGGTACATGCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGTGGAACATGACCTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGACCTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACCTACGCTATCTATATGAAGATTAATTAAGGCCAAAGCACTGCTTAA 780
DB 721 ACCACTCTGACCTACGCTATCTATATGAAGATTAATTAAGGCCAAAGCACTGCTTAA 780
QY 781 TATGTGCTGATATCGAATCAAAAGCAAGCATGGCTCAGACCACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAGCAAGCATGGCTCAGACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900

DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGACGTCTCATCTGCTGATGTGGATACAGCAATGA 960
DB 901 CTGATATGATATGGAAGACGTCTCATCTGCTGATGTGGATACAGCAATGA 960
QY 961 GTCACTTCTTCACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTCACTTCTTCACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTTACATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTTACATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATCTAAAAATCTCTGTAACCAACCCAGAACAAACTTTAAG 1140
DB 1081 AAGAAAAACAGATCTAAAAATCTCTGTAACCAACCCAGAACAAACTTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAGTTCAAAAGCAAGTAATAGCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAGTTCAAAAGCAAGTAATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGGTGGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAAGATGTGATAGAGGTGGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATTAAGTGGATTACTGAGAAACCTGACTAATGTGTCACTGGC 1320
DB 1261 AAGCATGAAGTAATTAAGTGGATTACTGAGAAACCTGACTAATGTGTCACTGGC 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGACAGAACACTGAAATAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGACAGAACACTGAAATAGCAATTT 1380
QY 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAACCCAGAACCAAGACTTAAGCTGAGA 1500
DB 1441 AAACAGATGCCAAATTAATCTTCTGAAACCCAGAACCAAGACTTAAGCTGAGA 1500
QY 1501 TCAGAGGAAGTGTCAAAAAGCTTGAAGGCAAGTGAATAATGGCCAGAGCTAGAAT 1560
DB 1501 TCAGAGGAAGTGTCAAAAAGCTTGAAGGCAAGTGAATAATGGCCAGAGCTAGAAT 1560
QY 1561 TTTATGCTATGGAAGAAATGAAGAGCAAGAGTACTCATGTGGAATTCAGAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGAGCAAGAGTACTCATGTGGAATTCAGAAAC 1620
QY 1621 CTGACTTAATGTGCACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAAAGC 1680
DB 1621 CTGACTTAATGTGCACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAAAGC 1680
QY 1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAAGATATCAAGTACGA 1740
DB 1681 AGAACACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAAGATATCAAGTACGA 1740
QY 1741 CAAATATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB 1741 CAAATATGATCTCAGAAAGATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCAGAGAAAGAGAGATGAAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
DB 1801 ATTCTGATTCAGAGAAAGAGAGATGAAGGTGTTGAAAAATGAATTTGAGCTTTCT 1860
QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAATAATGATAGTTGGGGAAGAAAT 1920
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAATAATGATAGTTGGGGAAGAAAT 1920
QY 1921 GGCATGCTTAAGACTGAGAGTGAACAATGAAGATCAGAGCCAGCTAATAAAAA 1980
DB 1921 GGCATGCTTAAGACTGAGAGTGAACAATGAAGATCAGAGCCAGCTAATAAAAA 1980

QY 1981 AAAAAAAAAAAAAAAAAA 2000
1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
AAH93715 standard; cDNA; 2000 BP.
ID AAH93715
XX AAH93715;
AC
XX
XX
DT 04-OCT-2001 (first entry)
XX
XX Human prostate-specific cDNA sequence B305D splice variant #9.
DE
XX Human prostate cancer; prostate-specific; diagnosis; vaccine;
KM cytolethal; gene therapy; metastasis; ss.
XX
XX Homo sapiens.
OS
XX MO200151633-A2.
XX
XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001MO-US001574.
PF
XX 14-JAN-2000; 2000US-00483672.
PR
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM,
PI Wang A, Mesgher MJ;
XX
XX MPI; 2001-425873/45.
DR
XX
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
PT
XX
XX
XX Claim 1; Page 347-348; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH0115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
CC
CC
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX

Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTTGTAAGAAGCATTTGGTCTC 60
1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTTGTAAGAAGCATTTGGTCTC 60
Db 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTTGTAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGATGAAACATCAGAGGACAG 180

Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGATGAAACATCAGAGGACAG 180
QY 181 ATGGGCAAGTGGTGGCGCCATGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
181 ATGGGCAAGTGGTGGCGCCATGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
Db 241 GGGGCTTCTGAGACCAAGACGACTCTGCTATGAAAGCACTGAGAAAGATGGGCAAG 300
241 GGGGCTTCTGAGACCAAGACGACTCTGCTATGAAAGCACTGAGAAAGATGGGCAAG 300
Db 241 GGGGCTTCTGAGACCAAGACGACTCTGCTATGAAAGCACTGAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCTGACCTGCTTCCCTGCTGCAAGGAGAGGCAAGGAGGCGCTTGG 360
301 TGGTGTGCTGACCTGCTTCCCTGCTGCAAGGAGAGGCAAGGAGGCGCTTGG 360
Db 361 GGAAGCTAGATGACAGTGCCTTCAATGAGAGCCAGGTACAGTCCGTGGAAGATCTG 420
361 GGAAGCTAGATGACAGTGCCTTCAATGAGAGCCAGGTACAGTCCGTGGAAGATCTG 420
Db 421 GACAACTTCAAGAGCTGCTGCTGGGCTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
421 GACAACTTCAAGAGCTGCTGCTGGGCTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
QY 481 CTCAGGGAACCTGAGCTGGAACAAGAGCAAGCAAAAGAGAGGATCTCATGCTCAG 540
481 CTCAGGGAACCTGAGCTGGAACAAGAGCAAGCAAAAGAGAGGATCTCATGCTCAG 540
Db 541 TCTGCCAATGGGAATTCAGAGATGATTAATCTCTGCTGGAAGACAGATGCACTTAAT 600
541 TCTGCCAATGGGAATTCAGAGATGATTAATCTCTGCTGGAAGACAGATGCACTTAAT 600
QY 601 GTTCCTTGACACAAAGAGAGAGAGCTGATTAAGGCGGTACATGCAAGAAATGAA 660
601 GTTCCTTGACACAAAGAGAGAGAGCTGATTAAGGCGGTACATGCAAGAAATGAA 660
Db 601 GTTCCTTGACACAAAGAGAGAGAGCTGATTAAGGCGGTACATGCAAGAAATGAA 660
QY 661 TGTGGTTAATGTGTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
661 TGTGGTTAATGTGTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGTTAATGTGTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACATGAGCTATCTATATGAAAGATTAATGAGCCAAAGCATGCTCTTA 780
721 ACCACTCTGACATGAGCTATCTATATGAAAGATTAATGAGCCAAAGCATGCTCTTA 780
Db 721 ACCACTCTGACATGAGCTATCTATATGAAAGATTAATGAGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAAAGAGATGCGCTCAACCACTGTTACTTGGTGA 840
781 TATGTGCTGATATGCAATCAAAAAAGAGATGCGCTCAACCACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAAGAGATGCGCTCAACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAACAGAGAGTGGTGAATTTAATCAAGAAAAGCGAATTAATGCA 900
841 CATGAGCAAAACAGAGAGTGGTGAATTTAATCAAGAAAAGCGAATTAATGCA 900
Db 841 CATGAGCAAAACAGAGAGTGGTGAATTTAATCAAGAAAAGCGAATTAATGCA 900
QY 901 CTGAGATAGATAGAAAGAGCTGCTCATATCTGCTGATGTGTGATCAGCAAGTATA 960
901 CTGAGATAGATAGAAAGAGCTGCTCATATCTGCTGATGTGTGATCAGCAAGTATA 960
Db 901 CTGAGATAGATAGAAAGAGCTGCTCATATCTGCTGATGTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GGCAGAGATAGCTGTTCTGATCATCATCATGTAATTTGCAAGTACTTTCTGACTAG 1080
1021 GGCAGAGATAGCTGTTCTGATCATCATCATGTAATTTGCAAGTACTTTCTGACTAG 1080
Db 1021 GGCAGAGATAGCTGTTCTGATCATCATCATGTAATTTGCAAGTACTTTCTGACTAG 1080
QY 1081 AAAAGAAAAAGATGCTAAATAATCTCTTCTGAAAAAGCAATCCAGAACAGCTTAAAG 1140
1081 AAAAGAAAAAGATGCTAAATAATCTCTTCTGAAAAAGCAATCCAGAACAGCTTAAAG 1140
Db 1081 AAAAGAAAAAGATGCTAAATAATCTCTTCTGAAAAAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCAAAAGGTTCAAAAGGATGAAATAGCCAGCAAGAGAA 1200
1141 CTGACATCAGAGAGAGATCAAAAGGTTCAAAAGGATGAAATAGCCAGCAAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCAAAAGGTTCAAAAGGATGAAATAGCCAGCAAGAGAA 1200
QY 1201 ATGTCGAAAGACCAAGAAATTAATAGATGAGATGAGAGGTTGAAGAAATGAAG 1260

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Db      1201 ATGTCTCAAGAACACAGAAATTAATAAGATGATGATGAGAGGTGAAGAAGAAATGAG 1260
Qy      1261 AAGCATGAAGATTAATATGATGATTAATCAAGAAAACCTGATTAATGATGATGATGATGATG 1320
Db      1261 AAGCATGAAGATTAATATGATGATTAATCAAGAAAACCTGATTAATGATGATGATGATGATG 1320
Qy      1321 AATGATGATTAATGATTAATGATGATTAATCAAGAAAACCTGATTAATGATGATGATGATGATG 1380
Db      1321 AATGATGATTAATGATTAATGATGATTAATCAAGAAAACCTGATTAATGATGATGATGATGATG 1380
Qy      1381 CCTGACACAGAAAGTGAAGATGATCAAGAAATTTGCGAAATTAATGATGATTAATGATGATG 1440
Db      1381 CCTGACACAGAAAGTGAAGATGATCAAGAAATTTGCGAAATTAATGATGATTAATGATGATG 1440
Qy      1441 AAACGATGCGCAAAATTAATCTCTGAAAACAGCAACCCGAACTTAATGATGATTAATGATGATG 1500
Db      1441 AAACGATGCGCAAAATTAATCTCTGAAAACAGCAACCCGAACTTAATGATGATTAATGATGATG 1500
Qy      1501 TCAGAGGAAGAGTCAAGAAAGCTTGAAGGCAAGTAAATGCGCAGCCAGAGCTAGAAAT 1560
Db      1501 TCAGAGGAAGAGTCAAGAAAGCTTGAAGGCAAGTAAATGCGCAGCCAGAGCTAGAAAT 1560
Qy      1561 TTTATGCTATGGAAGAAATGAAGAACACGAAAGTACTCATGTCGAAATTCGAGAAAC 1620
Db      1561 TTTATGCTATGGAAGAAATGAAGAACACGAAAGTACTCATGTCGAAATTCGAGAAAC 1620
Qy      1621 CTGACTAATGATGCGCACTGCTGCAATGATGATGATTAATTCCTCAAGAAAGAC 1680
Db      1621 CTGACTAATGATGCGCACTGCTGCAATGATGATGATTAATTCCTCAAGAAAGAC 1680
Qy      1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATGATCAAGTACGAA 1740
Db      1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATGATCAAGTACGAA 1740
Qy      1741 CAAATGATGATGAGAAAGCAATTTGTGAAGAACAGAACCTGAAATTAATTAACGATGAG 1800
Db      1741 CAAATGATGATGAGAAAGCAATTTGTGAAGAACAGAACCTGAAATTAATTAACGATGAG 1800
Qy      1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
Qy      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATTAATGATGATGCGGAAAGAAAT 1920
Db      1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATTAATGATGATGCGGAAAGAAAT 1920
Qy      1921 GCCATGCTAAGACTGAGCTGAGACACATGAATGAATCATCAGAGCCAGCTAAATTAATTAAT 1980
Db      1921 GCCATGCTAAGACTGAGCTGAGACACATGAATGAATCATCAGAGCCAGCTAAATTAATTAAT 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3
AA167212
ID AA167212 standard; cDNA; 2000 BP.
XX AA167212;
XX
XX 11-FEB-2002 (first entry)
XX
XX B305D isoform C splice variant 2 encoding cDNA.
XX
XX Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1971
XX FT
XX /tag= a

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FT      /product= "B305D isoform C splice variant"
XX
XX MO200175171-A2.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001MO-US010631.
XX
XX 03-APR-2000; 2000US-0194241P.
XX 20-JUL-2000; 2000US-0219862P.
XX 27-JUL-2000; 2000US-0221300P.
XX 18-DEC-2000; 2000US-0256592P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton RI, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH,
XX P-PSDB; AM65977.
XX
XX WPI; 2001-626449/72.
XX
XX P-PSDB; AM65977.
XX
XX Identifying tissue (tumor)-specific polynucleotides overexpressed in
XX tissue of interest as compared to control tissue, for detecting cancer
XX cells in patient, comprises DNA microarray analysis or quantitative
XX polymerase chain reaction.
XX
XX Claim 4; Page 94; 127pp; English.
XX
XX The invention relates to identifying tissue-specific polynucleotides (P)
XX that involves performing a genetic subtraction to identify pool of (P)
XX from tissue of interest (TI), performing DNA microarray analysis to
XX identify first subset of polynucleotides (SPI) at least 2-fold over
XX expressed in TI, and performing quantitative polymerase chain reaction
XX (PCR) analysis on SPI to identify second subset of (P). The method is
XX useful for determining the presence or absence of a cancer cell in a
XX patient, monitoring the progression of cancer in a patient using a
XX biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX urine or a tumour biopsy sample. The methods are useful for determining
XX the presence or absence of or monitoring progression of prostate, breast,
XX colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
XX gastric, kidney, bladder, pancreatic or endometrial cancer. The present
XX sequence represents a cDNA encoding a B305D isoform C splice variant
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2000; DB 4; Length 2000;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGTGTGAGAGTGAATTCATGCGGCTGCTCTTCTGTAAGAAAGCAATTTGATCTC 60
XX 1 ATGGTGTGAGAGTGAATTCATGCGGCTGCTCTTCTGTAAGAAAGCAATTTGATCTC 60
XX
XX 61 AGAGCAAGATGAGGCAAGTGTGCTGCGGCTTCCCTGCTGAGGAGAGCGCAAG 120
XX 61 AGAGCAAGATGAGGCAAGTGTGCTGCGGCTTCCCTGCTGAGGAGAGCGCAAG 120
XX
XX 121 AGCAACGTGCGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
XX 121 AGCAACGTGCGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
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XX 121 AGCAACGTGCGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
XX 121 AGCAACGTGCGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
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XX 181 ATGGCAAGATGAGTGCAGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGCTG 240
XX 181 ATGGCAAGATGAGTGCAGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGCTG 240
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XX 241 GCGGCTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
XX 241 GCGGCTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
XX
XX 301 TGTGCTGCTCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
XX 301 TGTGCTGCTCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
XX
XX 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGAGTACACAGTCCGTGAGAAAGATCTG 420
XX 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGAGTACACAGTCCGTGAGAAAGATCTG 420

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Db 361 GGAGACTACGATGACAGTGGCTTCATGAGACCAGAGGTACCACTCCGTGGAGAAAGATCTG 420
 QY 421 GACAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480
 Db 421 GACAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480
 QY 481 CTCAGGAGACCTGACGTGAACAGAAAGAACAGCAAAAGAGAGCTGCTCAACATCTGGCC 540
 Db 481 CTCAGGAGACCTGACGTGAACAGAAAGAACAGCAAAAGAGAGCTGCTCAACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGGACAGACGATGCACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGGACAGACGATGCACTTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGACAGCTGTGATAAAGCCGTACATGCGACAGAAAGATGAA 660
 Db 601 GTCTTGAACAACAAAAGAGACAGCTGTGATAAAGCCGTACATGCGACAGAAAGATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACTGGAATCCAAATTTCCAGATGATGGAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACTGGAATCCAAATTTCCAGATGATGGAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGGCAAGCACTGCTTAA 780
 Db 721 ACCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGGCAAGCACTGCTTAA 780
 QY 781 TATGATGCTGATATCGAATCAAAAACAGCATGGCTCCACACACTGTTACTTGTGTA 840
 Db 781 TATGATGCTGATATCGAATCAAAAACAGCATGGCTCCACACACTGTTACTTGTGTA 840
 QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGGAGCTGCTCATATCTGTGATGTTGTGGATCAGCAAGATTA 960
 Db 901 CTGGATAGATATGGAAGGAGCTGCTCATATCTGTGATGTTGTGGATCAGCAAGATTA 960
 QY 961 GTGAGCGTTCTTACTTGAACAAAATATTGATGTACTTCTCAAGATCTATCGACAGACG 1020
 Db 961 GTGAGCGTTCTTACTTGAACAAAATATTGATGTACTTCTCAAGATCTATCGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCGACAGAACAGACTTAAAG 1140
 Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCGACAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGCATGTAATAGCCAGCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGCATGTAATAGCCAGCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACCAAGATTAATAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAACCAAGATTAATAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AAGCAGAAAGTAAATATGAGGATTAATAGAAAACCTGACTAATGCTGCTGCG 1320
 Db 1261 AAGCAGAAAGTAAATATGAGGATTAATAGAAAACCTGACTAATGCTGCTGCG 1320
 QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACACTGTAATCAGCAATTT 1380
 Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGACACTGTAATCAGCAATTT 1380
 QY 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
 Db 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500

Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
 QY 1501 TCAGAGAAAGAGTCACAAAGCTTGAAGGCAAGTGAATGGCCAGACGTTAGAAAAT 1560
 Db 1501 TCAGAGAAAGAGTCACAAAGCTTGAAGGCAAGTGAATGGCCAGACGTTAGAAAAT 1560
 QY 1561 TTTATGGCTATGCAAGAAATGGAAGACAGGAAGTCACTCATGTCGATTTCCAGAAAAC 1620
 Db 1561 TTTATGGCTATGCAAGAAATGGAAGACAGGAAGTCACTCATGTCGATTTCCAGAAAAC 1620
 QY 1621 CTGACTAATATGATGTCACCTGCTGCAATGATGATGATTAATTTCTCCAGAAAGAGC 1680
 Db 1621 CTGACTAATATGATGTCACCTGCTGCAATGATGATGATTAATTTCTCCAGAAAGAGC 1680
 QY 1681 AGAACCTGAAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAA 1740
 Db 1681 AGAACCTGAAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAAGTACGAA 1740
 QY 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
 Db 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACGATGAG 1800
 QY 1801 ATTCTGATTCATGAGAAAGAGAGATGAGTGAAGTGAAGAAATGAATTTCTGAGCTTTCT 1860
 Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGTGAAGTGAAGAAATGAATTTCTGAGCTTTCT 1860
 QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAATATGTAAGTTGGGGAAGAAAT 1920
 Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAAATATGTAAGTTGGGGAAGAAAT 1920
 QY 1921 GCCATGCTTAAGACTGAGAGTGAACAGAAATCATCAGAGCAGCTTAAAAA 1980
 Db 1921 GCCATGCTTAAGACTGAGAGTGAACAGAAATCATCAGAGCAGCTTAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAA 2000
 RESULT 4
 AAS63808
 ID AAS63808 standard; cdna; 2000 BP.
 XX
 AC AAS63808;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cdna clone B305D splice variant #9.
 XX
 KW Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN MO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WC-US009919.
 XX
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 XX
 PA (CORI-) CORIXA CORP.
 XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Rietter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX MPI, 2001-639232/73.
DR P-PSDB; AAU69778.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
PT
PS Claim 1, Page 349-350, 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGAGCAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGACGGCAAG 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGACGGCAAG 120
QY 121 ACCAAGCTGGGCACTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180
DB 121 ACCAAGCTGGGCACTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGT 240
QY 241 GGCGCTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAAACAAGATGGGCAAG 300
DB 241 GGCGCTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAAACAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGAGGCAAGGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGAGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
DB 361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTTGGTGAAGATGCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAACTCCACAGAGCTGCTGTTGGTGAAGATGCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGAGACCTGACCTGTAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
DB 481 CTCAGGAGACCTGACCTGTAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTCTGGAAGAGAGATGTCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTCTGGAAGAGAGATGTCACTTAAT 600
QY 601 GTCTTTGACAAAGAGAGCAAGCTTGATTAAGGCGGTACATGCGAGGAAGATGA 660
DB 601 GTCTTTGACAAAGAGAGCAAGCTTGATTAAGGCGGTACATGCGAGGAAGATGA 660

DB 601 GTCTTTGACAAAGAGAGCAAGCTTGATTAAGGCGGTACATGCGAGGAAGATGA 660
QY 661 TGTGGTTAAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGATGAAT 720
DB 661 TGTGGTTAAATGTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGATGAAT 720
QY 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTTGCTGATATGATCAAAAAAAGAGATGCTTCACCACTGTTACTTGATGTA 840
DB 781 TATGTTGCTGATATGATCAAAAAAAGAGATGCTTCACCACTGTTACTTGATGTA 840
QY 841 CATGAGCAAAAAACACCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACACCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATATGAAAGAGCTGCTCATACTTGCTGATGTTGTGATCAGACAGTATA 960
DB 901 CTGATATGATATGAAAGAGCTGCTCATACTTGCTGATGTTGTGATCAGACAGTATA 960
QY 961 GTGAGCTTTCTATCTGAGCAAAAAATTAATGATCTTCAAGATCTATCTGAGACAGC 1020
DB 961 GTGAGCTTTCTATCTGAGCAAAAAATTAATGATCTTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAAGAGTATGCTGTTCTGATGATCATCATATTTGGCACTTCTTCTGATC 1080
DB 1021 GCCAAGAGTATGCTGTTCTGATGATCATCATATTTGGCACTTCTTCTGATC 1080
QY 1081 AAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
DB 1081 AAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGCATGAAATATGCGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGCATGAAATATGCGCCAGAGAAA 1200
QY 1201 ATGTTCTAAGAACCAAGAAATTAATGAATGTTGTATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTTCTAAGAACCAAGAAATTAATGAATGTTGTATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGATTAATCTAGAAAACTGCAATATGTTGCTGCTGAC 1320
DB 1261 AAGCATGAAGATTAATATGTTGGATTAATCTAGAAAACTGCAATATGTTGCTGCTGAC 1320
QY 1321 AATGTTGATTAATGATTAATTTCTCAAGAAAGAGCAAGCACTGAAATGAGCAATTT 1380
DB 1321 AATGTTGATTAATGATTAATTTCTCAAGAAAGAGCAAGCACTGAAATGAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGATCTGACATCAAGAAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGATCTGACATCAAGAAA 1440
QY 1441 AAAAGATGSCAAAATTAATCTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
DB 1441 AAAAGATGSCAAAATTAATCTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCAAAAAGGCTTGAAGGCAAGTGAATGAGCCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGAAAGAGTCAAAAAGGCTTGAAGGCAAGTGAATGAGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGGCTATGGAAGAAATGAAGAAAGCAAGAAATTAATCTCAATGTTCCCAAGAAAAC 1620
DB 1561 TTTATGGCTATGGAAGAAATGAAGAAAGCAAGAAATTAATCTCAATGTTCCCAAGAAAAC 1620
QY 1621 CTGACTTAATGAGCACTGCTGCAATGTTGATGATTAATTTCTTCAAGAAAGAC 1680
DB 1621 CTGACTTAATGAGCACTGCTGCAATGTTGATGATTAATTTCTTCAAGAAAGAC 1680
QY 1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGATGCGAA 1740
DB 1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGATGCGAA 1740

QY 1741 CAAATGATATCTGAGAGCAATTTTGTGAGAACAGAACCTGGATATTTACGATGAG 1800
DB 1741 CAAATGATATCTGAGAGCAATTTTGTGAGAACAGAACCTGGATATTTACGATGAG 1800
QY 1801 ATTCTGATTCATGAGAGAGAGAGATGAGAGTGGTTGAAATTTGAAATTTCTGACTTTCT 1860
DB 1801 ATTCTGATTCATGAGAGAGAGAGATGAGAGTGGTTGAAATTTGAAATTTCTGACTTTCT 1860
QY 1861 CTTAGTTGTGAGAGAGAGAGAGAGATCTTTGATGAAATTTGTAAGTTGCGGAGAGAAAT 1920
DB 1861 CTTAGTTGTGAGAGAGAGAGAGAGATCTTTGATGAAATTTGTAAGTTGCGGAGAGAAAT 1920
QY 1921 GCCATGCTAG 1980
DB 1921 GCCATGCTAG 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 5

AAH02780 standard; cDNA; 2000 BP.

AAH02780;

14-JUN-2001 (first entry)

Prostate tumour antigen determined cDNA splice variant of B305D #9.

Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
prostate cancer; immunogenic; cytotoxic; vaccine; ss.

Homo sapiens.

MO200125272-A2.

12-APR-2001.

04-OCT-2000; 2000MO-US027464.

04-OCT-1999; 99US-0157455P.

(CORI-) CORIXA CORP.

Xu J, Skeiky YAW, Reed SG, Cheever MA;

WPI, 2001-245062/25.

P-PSDB; AAB74816.

Prostate specific protein and its encoding polynucleotide, useful for the

treatment and diagnosis of prostate cancer.

Claim 50; Page 232; 276pp; English.

The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytotoxic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of the cancer. Progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention

Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match	100.0%	Score 2000;	DB 4;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 2000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAGAGCATTTGGTCTC 60				
DB 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAGAGCATTTGGTCTC 60				
QY 61 AGAGCAAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGCAAGAGAGCGCAAG 120				
DB 61 AGAGCAAGATGAGGCAAGTGTGCTGCGTGTCTTCCCTGCTGCAAGAGAGCGCAAG 120				
QY 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180				
DB 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180				
QY 181 ATGAGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGAGAGAGAGAGAGAGAGAG 240				
DB 181 ATGAGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGAGAGAGAGAGAGAGAGAG 240				
QY 241 GCGGCTTGTGAG 300				
DB 241 GCGGCTTGTGAG 300				
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360				
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360				
QY 361 GGAAGCTAG 420				
DB 361 GGAAGCTAG 420				
QY 421 GACAACTCCAG 480				
DB 421 GACAACTCCAG 480				
QY 481 CTCAGGAG 540				
DB 481 CTCAGGAG 540				
QY 541 TCTGCAATGGGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600				
DB 541 TCTGCAATGGGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600				
QY 601 GTCTTGAACAACAAAG 660				
DB 601 GTCTTGAACAACAAAG 660				
QY 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGAGATGGAAT 720				
DB 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGAGATGGAAT 720				
QY 721 ACCACTCTGACATGCTATCTAATATGAAATTAATTAATTAATTAATTAATTAATTA 780				
DB 721 ACCACTCTGACATGCTATCTAATATGAAATTAATTAATTAATTAATTAATTAATTA 780				
QY 781 TATGCTGATATGCAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840				
DB 781 TATGCTGATATGCAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840				
QY 841 CATGAGCAAAAAAG 900				
DB 841 CATGAGCAAAAAAG 900				
QY 901 CTGATAGATATGAG 960				
DB 901 CTGATAGATATGAG 960				
QY 961 GTGAGCTTCTAATGAG 1020				
DB 961 GTGAGCTTCTAATGAG 1020				
QY 1021 GCCAGAGATATGCTGTTCTAGTATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080				

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Db 1021 GCAGAGATAGCTGTTCTAGTCATCATGTAATTTGCGAGTTACTTTCTGACTAC 1080
QY 1081 AAGAGAAAAACAGATGCTTAAATCTCTTCTGAAAAAGCAATTCAGAACCAAGCTTAAAG 1140
Db 1081 AAGAGAAAAACAGATGCTTAAATCTCTTCTGAAAAAGCAATTCAGAACCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCACTAAAGGTTCAAAAGGAGTGAATAATGCGAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCACTAAAGGTTCAAAAGGAGTGAATAATGCGAGCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTGAAGAGAAATGAAG 1260
Db 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTGAAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGAGGATTAATGATGAGGATTAATGATGAGGATTAATGATGAG 1320
Db 1261 AAGCATGAAGATTAATGATGAGGATTAATGATGAGGATTAATGATGAGGATTAATGATGAG 1320
QY 1321 AATGATGATTAATGATTAATTTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGATGATTAATGATTAATTTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACACGAAAGTGAAGAGATCAAGAAATTTGCGAAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAAGTGAAGAGATCAAGAAATTTGCGAAATTTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAAATATCTCTTCTGAAAAAGCAATTCAGAACCAAGCTTAAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAAATATCTCTTCTGAAAAAGCAATTCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCACTAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGAGTCACTAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACATTAATGAGTGCCTGCTGCGAATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 CTGACATTAATGAGTGCCTGCTGCGAATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 AGAACAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAACAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 CAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 ATTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 1801 ATTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
```

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RESULT 6
AAH85029
ID AAH85029 standard; cDNA, 2000 BP.
XX
AC AAH85029;
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```
XX 25-SBP-2001 (first entry)
DT Human prostate-specific cDNA sequence B305D splice variant #9.
XX
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
XX Homo sapiens.
XX WO200134802-A2.
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US030904.
XX
XX 12-NOV-1999; 99US-00439313.
XX
XX 18-NOV-1999; 99US-00443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Haylocke SL, Jiang Y, Reed SG;
XX Kalos MD, Rector MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX MPI; 2001-308785/32.
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
XX prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer.
XX
XX Claim 31; Page 247-248; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
XX at least an immunogenic portion of a prostate-specific protein, or its
XX variant. Also described are polynucleotides (N1) encoding (P1) and
XX (N1) have cytostatic activity and can be used in vaccine production. The
XX polypeptides, nucleic acids and antibodies from the present invention are
XX useful in the diagnosis and therapy of prostate cancer. Prostate specific
XX genes P704P, P712P, P774P, P775P and B305D are located in a genomic
XX region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
XX CC Prostate specific antigen (PSA) P5018 was located on chromosome 1.
XX CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
XX CC and polypeptide sequences used in the exemplification of the present
XX CC invention.
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2000; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTGTTGAGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCATTTGGTCTC 60
Db 1 ATGTTGTTGAGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGGAAGTGGCTGCGTTCCTCCCTGCTGAGAGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGGAAGTGGCTGCGTTCCTCCCTGCTGAGAGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGGCGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGGCGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
```


Db 301 TGGTGTGGCACTGCTTCCCTCTGCTCAGAGGAGGCGAGAGCAAGGTGGCGCTTGG 360
 QY 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
 Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
 QY 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
 Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
 QY 481 CTCAGGAGACCTGACCTGAGCAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACCTGACCTGAGCAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAAGAGTAAATCTCTGCTGAGCAGAGATGCTCAATCTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAAGAGTAAATCTCTGCTGAGCAGAGATGCTCAATCTTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAATGAA 660
 Db 601 GTCTTGAACAACAAAAGAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGAAATGAA 660
 QY 661 TGTGGCTTAATGTTGCTGGAGCATGGCACTGATCCAAATATTCAGATGATGTAATGAAAT 720
 Db 661 TGTGGCTTAATGTTGCTGGAGCATGGCACTGATCCAAATATTCAGATGATGTAATGAAAT 720
 QY 721 ACCACTCTGACACTACCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTAA 780
 Db 721 ACCACTCTGACACTACCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTAA 780
 QY 781 TATGTCCTGATATGCAATCAAAAAAACAAGATGGCTCAACACTGTTACTTGGTGA 840
 Db 781 TATGTCCTGATATGCAATCAAAAAAACAAGATGGCTCAACACTGTTACTTGGTGA 840
 QY 841 CATGACCAAAAAACAGAAAGTCGTGAATTTTAAATGAAGAAAAAAGCAATTTAAATGCA 900
 Db 841 CATGACCAAAAAACAGAAAGTCGTGAATTTTAAATGAAGAAAAAAGCAATTTAAATGCA 900
 QY 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTTGGATCAGCAATATTA 960
 Db 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTTGGATCAGCAATATTA 960
 QY 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 Db 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTCTACTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTCTACTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
 QY 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCTCAGAACAGATTAAG 1140
 Db 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACAGCAATCTCAGAACAGATTAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATAATGCAAGCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATAATGCAAGCCAGAGAAA 1200
 QY 1201 ATGCTCCAAGAACCAAGAAATTAATAGATGATGATGATGATGATGATGATGATGATG 1260
 Db 1201 ATGCTCCAAGAACCAAGAAATTAATAGATGATGATGATGATGATGATGATGATGATG 1260
 QY 1261 AAGCATGAAGTAAATGATGAGGATTAAGTAAAGAACTGATGATGATGATGATGATGATG 1320
 Db 1261 AAGCATGAAGTAAATGATGAGGATTAAGTAAAGAACTGATGATGATGATGATGATGATG 1320
 QY 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGAAATTCAGCAATTT 1380
 Db 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGAAATTCAGCAATTT 1380
 QY 1381 CCTGACACGAAGTGAAGATTCACAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
 Db 1381 CCTGACACGAAGTGAAGATTCACAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440

Db 1381 CCTGACACGAAGTGAAGATTCACAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
 QY 1441 AAAAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
 Db 1441 AAAAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
 QY 1501 TCAGAGGAAGATTCACAAAGGCTTTGAGGCGCATGAAAAATGGCCAGCCAGAGCTAGAAAT 1560
 Db 1501 TCAGAGGAAGATTCACAAAGGCTTTGAGGCGCATGAAAAATGGCCAGCCAGAGCTAGAAAT 1560
 QY 1561 TTTATGCTATGCAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
 Db 1561 TTTATGCTATGCAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
 QY 1621 CTGACTAATGATGCACTGCTGGCAATGGTGAATGATGATTAATTTCTCAAGAAAGAC 1680
 Db 1621 CTGACTAATGATGCACTGCTGGCAATGGTGAATGATGATTAATTTCTCAAGAAAGAC 1680
 QY 1681 AGAACACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTACGAA 1740
 Db 1681 AGAACACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTACGAA 1740
 QY 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATTAACACGATGAG 1800
 Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATTAACACGATGAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATGAAATTCAGAGCTTCT 1860
 Db 1801 ATTCTGATTCATGAAGAAAGAGATAGAAAGTGTGTAAGAAATGAAATTCAGAGCTTCT 1860
 QY 1861 CTTAGTTGAAGAAAGAAAGACATCTTGACATGAATAATGATGCTGGCGAGAAATTT 1920
 Db 1861 CTTAGTTGAAGAAAGAAAGACATCTTGACATGAATAATGATGCTGGCGAGAAATTT 1920
 QY 1921 GCCATGCTAAGCTGAGAGCTAGACAAATGAATGAAATCAGAGCAGCTAATAAAAAA 1980
 Db 1921 GCCATGCTAAGCTGAGAGCTAGACAAATGAATGAAATCAGAGCAGCTAATAAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 RESULT 7
 ACAS9616
 ID ACAS9616 standard; cDNA; 2000 BP.
 XX
 ACAS9616;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Prostate cancer therapy associated cDNA #359.
 XX
 KW prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSM; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002192763-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 29-JUN-2001; 2001US-00895793.
 XX
 PR 04-OCT-1999; 99US-0157455F.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHEM J L.

PA (HARL/) HARLOCKER S. L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELLY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P. D.
 PA (HOUN/) HOUGHTON R. L.
 PA (DBAS/) Y. DE BASSOLS C. V.
 PA (FOYT/) FOY T. M.

PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SK, Wang A, Skelky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; ABU71669.

PT Prostate specific protein and its encoding polynucleotide, useful for the
 XX treatment and diagnosis of prostate cancer.
 PS Example 11; SEQ ID NO 374; 85bp; English.

XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 3 sequences defined in the USPO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated cDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 5; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGCTTC 60
 DB 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGCTTC 60
 QY 61 AGAAGCAAGTGGGCAAGTGTCTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
 DB 61 AGAAGCAAGTGGGCAAGTGTCTGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGGAGACGACGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGGAGACGACGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
 DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
 QY 241 GGGGCTTTGGAGACCAAGCAAGCTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
 DB 241 GGGGCTTTGGAGACCAAGCAAGCTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300

1

QY 301 TGGTGTGCACTGCTCCCTGCTGCAAGGGAGCGGCAAGGATGGGCGCTTGG 360
 DB 301 TGGTGTGCACTGCTCCCTGCTGCAAGGGAGCGGCAAGGATGGGCGCTTGG 360
 QY 361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCAGGTACACGTCGTTGAGAAATCTG 420
 DB 361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCAGGTACACGTCGTTGAGAAATCTG 420
 QY 421 GACCAAGCTTCAAGAGTGTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTATCGTCAG 480
 DB 421 GACCAAGCTTCAAGAGTGTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTATCGTCAG 480
 QY 481 CTCAGAGCACTGAGGTGAACAAGAGGCAAGCAAAAAGAGAGTCTTCAATCTGAGCC 540
 DB 481 CTCAGAGCACTGAGGTGAACAAGAGGCAAGCAAAAAGAGAGTCTTCAATCTGAGCC 540
 QY 541 TCTGCAATGGGAATTCAGAAAGTAAAGCTCTGCTGAGCAGAGATGTCAATTAAT 600
 DB 541 TCTGCAATGGGAATTCAGAAAGTAAAGCTCTGCTGAGCAGAGATGTCAATTAAT 600
 QY 601 GTCTTTGACAAACAAAAGAGGACAGCTGTGATTAAGGCGGTACATGCCAGAAATGAA 660
 DB 601 GTCTTTGACAAACAAAAGAGGACAGCTGTGATTAAGGCGGTACATGCCAGAAATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
 DB 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTGTGCACTAGCTATCTATATGAAATTAATTAAGCCAAAGACATGCTCTTA 780
 DB 721 ACCACTGTGCACTAGCTATCTATATGAAATTAATTAAGCCAAAGACATGCTCTTA 780
 QY 781 TATGTGTGCTGATATGGAATCAAAAACAGATGAGCTTCAACACCTGTACTTGGTGA 840
 DB 781 TATGTGTGCTGATATGGAATCAAAAACAGATGAGCTTCAACACCTGTACTTGGTGA 840
 QY 841 CATGAGCAAAAACAGATGAGCTGTAATTTTATCAAGAAAGGCAATTTAAATGCA 900
 DB 841 CATGAGCAAAAACAGATGAGCTGTAATTTTATCAAGAAAGGCAATTTAAATGCA 900
 QY 901 CTGGATATGATATGAAAGGACATGCTCTCATATCTGTTGATGTTGGATCAAGATATA 960
 DB 901 CTGGATATGATATGAAAGGACATGCTCTCATATCTGTTGATGTTGGATCAAGATATA 960
 QY 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
 DB 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAAGAGTATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
 DB 1021 GCCAAGAGTATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAACAGATCTAAAAATCTCTTGTAAAAACAGAAATCCAGAACAGACTTAAAG 1140
 DB 1081 AAAAGAAAACAGATCTAAAAATCTCTTGTAAAAACAGAAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGCAAGTAAATAGCCAGCAAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGATCAAAAGGTTCAAAAGCAAGTAAATAGCCAGCAAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTAGAGAGTTGAAGAAATGAAG 1260
 DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGTAGAGAGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATATGTGGAAATTAAGAAAACTTGAATATGTGTCACTGTGAC 1320
 DB 1261 AAGCATGAAAGTAAATATGTGGAAATTAAGAAAACTTGAATATGTGTCACTGTGAC 1320
 QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAAGAACCTGTAATATCAGCAATTT 1380
 DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAAGAACCTGTAATATCAGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAAATTAAGTTTCTGACTCAAAAGAA 1440

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Db      1381 CCTGACACGAAAGTGAAGGTATCACAGAAATTTGGCAATTTAGTTTCTGACTCAAGAA 1440
Qy      1441 AAACAGATGCCAAATATCTCTTGTGAAAAGCAAGACCAGAACAGACTTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATATCTCTTGTGAAAAGCAAGACCAGAACAGACTTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGTCAACAAAGCTTGAAGGCGAGTGAATAATGGCCAGGCTAGTGAATAAT 1560
Db      1501 TCAGAGAAAGTCAACAAAGCTTGAAGGCGAGTGAATAATGGCCAGGCTAGTGAATAAT 1560
Qy      1561 TTTATGGCTATCGAAGAAATGAAAGACGAGAAAGTACTATGTCGGATTCGCCAGAAAC 1620
Db      1561 TTTATGGCTATCGAAGAAATGAAAGACGAGAAAGTACTATGTCGGATTCGCCAGAAAC 1620
Qy      1621 CTGACTAATGTCGCACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAAAGGC 1680
Db      1621 CTGACTAATGTCGCACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAAAGGC 1680
Qy      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGTATCAAGTGAAGAA 1740
Db      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGTATCAAGTGAAGAA 1740
Qy      1741 CAAAATGATATCTGAGAAAGCAATTTGTGAAGAAAGCAAGCACTGGAATATTAACAGATGAG 1800
Db      1741 CAAAATGATATCTGAGAAAGCAATTTGTGAAGAAAGCAAGCACTGGAATATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGCAAGTAAAGTGTGAAATTTGAATTCGACTTCTT 1860
Db      1801 ATTCTGATTCATGAGAAAGCAAGTAAAGTGTGAAATTTGAATTCGACTTCTT 1860
Qy      1861 CTTAGCTTTGAAGAAAGAAAGCATTTTGCATGAAATTTGTAAGCTTGGGAAAGAAATT 1920
Db      1861 CTTAGCTTTGAAGAAAGAAAGCATTTTGCATGAAATTTGTAAGCTTGGGAAAGAAATT 1920
Qy      1921 GCCATGCTAGAGCTGAGCTGAGACAAATGAATCATCAGAGCCAGCTAAATTAATTAAT 1980
Db      1921 GCCATGCTAGAGCTGAGCTGAGACAAATGAATCATCAGAGCCAGCTAAATTAATTAAT 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
ABL95179
ID      ABL95179 standard; cDNA; 2000 BP.
XX
AC      ABL95179;
XX
DT      19-JUL-2002 (first entry)
XX
DE      Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
KW      Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX      gene therapy; gene; ss.
OS      Homo sapiens.
XX
PN      US2002022248-A1.
XX
PD      21-FEB-2002.
XX
PF      12-JAN-2001; 2001US-00759143.
XX
PR      25-FEB-1997; 97US-00806099.
PR      01-AUG-1997; 97US-00904804.
PR      10-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.

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PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00443686.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-00568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      10-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651236.
PR      06-SEP-2000; 2000US-00657279.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
XX
XX      (XUJ/) XU J.
PA      (DILL/) DILLON D C.
PA      (MITC/) MITCHAM J L.
PA      (HARL/) HARLOCKER S L.
PA      (JIAN/) JIANG Y.
PA      (KALO/) KALOS M D.
PA      (FANG/) FANGER G R.
PA      (RETT/) RETTER M W.
PA      (STOL/) STOLK J A.
PA      (DAYC/) DAY C H.
PA      (VEDV/) VEDVICK T S.
PA      (CART/) CARTER D.
PA      (LISX/) LI S X.
PA      (WANG/) WANG A.
PA      (SKEI/) SKEIKY Y A W.
PA      (HEPL/) HEPLER W T.
PA      (HEND/) HENDERSON R A.
XX
XX      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI      Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX      WPI; 2002-255649/30.
XX
XX      New prostate-specific polynucleotides for diagnosing and treating
PT      diseases, in particular prostate cancer, and as markers for the
PT      progression of cancer.
XX
XX      Claim 1; SEQ ID NO 374; 87bp; English.
XX
XX      The present invention provides prostate-specific coding sequences and
CC      CC their encoded proteins. These can be used in the diagnosis and treatment
CC      of cancers, particularly prostate cancer. The present sequence is a cDNA
CC      described in the invention
XX
XX      Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2000; Conservative 0;
Qy      1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGGTCTC 60
Db      1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGGTCTC 60
Qy      61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db      61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy      121 AGCAAGTGGGCACTTGTGAAGCAAGCAAGCACTGTATGAAGACACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTGTGAAGCAAGCAAGCACTGTATGAAGACACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Qy      241 GGGCTTCTGAGAGCAAGCAAGCACTGTGTAAGACACTCAGAGCAAGAGTGGCAAG 300

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Db      241 GGGGCTTCTGGAGACCAAGCAGCTGCTATGAAACACTCAGAAACAAGATGGCAAG 300
Qy      301 TGGTGTGCGACATGCTTCCCTGCTGACAGGGGGAGGGAAGGCAAGGTGGCGCTTGG 360
Db      301 TGGTGTGCGACATGCTTCCCTGCTGACAGGGGGAGGGAAGGCAAGGTGGCGCTTGG 360
Qy      361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCAGGTACACGCTCCGTGAGAGATCTG 420
Db      361 GGAAGCTAGATGACAGTGTCTTCAATGAGCCAGGTACACGCTCCGTGAGAGATCTG 420
Qy      421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db      421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Qy      481 CTCAGGGAACATGACGCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACACTGGCC 540
Db      481 CTCAGGGAACATGACGCTGAAACAAGAGCAAGCAAAAGAGAGCTGCTACACTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTATGAAATCTCTGCTGACAGAGATGCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTATGAAATCTCTGCTGACAGAGATGCACTTAAT 600
Qy      601 GTCTTGAACAACAAGAGGACAGCTCTGATTAAGCCGTACATGCCAGAAAGATGAA 660
Db      601 GTCTTGAACAACAAGAGGACAGCTCTGATTAAGCCGTACATGCCAGAAAGATGAA 660
Qy      661 TGTGCGTTATGTTGTGGAAACATGGACCTGATCCAAATATTCGAATAGATGGAAT 720
Db      661 TGTGCGTTATGTTGTGGAAACATGGACCTGATCCAAATATTCGAATAGATGGAAT 720
Qy      721 ACCACTCTGCACTACGCTATCTATTAATGAAGATAAATTAATGCGCAAGCACTGCTTA 780
Db      721 ACCACTCTGCACTACGCTATCTATTAATGAAGATAAATTAATGCGCAAGCACTGCTTA 780
Qy      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCATGTTACTTGGTGA 840
Db      781 TATGTGCTGATATGCAATCAAAAAACAAGCATGGCTCACAACCATGTTACTTGGTGA 840
Qy      841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Db      841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
Qy      901 CTGGATAGATATGGAAGGACGTGCTCATACTTGTATGTTGTGATCAGCAAGTATA 960
Db      901 CTGGATAGATATGGAAGGACGTGCTCATACTTGTATGTTGTGATCAGCAAGTATA 960
Qy      961 GTACGCTTCTACTTGAAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Db      961 GTACGCTTCTACTTGAAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Qy      1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
Db      1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
Qy      1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCATCCAGAACAGCTTAAG 1140
Db      1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCATCCAGAACAGCTTAAG 1140
Qy      1141 CTGACATCAGAGGAAGATCAAAAGTTCAAAAGGCAAGTAATAGCCAGCCAGAGAAA 1200
Db      1141 CTGACATCAGAGGAAGATCAAAAGTTCAAAAGGCAAGTAATAGCCAGCCAGAGAAA 1200
Qy      1201 ATGCTCAAGAACACAGAAATTAATAGATGATAGAGAGGTTGAAGAAAGAAAGAG 1260
Db      1201 ATGCTCAAGAACACAGAAATTAATAGATGATAGAGAGGTTGAAGAAAGAAAGAG 1260
Qy      1261 AAGCATGAAGATATATATGAGATTAGAAAACTGACTATATGATGCTGCTGAC 1320
Db      1261 AAGCATGAAGATATATATGAGATTAGAAAACTGACTATATGATGCTGCTGAC 1320
Qy      1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGCAACCTGAAATACGCAATTT 1380

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Db      1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGACAGAACACTGAAATACGCAATTT 1380
Qy      1381 CCTGACAAGAAAGTAAAGATATCAAGAAATTTGCGAAATTTGTTCTGACTACAAAGAA 1440
Db      1381 CCTGACAAGAAAGTAAAGATATCAAGAAATTTGCGAAATTTGTTCTGACTACAAAGAA 1440
Qy      1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA 1500
Qy      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCAAGTAAATGGCCAGCAGAGCTAGAAAAAT 1560
Db      1501 TCAGAGAAAGATCACAAAAGCTTGAAGGCAAGTAAATGGCCAGCAGAGCTAGAAAAAT 1560
Qy      1561 TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
Db      1561 TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAAC 1620
Qy      1621 CTGACTAATGGTGCCACTGCTGGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
Db      1621 CTGACTAATGGTGCCACTGCTGGCAATGATGATGATTAATTTCTTCAAGAAAGAC 1680
Qy      1681 AGAACACTGAAAGCCAGCAATTTCTGCACTGAGATGAAGATATCACTGACGAA 1740
Db      1681 AGAACACTGAAAGCCAGCAATTTCTGCACTGAGATGAAGATATCACTGACGAA 1740
Qy      1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACCTGGAATTAACAGATGAG 1800
Db      1741 CAAATGATATCTCAGAGCAATTTTGTGAAGACAGAACCTGGAATTAACAGATGAG 1800
Qy      1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTAAGAAATTAATTTCTGAGCTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGTGTAAGAAATTAATTTCTGAGCTTCT 1860
Qy      1861 CTTAGTTTGAAGAAAGAAAGACATCTTGCATGAAATATGATCGTTGGGGAAGAAAT 1920
Db      1861 CTTAGTTTGAAGAAAGAAAGACATCTTGCATGAAATATGATCGTTGGGGAAGAAAT 1920
Qy      1921 GCCATGCTAAGCTGAGAGTACACAAATGAAACATCAGAGCAGCTAAAAAAGAAAA 1980
Db      1921 GCCATGCTAAGCTGAGAGTACACAAATGAAACATCAGAGCAGCTAAAAAAGAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 9
AAS99858
ID AAS99858 standard; cDNA; 2000 BP.
XX
AC AAS99858;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11g1 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosolic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN M0200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX

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(CORI-) CORIXA CORP.

PA Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
XX Wang A, Skeiky YAM, Harlocker SL, Day CH;
PI WPI; 2002-089919/12.
XX P-PSDB; AAU74378.

PT New breast tumor proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response.

XX Claim 1: Page 224; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response.
XX Particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation, in the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumour polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS99570-AAS99888
XX represent novel human breast cancer protein coding sequences and PCR
XX primers of the invention

SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 6; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCATGCGGCTCCTCTTGTGTGAAGAAGCCATTGTGCTC 60
DB 1 ATGGTGTGAGGTTGATTCATGCGGCTCCTCTTGTGTGAAGAAGCCATTGTGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGGAACACACAGACACTCTGTATGAAGACACTCAGGAACAAGATGGCAAG 300
DB 241 GGGGCTTCTGGAACACACAGACACTCTGTATGAAGACACTCAGGAACAAGATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGTACGATACAGTGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
DB 361 GGAAGTACGATACAGTGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420
QY 421 GACAACTCCACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTCCACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTGAGGGAACAATGAGGGAACAAGGGAACAAGGGAACAAGGGAACAAGGGAACAAG 540
DB 481 CTGAGGGAACAATGAGGGAACAAGGGAACAAGGGAACAAGGGAACAAGGGAACAAG 540
QY 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGGAACAAGATGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGGAACAAGATGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAGGAGCAAGCTGTATTAAGCGCTACAAATGCCAGGAAGTGA 660

DB 601 GTCTTGAACAACAAAGGAGCAAGCTGTATTAAGCGCTACAAATGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTGCTGGAACATGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTATTAATGAAGTAATTAATGCGCAAGACTGCTT 780
DB 721 ACCACTCTGCACTAGCTATCTATTAATGAAGTAATTAATGCGCAAGACTGCTT 780
QY 781 TATGGTGTGATGATGAATCAAAAACAAGATGCTGCAACAATGCTTATCTGCTGTA 840
DB 781 TATGGTGTGATGATGAATCAAAAACAAGATGCTGCAACAATGCTTATCTGCTGTA 840
QY 841 CATGACAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAACGCAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAACGCAATTTAAATGCA 900
QY 901 CTGATATGATGGAAGACTGCTCATCTTGTCTGATATGTTGGATCAGCAAGTATA 960
DB 901 CTGATATGATGGAAGACTGCTCATCTTGTCTGATATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATTAATGATGATCTTCCAGATCTATCTGGAACAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATTAATGATGATCTTCCAGATCTATCTGGAACAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCAAGTCTTCTGCACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCAAGTCTTCTGCACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACGCAATCCAGAACAACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACGCAATCCAGAACAACTTAAG 1140
QY 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGCAAGTAATGACGACAGAGAA 1200
DB 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGCAAGTAATGACGACAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATATGATGATTAATGATTAATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAGTATATGATGATTAATGATTAATGATGATGATGATGATGATGATG 1320
QY 1321 AATGGTATTAATGATTAATTTCTCAAGAGAGACAGAACCTGAATAATGACAAATT 1380
DB 1321 AATGGTATTAATGATTAATTTCTCAAGAGAGACAGAACCTGAATAATGACAAATT 1380
QY 1381 CCTGACAAAGAGAGAGATATCAAGAAATTTGCAATTAATGATGATGATGATGATG 1440
DB 1381 CCTGACAAAGAGAGAGATATCAAGAAATTTGCAATTAATGATGATGATGATGATG 1440
QY 1441 AAACAGATCCAAAAATCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATCCAAAAATCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
QY 1501 TCAAGAGAAAGTCAAAAGGCTTGAAGGCAATGAAATGAGGCAAGCTAAGAAAT 1560
DB 1501 TCAAGAGAAAGTCAAAAGGCTTGAAGGCAATGAAATGAGGCAAGCTAAGAAAT 1560
QY 1561 TTTATGCTATGAGAAATTAAGAAAGCAGGAAGTACTATGCGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGAGAAATTAAGAAAGCAGGAAGTACTATGCGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGTGCACTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAC 1680
DB 1621 CTGACTAATGTGCACTGCTGCAATGATGATGATTAATTTCTCAAGAAAGAC 1680
QY 1681 AGAACCTGAAGACAGAAATTTCTGCACTGGAAGAAAGATATCAAGTGAAGAA 1740

Db 1681 AGAACAAGCTGAAAGCAATTTCTGACACTGAGATGAAGATGATCACTGACGAA 1740
QY 1741 CAAAATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAATATTACACGATGAG 1800
Db 1741 CAAAATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAATATTACACGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGTAAGAAATGAAATCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGAGAGATGAGAGTGTGTAAGAAATGAAATCTGAGCTTCT 1860
QY 1861 CTTAGTGTGTAAGAAAGAGAGATGAGAGTGTGTAAGAAATGAAATCTGAGCTTCT 1920
Db 1861 CTTAGTGTGTAAGAAAGAGAGATGAGAGTGTGTAAGAAATGAAATCTGAGCTTCT 1920
QY 1921 GCCATGCTAGAGCTGAGAGCTGAGACAGATGAAACATGAGCGAGCTTAAAAA 1980
Db 1921 GCCATGCTAGAGCTGAGAGCTGAGACAGATGAAACATGAGCGAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
RESULT 10
ACC95343
ID ACC95343 standard; cDNA; 2000 BP.
XX
AC ACC95343;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SFG ID 374.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW Immune response; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN MO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002MO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
XX
PR 29-JUN-2001; 2001US-0085814.
XX
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA,
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CR, Vedrick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepner WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Baesisc, Foy TM, Watanabe Y;
PI Deng T;
XX
DR MPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 11; Page 415-416; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGTAAGTGAATTCATGCGCGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
Db 1 ATGGTGTGTAAGTGAATTCATGCGCGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
QY 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGACAGAGCACTGCTGATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAAGACAGAGCACTGCTGATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
QY 241 GCGGCTTCTGAGACCAAGCACTGCTTATGAAGACCTAGAGAACAAATGGGCAAG 300
Db 241 GCGGCTTCTGAGACCAAGCACTGCTTATGAAGACCTAGAGAACAAATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGGAGTGGGCGCTTGG 360
QY 361 GGAAGCTAGATGAGAGTGCCTTCAATGAGAGCCAGGTACACGCTCGTGGAGAGTCTG 420
Db 361 GGAAGCTAGATGAGAGTGCCTTCAATGAGAGCCAGGTACACGCTCGTGGAGAGTCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGAGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGAGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGAGACCTGAGGTGAAGAAAGCAAGCAAGAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGAGGTGAAGAAAGCAAGCAAGAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGACAGAGATGCACTTAAT 600
QY 601 GTCTTGTGACAAAGAAAGAGACAGCTGATTAAGGCGGTACATGCGAGAAAGTGA 660
Db 601 GTCTTGTGACAAAGAAAGAGACAGCTGATTAAGGCGGTACATGCGAGAAAGTGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTAATAGAAATTAATTAAGGCCAAGCACTGCTTGA 780
Db 721 ACCACTCTGCACTAGCTATCTAATAGAAATTAATTAAGGCCAAGCACTGCTTGA 780
QY 781 TATGCTGCTGATATGATCAAAAAAGCAATGGCTTCAACCACTGTTACTTGTGTGA 840
Db 781 TATGCTGCTGATATGATCAAAAAAGCAATGGCTTCAACCACTGTTACTTGTGTGA 840
QY 841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATGAGAGAGCTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATGAGAGAGCTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
 |||||
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
 QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGTGAAAAAGCAATCCAGAACAGACTTAAG 1140
 |||||
 Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGTGAAAAAGCAATCCAGAACAGACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGCGTGAATAATAGCCAGAGAAA 1200
 |||||
 Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGGCGTGAATAATAGCCAGAGAAA 1200
 QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
 |||||
 Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAATTAATTAATGAGGATTAAGGAAATCTGAACTAATGCTGCTGCGC 1320
 |||||
 Db 1261 AAGCATGAAAATTAATTAATGAGGATTAAGGAAATCTGAACTAATGCTGCTGCGC 1320
 QY 1321 AATGCTAATATGATTAATTTCTCTCAAAAGAGAGCAACACTGAAATCAAGCAATTT 1380
 |||||
 Db 1321 AATGCTAATATGATTAATTTCTCTCAAAAGAGAGCAACACTGAAATCAAGCAATTT 1380
 QY 1381 CTGACACACGAAAGTGAAGAGTATCAGAAATTTGCGAATTAAGTTGCTGCTACAAAGAA 1440
 |||||
 Db 1381 CTGACACACGAAAGTGAAGAGTATCAGAAATTTGCGAATTAAGTTGCTGCTACAAAGAA 1440
 QY 1441 AAAAGATGCAAAATCTCTTCTGAAAAGAGCAACCCAGAACAGACTTAAGGCTGACA 1500
 |||||
 Db 1441 AAAAGATGCAAAATCTCTTCTGAAAAGAGCAACCCAGAACAGACTTAAGGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAATAATGCGCAAGCTAAGAAAT 1560
 |||||
 Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAATAATGCGCAAGCTAAGAAAT 1560
 QY 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAGTCTCATGTCGATTCCTCCAGAAAC 1620
 |||||
 Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAGTCTCATGTCGATTCCTCCAGAAAC 1620
 QY 1621 CTGACTAATGATGCTGCTGCGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC 1680
 |||||
 Db 1621 CTGACTAATGATGCTGCTGCGCAATGATGATGATGATTAATTCCTCCAGAAAGAGC 1680
 QY 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGACAGTGAAGCA 1740
 |||||
 Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGACAGTGAAGCA 1740
 QY 1741 CAAAAATGATCTCGAAGAACTTTTGTGAAGAAAGCAAGCACTGGAATTTACAGATGAG 1800
 |||||
 Db 1741 CAAAAATGATCTCGAAGAACTTTTGTGAAGAAAGCAAGCACTGGAATTTACAGATGAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGGTGAAGAAATGAAATCTGAGCTTTCT 1860
 |||||
 Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGGTGAAGAAATGAAATCTGAGCTTTCT 1860
 QY 1861 CTTAGTTTGAAGAAAGAAAGACATCTTGCATGAATAATGATGCTGCGGAGAAATTT 1920
 |||||
 Db 1861 CTTAGTTTGAAGAAAGAAAGACATCTTGCATGAATAATGATGCTGCGGAGAAATTT 1920
 QY 1921 GCCATCTTAAGACTGAGAGCTAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
 |||||
 Db 1921 GCCATCTTAAGACTGAGAGCTAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAA 2000
 |||||
 Db 1981 AAAAAAAAAAAAAAAAAA 2000
 RESULT 11
 ADA11381
 XX ADA11381 standard; cDNA; 2000 BP.
 XX

AC ADA11381;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human breast cancer specific cDNA B11C-8.
 XX
 KW seq; gene; human; breast cancer; cyrostatic; tumour; gene therapy.
 OS Homo sapiens.
 XX
 PN US2002165371-A1.
 XX
 PD 07-NOV-2002.
 XX
 PF 07-AUG-2001; 2001US-00924400.
 XX
 PR 11-JAN-1996; 96US-00585392.
 PR 10-JAN-1997; 97MC-US000485.
 PR 09-APR-1997; 97US-00838762.
 PR 11-DEC-1997; 97US-00991789.
 PR 17-APR-1998; 98US-0062451.
 PR 09-APR-1999; 99US-00289198.
 PR 28-OCT-1999; 99US-00429755.
 PR 23-MAR-2000; 2000US-00534825.
 PR 24-MAY-2000; 2000US-00577505.
 PR 08-JUN-2000; 2000US-00590583.
 PR 26-OCT-2000; 2000US-00699295.
 PR 16-MAR-2001; 2001US-00810936.
 XX
 PA (FRUD/) FRUDAKIS T N.
 PA (REED/) REED S G.
 PA (SMIT/) SMITH J M.
 PA (MISH/) MISHNER L E.
 PA (DILL/) DILLON D C.
 PA (RETT/) RETTER M W.
 PA (WANG/) WANG A.
 PA (SKEK/) SKEIKY Y A W.
 PA (HARL/) HARLOCKER S L.
 PA (DAYC/) DAY C H.
 PA (LISX/) LI S X.
 PA (DENG/) DENG T.
 XX
 PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;
 DR P-PSDB; ADA11384.
 XX
 PT MPI; 2003-247262/24.
 PT
 PT New breast tumor proteins nucleic acids encoding such proteins, useful in
 PT diagnosing, preventing and/or treating diseases such as cancer,
 PT particularly breast cancer, and as markers for detecting the presence of
 PT a cancer.
 XX
 PS Claim 1, Page 140, 190pp; English.
 XX
 CC The invention relates to a breast tumour polynucleotide selected from one
 CC of the 275 fully defined nucleotide sequences (a) given in the
 CC specification, including their complements, sequences consisting of at
 CC least 20 contiguous residues of a sequence in (a), sequences that
 CC hybridise to a sequence in (a) under moderately stringent conditions,
 CC sequences having at least 75% or 90% identity to a sequence in (a), or
 CC degenerate variants of a sequence in (a). Also included are an isolated
 CC polypeptide (ii) (comprising an amino acid sequence selected from
 CC sequences encoded by (a), sequences having at least 70% or 90% identity
 CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
 CC sequences (c), and sequences having at least 70% or 90% identity to a
 CC sequence in (c)), expression vectors comprising (a), a host cell
 CC transformed or transfected with the expression vector, an isolated
 CC antibody or its antigen-binding fragment that specifically binds to (ii),
 CC a method for detecting the presence of a cancer in a patient, a fusion
 CC protein comprising at least one polypeptide (ii), an oligonucleotide that
 CC hybridises to (a), under moderately stringent conditions, a method for
 CC stimulating and/or expanding T cells specific for a tumour protein (by

CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii), an isolated T cell
CC population comprising T cells prepared from as detailed above, a T cell
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX
Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 2000; DB 8; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
DB 1 ATGTGTTGATGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
QY 61 AGGAGCAAGATGAGGCAAGTGTGCTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGAGGCAAGTGTGCTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGCACTGCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGCACTGCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTGTATGAAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTGTATGAAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCGCACTGCTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTG 360
DB 301 TGGTGTGCGCACTGCTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTG 360
QY 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGTACCACTGCTGGAAGAGTCTG 420
DB 361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGTACCACTGCTGGAAGAGTCTG 420
QY 421 GACAAAGCTCCAGAGCTGCTGAGTGGGCTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
DB 421 GACAAAGCTCCAGAGCTGCTGAGTGGGCTAAAGTCCCAAGAAAGATCTCATGCTCAG 480
QY 481 CTGAGGAGCACTGAGCGTGAACAAAGAGCAAGCAAGAAAGAGCACTGCTTCAATCTGG 540
DB 481 CTGAGGAGCACTGAGCGTGAACAAAGAGCAAGCAAGAAAGAGCACTGCTTCAATCTGG 540
QY 541 TCTGCGCAATGGGAATTCAGAAAGTAAACTCTCTGTGAGCAGAGATGCTCAACTTAAT 600
DB 541 TCTGCGCAATGGGAATTCAGAAAGTAAACTCTCTGTGAGCAGAGATGCTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATTAAGGCGGTACATGCGCAAGAGATGA 660
DB 601 GTCTTGAACAACAAAAAGAGAGAGCTGTATTAAGGCGGTACATGCGCAAGAGATGA 660
QY 661 TGTGCGTAAATGTTGCTGAACAATGCACTGATCCAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTAAATGTTGCTGAACAATGCACTGATCCAATATTCAGATGATGAGAAAT 720
QY 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAAGCCCAAGAGCACTGCTT 780
DB 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAAGCCCAAGAGCACTGCTT 780

QY 781 TATGGTGTGATATGGAATCAAAAAACAGAGAGGCTTCACACCACTGTACTGTGTTGA 840
DB 781 TATGGTGTGATATGGAATCAAAAAACAGAGAGGCTTCACACCACTGTACTGTGTTGA 840
QY 841 CATGAGCAAAAAACAGAGAGTGTGAAATTTTATCAAGAAAAACGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGAGAGTGTGAAATTTTATCAAGAAAAACGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAAAGAGCTGCTCATCTTGTGATATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAAGAGCTGCTCATCTTGTGATATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACGCAATCCAGAACATACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACGCAATCCAGAACATACTTAAG 1140
QY 1141 CTGACATCAGAGAAAGATCAGAAAGGTTCAAGGCAAGTAAATAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAAAGATCAGAAAGGTTCAAGGCAAGTAAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGGTTGAAGAAATAGAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGGTTGAAGAAATAGAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGATTAATCTGAAAAACCTGATTAATGATGATGATG 1320
DB 1261 AAGCATGAAAGTAAATATGATGATTAATCTGAAAAACCTGATTAATGATGATGATG 1320
QY 1321 AATGGTATATGATTAATTTCTCAAGAGAGAGAGAGCACTGAAATATCAGCAATTT 1380
DB 1321 AATGGTATATGATTAATTTCTCAAGAGAGAGAGAGCACTGAAATATCAGCAATTT 1380
QY 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
DB 1381 CCTGCAACAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
DB 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
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DB 1501 TCAGAGAAAGATCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGCTAGAAAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGAGAGTACTCATGTGCGATTTCCAGAAAAAC 1620
DB 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGAGAGTACTCATGTGCGATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATATGATGCACTGCTGCAATGATGATTAATTTCTTCAAGAAAGAGAC 1680
DB 1621 CTGACTAATATGATGCACTGCTGCAATGATGATTAATTTCTTCAAGAAAGAGAC 1680
QY 1681 AGAAGCACTGGAAGCAGAGCAATTTCTGCACTGAGAAATGAAGAGATCAGAGTGA 1740
DB 1681 AGAAGCACTGGAAGCAGAGCAATTTCTGCACTGAGAAATGAAGAGATCAGAGTGA 1740
QY 1741 CAAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
DB 1741 CAAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
QY 1801 ATTTGATTTCAATGAAGAAAGAGAGATGAGAGTGTGAAAAATTAATTTCTGAGCTTTCT 1860
DB 1801 ATTTGATTTCAATGAAGAAAGAGAGATGAGAGTGTGAAAAATTAATTTCTGAGCTTTCT 1860


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Db      1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACCGAAATTAATAGATGATGATGAGAGCTTGAATAAATAATGAG 1260
Db      1201 ATGTCTCAAGAACCGAAATTAATAGATGATGATGAGAGCTTGAATAAATAATGAG 1260
Qy      1261 AAGCATGAAAGTATATATGATGGAATTACTAGAAAACCTGACTATATGATGCTGCTGAC 1320
Db      1261 AAGCATGAAAGTATATATGATGGAATTACTAGAAAACCTGACTATATGATGCTGCTGAC 1320
Qy      1321 AATGTGATATATGATTAATTTCTCTCAAGAGAAAGAGACACCTGAAATATGACAAATT 1380
Db      1321 AATGTGATATATGATTAATTTCTCTCAAGAGAAAGAGACACCTGAAATATGACAAATT 1380
Qy      1381 CCTGACAAAGAAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db      1381 CCTGACAAAGAAAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy      1441 AAACAGATGCCAAAATCTCTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAAATCTCTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Qy      1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCGAGTGAATGCGCAGCCAGAGCTGAGAAAT 1560
Db      1501 TCAGAGAAAGAGTCACAAAAGCTTGAAGGCGAGTGAATGCGCAGCCAGAGCTGAGAAAT 1560
Qy      1561 TTTATGGCTATGAGAAATGAAAGACCGAAGTACTCATGTGGATTTCCCAAGAAAAC 1620
Db      1561 TTTATGGCTATGAGAAATGAAAGACCGAAGTACTCATGTGGATTTCCCAAGAAAAC 1620
Qy      1621 CTGACTAATGATGCGCACTGCTGCGCAATGATGATGATGATTAATTTCTCTCAAGAAAGAC 1680
Db      1621 CTGACTAATGATGCGCACTGCTGCGCAATGATGATGATGATTAATTTCTCTCAAGAAAGAC 1680
Qy      1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGATATACAGTACGAA 1740
Db      1681 AGAACAACCTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAAGATATACAGTACGAA 1740
Qy      1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACACATGAG 1800
Db      1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACACATGAG 1800
Qy      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGTAAGAAATGATTTCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAAAGAGAGATAGAGTGTGTAAGAAATGATTTCTGAGCTTTCT 1860
Qy      1861 CTTAGTTGTTAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGATGAT 1920
Db      1861 CTTAGTTGTTAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGATGAT 1920
Qy      1921 GCCATGCTAAGCTGGAGCTAGACAAATGAAACATCAGAGCAGCTAATAAAAAAAAAA 1980
Db      1921 GCCATGCTAAGCTGGAGCTAGACAAATGAAACATCAGAGCAGCTAATAAAAAAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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XX      XX Homo sapiens.
OS      XX
XX      XX US2003185830-A1.
XX      XX
XX      XX 02-OCT-2003.
XX      XX
XX      XX 12-NOV-2002; 2002US-00294025.
XX      XX
XX      XX 25-FEB-1997; 97US-00806099.
XX      XX 01-AUG-1997; 97US-00904804.
XX      XX 09-FEB-1998; 98US-00202056.
XX      XX 25-FEB-1998; 98US-00030607.
XX      XX 14-JUL-1998; 98US-00115453.
XX      XX 23-SEP-1998; 98US-00159812.
XX      XX 15-JAN-1999; 99US-00232149.
XX      XX 09-APR-1999; 99US-00288946.
XX      XX 13-JUL-1999; 99US-00352616.
XX      XX 12-NOV-1999; 99US-00439313.
XX      XX 18-NOV-1999; 99US-00443686.
XX      XX 14-JAN-2000; 2000US-00483672.
XX      XX 27-MAR-2000; 2000US-00536857.
XX      XX 09-MAY-2000; 2000US-00568100.
XX      XX 12-MAY-2000; 2000US-00570737.
XX      XX 13-JUN-2000; 2000US-00593793.
XX      XX 27-JUN-2000; 2000US-00605763.
XX      XX 09-AUG-2000; 2000US-00636215.
XX      XX 29-AUG-2000; 2000US-00651236.
XX      XX 06-SEP-2000; 2000US-00657279.
XX      XX 02-OCT-2000; 2000US-00679426.
XX      XX 10-OCT-2000; 2000US-00685166.
XX      XX 09-NOV-2000; 2000US-00709729.
XX      XX 12-JAN-2001; 2001US-00759143.
XX      XX 09-FEB-2001; 2001US-00780669.
XX      XX 09-MAY-2001; 2001US-00852911.
XX      XX 29-JUN-2001; 2001US-00895814.
XX      XX 10-DEC-2001; 2001US-00012896.
XX      XX 09-MAY-2002; 2002US-00144678.
XX      XX
XX      XX (CORI-) CORIXA CORP.
XX      XX
XX      XX Xu J, Stolk JA, Kalos MD;
XX      XX MPI: 2003-756193/71.
XX      XX P-PSDB; ADB13829.
XX      XX
XX      XX New isolated polypeptide for use in a vaccine for stimulating an immune
XX      XX response, or for treating or diagnosis cancer, preferably prostate
XX      XX cancer.
XX      XX
XX      XX Example 11; Page; 101pp; English.
XX      XX
XX      XX The invention relates to an isolated polypeptide comprising no more than
XX      XX 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
XX      XX peptides comprise a fragment ADB13563 of that contain naturally processed
XX      XX T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX      XX alleles. ADB13563 is a polypeptide encoded by a human prostate specific
XX      XX cDNA, one of 648 disclosed as new. Also included are nucleic acids
XX      XX encoding the proteins and peptides, expression vectors, a host cell
XX      XX transformed with the vector, an isolated antibody (or antigen binding
XX      XX fragment) that specifically binds to the protein or peptide, detecting
XX      XX the presence of a cancer in a patient (comprising contacting a patient
XX      XX sample with a binding agent that binds to the peptide or a polypeptide
XX      XX appearing as ADB13558, detecting the amount of polypeptide that binds to
XX      XX the agent and comparing the amount of polypeptide to a predetermined cut-
XX      XX off value to determine the presence of cancer), a fusion protein
XX      XX comprising the peptides or proteins, stimulating or expanding T cells
XX      XX specific for a tumour protein comprising contacting T cells with the
XX      XX peptides or the isolated T cell population, treating prostate cancer in a
XX      XX patient comprising administering a composition comprising the peptides,
XX      XX nucleic acids, antibodies or compounds, determining the presence of a
XX      XX cancer in a patient and treating prostate cancer in a patient comprising
XX      XX incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

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from a patient with the peptides or antigen presenting cells that express the peptides so that the T cells proliferate, and administering the proliferated T cells to the patient. The peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a known cDNA showing sequence similarity to one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.

SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;

Query Match	Score	DB	Length
100.0%	2000	10	2000

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGTTAGGTTGATTCCATGCGCGGTGCTCTTCTGGAAGAAGCCATTGGCTC 60

Db 1 ATGGGGTTAGGTTGATTCCATGCGCGGTGCTCTTCTGGAAGAAGCCATTGGCTC 60

QY	QY
61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCGTTGCTTCCCTGCTGCAGGGAGAGCGCGAAG 120	61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCGTTGCTTCCCTGCTGCAGGGAGAGCGCGAAG 120

Oy 121 AGCAAGTGGGCACTTCTGAGAGCCAGCAGCACTCTGCTATGAGAGCACTCAGAGCAAG 180
 Db 121 AGCAAGTGGGCACTTCTGAGAGCCAGCAGCACTCTGCTATGAGAGCACTCAGAGCAAG 180

0Y 181 ATGGCAAGTGTGCGGCACTGCTTCCCCCTGTGACGGGGAGTGGCAAGCAACGTG 240

241 GGGCGTTCTGGAGACCAAGAGACTTGTCTATGAGACACTTCAGGAACAAGATGGCGAG 300

301 TGGTGTGCCACTGCTTCCCCCTGCTGCAGGGGAGCGCGCAAGCAAGTGGGCGCTTGG 360

DB 30 TGGTACCGCAGGCTCCATCATGAGGCCAAGGCACAAGTGAGGCTTTGG 360

OY 361 GGAGACTACGATGACGTGCTTCATGAGGCCAAGTACCAGTCCGTGGAAAGATCTG 420

Db 361 GGAGCTACGATGACAGTGCCTTCACGAGCCACAGTACCACGTCCGTGAGAAAGATCTG 420

Qy 421 GACAACTCCACAGAGTGCCTGTGTGGGTAAAGTCCCCAGAAAGATCTCATGCTATG 480

421 GACAAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480
481 CTGAGGGACACTGACGTGAACAAAGAGGACACAGCAAGAAAAGAGACTGCTTCAATCTGGCC 540

Db	481	CTCAGGGGACCTGACCTGAACAAAGAGGACAAGCAAGCAAAAGAGGACTGCTCTCATCTGGGCC	540
Ov	541	TCATCCCAATGGGAATTCAGAGTAGTAAATACTCCTGCTGGAAGAGCGATGTCAACTTAAT	600

Db 541 TCTGCCAATGGGAATTGAGAAGTAGTAAAACTCCTCTGGACAGACGATGCAACTTAAT 600

Db 601 GTCCCTGACACAAAGAGGACAGCTCTGATTAAGGCCGTCATCCACGAGAAAGATGAA 660

Db 661 TGTGGCTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGAGTATGGAAAT 720

Dbb 721 ACCACTCTGCATACGCTATCTATAATGAAAGTAAATTAATGGCCAAAGCACTGCTCTTA 780

Qy 781 TATGGTCTGATATCGAATCAAAAAACAGCATGGCTCACCACTGTTACTTGCTGA 840

841 CATGAGCAAAACAGACGAGTCGTGAATTTTAAATCAGAAAAAGCGAATTTAAATGCA 900

DB	84	CAATGCAAAAACAGCAGCTGCGTAAATTTTAAATCAAGAAAAAACGGAATTTAAATGCA	900
QY	901	CTGATAGATATGGAAGATGCTCTCATCTTGCCTATGTTGGATCAGCAAGTATA	960

Db 901 CTGATAGATATGGAAGSACTGCTCTCAATCTTGCTGATNTGTGGATCAGCAAGTATA 960

Qy 961 GTGACCTTCTACTTGAGCAAAATATGTGATATCTTCTCAAGATCTATCTGGACAGAGC 1022

Db 961 GTGAGCCTTCTACTTGAGCAAAATTTGATGTATCTTCTCAAGATCTATCTGGACAGACG 1022

Qy 1021 GCCAGAGATATGCTGTCTTCTAGTCATCATCATGTAATTTGCCAGATTACTTTCTGACTAC 1088

Db 1021 GCCGAGAGATATGCTGTTTCTAGTATCATCATGTAAATTGCCAGTTTACTTTCTGACTAC 108

[illegible]

Db 1141 CTGACATCAGAGGAGGTCACAAAGTTCAAAGCGAGTAAATATGCCAGCCAGAGAAA 120

Dbb 1201 ATGTCCTCAAGAACCCAGAAATAAATAGGATGCTATGAGAGCGTTGAAAGAAAGAAATGTAAG 1266

DB 1261 AAGCATGAAAGTAAATGATGGGATTACTAGAAAAAAGCTGACTAATGATGCTCACTGCTGGC 1322

QY 1332 ATGCTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACACCTGAAAAATCAGCAATT 138
 1321 AATGCTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACACCTGAAAAATCAGCAATT 138

Oy	1381	CCTGCAACGAAAGGAAAGTATGACAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	144
Db	1381	CCTGCAACGAAAGTGAAGATATACAGAAATTTGCGAATTAGTTCTGACTACAAAGAA	144

QY 1441 AAAACAGATGCCAAAATACCTTTCTGAAAACAGCAACCCAGAACCAAGACTTTAAAGCTGACA 150

Db 1441 AAAACAGATGCCAAAATACCTTTCTGAAAACAGCAACCCAGAACCAAGACTTTAAAGCTGACA 150

Qy 1501 TCAGGGAAGAGTCA CAAAGGCTTAGGCGCACTGTAATAATGGCCAGCAGACTAGAAAT 156

Dp 1501 TCAGGGAAGAGTCA CAAAGGCTTAGGCGCACTGTAATAATGGCCAGCAGACTAGAAAT 156

QY 1561 TTTATGCTATCGAAGAAATGAAGAACGCGAAGTACTCATGTGCGATTCCAGAAAC 1622
 1562 TTTTATGCTATCGAAGAAATGAAGAACGCGAAGTACTCATGTGCGATTCCAGAAAC 1623
 1563 TTTTATGCTATCGAAGAAATGAAGAACGCGAAGTACTCATGTGCGATTCCAGAAAC 1624

1621 CTGACTAATGCTGCACCTGCTGCATATGATGATTAAATTCCTCAAGAAGAC 168

1681 AGAACACTTGAAAGCCAGCAATTTCTGACACTGAGATGAGAGTATCACAGTACGAA 174

1741 CAAATGATACTCGAAGCAATTTGTGTGAACACGAACACTGGAATATTACACGATG 180

DB 174 CAAATGATACCTCAGAAAGCAATTTTGTAGAAACGAAACCTGAAATATTTACACGAG 180

QY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAACTGTTGAAAAAATGATTCGAGCTTCT 186

QY 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATAGTACGTTGGCGGAAGAATT 1920
PI |||||
DB 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGCATGAAATAGTACGTTGGCGGAAGAATT 1920
QY 1921 GCCATGCTTAAGACTGGAGCTGACACATGAAACATCAGAGCCAGCTTAATAAAAAA 1980
PI |||||
DB 1921 GCCATGCTTAAGACTGGAGCTGACACATGAAACATCAGAGCCAGCTTAATAAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
PI |||||
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
RESULT 14
ADG26240
ID ADG26240 standard; cDNA; 2000 BP.
AC ADG26240;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human prostate-specific CDNA #359.
XX
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN US2003157089-A1.
XX
PD 21-AUG-2003.
XX
PF 09-MAY-2002; 2002US-00144678.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA,
PI Kalos MD, Fanger GR, Rietter MW, Stolk JA, Day CH, Vedvick TS,
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J,
PI McNeill PD, Houghton RL, Vinals Y De Baesolc, Foy TM, Matanabe Y,
PI Meagher MJ, Deng T;
XX
DR WPI; 2003-777973/73.
DR P-PSDB; ADG26245.

XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 11; SEQ ID NO 374; 99p; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAAGCATTTGCTTC 60
DB 1 ATGTCGTTGAGAGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAAGCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGTCTATGAGAACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGTCTATGAGAACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGCAAGTGTGCCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGTTCTGAGACCAAGCAAGCTGTCTATGAGAACACTCAGAGCAAGTGGCAAG 300
DB 241 GGGCGTTCTGAGACCAAGCAAGCTGTCTATGAGAACACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACAGTCCGTGGAAGAATCTG 420
DB 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACAGTCCGTGGAAGAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTACGTCAG 480
DB 421 GACAAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGAAGAGATCTACGTCAG 480
QY 481 CTCAGGGAACCTGACGTGAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
DB 481 CTCAGGGAACCTGACGTGAACAAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAAAGCTCTGCTGAGACAGAGTCAATCTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAAAGCTCTGCTGAGACAGAGTCAATCTTAAT 600
QY 601 GTCTTGAACAATAAAGAGGACAGCTGTGAATAAGCCGTCAATGCCAGGAAGTGA 660
DB 601 GTCTTGAACAATAAAGAGGACAGCTGTGAATAAGCCGTCAATGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720

Db 661 TGTGCTTAATGTGTGCGAATGCGCATGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGACATACGATATCTATATGAAGATTAATATGCGCAAGACCTGCTTTA 780
Db 721 ACCACTCTGACATACGATATCTATATGAAGATTAATATGCGCAAGACCTGCTTTA 780
Qy 781 TATGTCCTGATATCGAATCAAAAAACAAGATGCGCTCACACACCTGATCTTGCTGA 840
Db 781 TATGTCCTGATATCGAATCAAAAAACAAGATGCGCTCACACACCTGATCTTGCTGA 840
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Db 841 CATGAGCAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTTAAATGCA 900
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Db 901 CTGATATGATATGGAAGAGACTGCTCTATATCTTGCTGATGTTGTGATGACAGATTA 960
Qy 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1081 AAAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
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Db 1141 CTGACATCAGAGAGAGGTGACAAAGGTTCAAGGCGTGAATAATGCGCGACAGAGAA 1200
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Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATGAGAGGTGGAAGAAATGTAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACTGACTATGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGGATTACTAGAAAACTGACTATGCTGCTGCGC 1320
Qy 1321 AATGATGATTAATGATTTAATCTCTCAAGAGAAAGACACCTGAAAATCAGCAATTT 1380
Db 1321 AATGATGATTAATGATTTAATCTCTCAAGAGAAAGACACCTGAAAATCAGCAATTT 1380
Qy 1381 CCTGACACGAAAGTAAAGATATCAAGAAATTTGCGAATTAATTTCTGACTCAAGAA 1440
Db 1381 CCTGACACGAAAGTAAAGATATCAAGAAATTTGCGAATTAATTTCTGACTCAAGAA 1440
Qy 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCGATGAGAAATGCGCAGAGCTAGAGAAAT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCGATGAGAAATGCGCAGAGCTAGAGAAAT 1560
Qy 1561 TTTATGCTATTCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGCGATTTCCAGAAAC 1620
Db 1561 TTTATGCTATTCGAAGAAATGAAGAAGCAGAAAGTACTCATGTGCGATTTCCAGAAAC 1620
Qy 1621 CTGACTTAATGTCGCACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAAAGC 1680
Db 1621 CTGACTTAATGTCGCACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAAAGC 1680
Qy 1681 AGAAGCCTGGAAGCAAGATTTCTGACACTGAGAAATGAAGATATCACTATGACGA 1740
Db 1681 AGAAGCCTGGAAGCAAGATTTCTGACACTGAGAAATGAAGATATCACTATGACGA 1740
Qy 1741 CAAATATGATCTGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
Db 1741 CAAATATGATCTGAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAG 1800

Qy 1801 ATTCTGATTCATGAAGAAAGCAGATGAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAGAGTGTGTAAGAAAAATGAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGACATCTGCAAGAAATATGATCGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTGCAAGAAATATGATCGTTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTGAGACACAAATGAAAACATCAGAGCCAGCTTAAAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTGAGACACAAATGAAAACATCAGAGCCAGCTTAAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 15
AAA06599 standard; cDNA; 2000 BP.
ID AAA06599; standard; cDNA; 2000 BP.
AC AAA06599;
XX
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
OS Homo sapiens.
XX
XX MO200004149-A2.
PN
XX
XX 27-JAN-2000.
PD
XX
XX 14-JUL-1999; 99WO-US015838.
PF
XX
XX 14-JUL-1998; 98US-00115453.
PR
XX 14-JUL-1998; 98US-00116134.
PR 23-SRP-1998; 98US-00159812.
PR 23-SRP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yuguu J, Xu J, Mitcham JL;
PI WPI; 2000-171268/15.
XX
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein.
XX
XX
XX Claim 50; Page 222-223; 263pp; English.
XX
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumor protein (prp). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express the
XX polypeptides, antibodies against the polypeptides and vaccines comprising
XX them can be used for inhibiting the development of prostate cancer in a
XX patient. The polypeptides can be used to generate antibodies or anti-
XX idiotypic antibodies for passive immuno therapy. A portion of the
XX polynucleotides encoding the polypeptides can be used as a probe or to
XX modulate the expression of the polypeptides. AAA06541 to AAA06691 and
XX CC AA082000 to AA082020 represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 2000 BP; 698 A; 387 C; 489 G; 426 T; 0 U; 0 Other;

Query Match 99.9%; Score 1998.4; DB 3; Length 2000;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGTGTGAAGTATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
DB 1 ATGGTGTGAAGTATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
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DB 61 AGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGTGCGAGGAGCGGCAAG 120
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Search completed: December 18, 2005, 08:17:04
 Job time : 1203.05 secs

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RESULT 2
US-09-352-616A-374
/ Sequence 374, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillon, David C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Uiang, Yungui
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352,616A
/ NUMBER OF SEQ ID NOS: 472
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 3
US-09-289-198-302
; Sequence 302, Applicant US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1921 GCCATGCTAAGACTGAGGCTGACACAAATGAAATCATCAGAGCCAGCTTAAAAA 1980
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Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-636-215-374
Sequence 374, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/636, 215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGAGAGTGAAGAAATGAAG 1260

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1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 5
US-09-685-166A-374
Sequence 374, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocke, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ronger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepier, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-685-166A-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1681 AGAAGCCTGAAAGCGAGCAATTTCTGCACTGAGAAATGAAGAGATACAGTGCAGAA 1740
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Db 1921 GCCATCTAAGACTGAGCTTACACATATGAAACATCAGAGCCGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 6
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda G.
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTTGATGATGATTCATGCGCGCTCTTCTGTAAGAGCAATTTGCTTC 60
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Qy      1141 CTGACATCAGAGAAAGAGTCACAAAAGTTCAAAAGCAGTGAATTTAGCCAGCAGAGAA 1200
Db      1141 CTGACATCAGAGAAAGAGTCACAAAAGTTCAAAAGCAGTGAATTTAGCCAGCAGAGAA 1200
Qy      1201 ATGTCTCAAGAACCGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACCGAAATTAATTAAGATGTTGATGAGAGGTTGAAGAAATGAAG 1260
Qy      1261 AAGCATGAAGATTAATGTTGGGATTACTAGAAAACTGATTAATGTTGCTGCTGGC 1320
Db      1261 AAGCATGAAGATTAATGTTGGGATTACTAGAAAACTGATTAATGTTGCTGCTGGC 1320
Qy      1321 AATGTGATATGATTAATTCCTCAAGAGAGAGCAACAAGTGAATGAGCAATTT 1380
Db      1321 AATGTGATATGATTAATTCCTCAAGAGAGAGCAACAAGTGAATGAGCAATTT 1380
Qy      1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGGAAATTTGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAGTGAAGATATCAGAAATTTGGAAATTTGTTCTGATCAAGAA 1440
Qy      1441 AAAACAGATGCCAAATATCTCTGTAACACCAACCCAGAACTTAATTAAGCTGACA 1500
Db      1441 AAAACAGATGCCAAATATCTCTGTAACACCAACCCAGAACTTAATTAAGCTGACA 1500
Qy      1501 TCAGAGGAAGATGCAAAAAGCTTGAAGGCACTGAAAATGAGCAGCAGAGCTAGAAT 1560
Db      1501 TCAGAGGAAGATGCAAAAAGCTTGAAGGCACTGAAAATGAGCAGCAGAGCTAGAAT 1560
Qy      1561 TTTATGGCTATGGAAGAAATGAAGAACCGAAAGTACTCATGTGGATTTCCAGAAAC 1620
Db      1561 TTTATGGCTATGGAAGAAATGAAGAACCGAAAGTACTCATGTGGATTTCCAGAAAC 1620

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Qy      1621 CTGACTAATGGTGGCACTGCTGGCAATGTTGATGATTAATTCCTTCAAGAAAGAC 1680
Db      1621 CTGACTAATGGTGGCACTGCTGGCAATGTTGATGATTAATTCCTTCAAGAAAGAC 1680
Qy      1681 AGAACAACCTGAAGAGCAGCAATTTCTCTGACATGAGAAATGAAGATATCACAGTGA 1740
Db      1681 AGAACAACCTGAAGAGCAGCAATTTCTCTGACATGAGAAATGAAGATATCACAGTGA 1740
Qy      1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACGAACCTGGAATATTACACATGAG 1800
Db      1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACGAACCTGGAATATTACACATGAG 1800
Qy      1801 ATTCTGATTCATGGAAGAAAGAGATAGAGTGTGAAAAATGAAATTCAGCTTCT 1860
Db      1801 ATTCTGATTCATGGAAGAAAGAGATAGAGTGTGAAAAATGAAATTCAGCTTCT 1860
Qy      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAATAATAGTACGTTGCGGAGAAATTT 1920
Db      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAATAATAGTACGTTGCGGAGAAATTT 1920
Qy      1921 GCCATGCTAAGACTGAGACTGAGACAAATGAACATCAGAGCCAGCTAAAAA 1980
Db      1921 GCCATGCTAAGACTGAGACTGAGACAAATGAACATCAGAGCCAGCTAAAAA 1980
Qy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 7
US-09-679-426-374
; Sequence 374, Application US/09679426
; Patent No. 6759315
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitchell, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Liang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-374

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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGATCTC 60
Db      1 ATGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGATCTC 60

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OY	61	AGGACCAAGATGGGCAATGGTGTGCTGCGCGTTCCTCCCTGCTGAGGGAAGGGCAAG	120
Db	61	AGGACCAAGATGGGCAAGTGGTGTGCTGCGCGTTCCTCCCTGCTGAGGGAAGGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGAGAGCCACGACGACTGTGCTATGAGAACACTGAGGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTTGAGAGCCACGACGACTGTGCTATGAGAACACTGAGGAGCAAG	180
OY	181	ATGGGCAAGTGTGTCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
Db	181	ATGGGCAAGTGTGTCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG	240
OY	241	GGCGCTTCTGAGAACGACGACGACTCTGCTATGAAGACACTGAGAACATATGGGCAAG	300
Db	241	GGCGCTTCTGAGAACGACGACGACTCTGCTATGAAGACACTGAGAACATATGGGCAAG	300
OY	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACATGATGGGCGCTTGG	360
Db	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGACATGATGGGCGCTTGG	360
OY	361	GGAGACTACATGACATGACGCTTCATGAGAGCCAGAGTACCAAGTCCGTGAGAAAGATCTG	420
Db	361	GGAGACTACATGACATGACGCTTCATGAGAGCCAGAGTACCAAGTCCGTGAGAAAGATCTG	420
OY	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAGATCTCATGCTCATG	480
Db	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGGACACTGAGCTGTGAACAAGAGGCAAGCAAAAGAGACTGCTCATCTGTGGCC	540
Db	481	CTCAGGGACACTGAGCTGTGAACAAGAGGCAAGCAAAAGAGACTGCTCATCTGTGGCC	540
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OY	601	GTCCTTGAACAACAAAGAGGACAGCTGTGTAAGGCCGTACCAATGCCAGGAAGATGAA	660
Db	601	GTCCTTGAACAACAAAGAGGACAGCTGTGTAAGGCCGTACCAATGCCAGGAAGATGAA	660
OY	661	TGTGGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATATGGAAT	720
Db	661	TGTGGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATATGGAAT	720
OY	721	ACCACTGCACTACGCTATCATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
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OY	781	TATGGTGTGATATCGAATCAAAAAACAAGATGGCCACACCACTGTATCTTGATGTA	840
Db	781	TATGGTGTGATATCGAATCAAAAAACAAGATGGCCACACCACTGTATCTTGATGTA	840
OY	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
OY	901	CTGATTAATATGGAAGGACGCTCTCATCTGCTGTGATTTGTGATGATGACAAAGTATA	960
Db	901	CTGATTAATATGGAAGGACGCTCTCATCTGCTGTGATTTGTGATGATGATGACAAAGTATA	960
OY	961	GTCAGCCCTTCACTTGAGCAAAAATATGATGATCTTCAAGATCTATCTGGACAGACG	1020
Db	961	GTCAGCCCTTCACTTGAGCAAAAATATGATGATCTTCAAGATCTATCTGGACAGACG	1020
OY	1021	GCACAGAGTATGCTGTTCTATGTCATCATCATGTAATTTCCAGTTACTTCTGACTAC	1080
Db	1021	GCACAGAGTATGCTGTTCTATGTCATCATCATGTAATTTCCAGTTACTTCTGACTAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTCTGTAAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTGTAAAAACAGCAATCCAGAACAAAGACTTAAAG	1140
OY	1141	CTGACATCAAGGAAGTCAACAAAGTTTCAAGGCAAGTGAATAAGCCAGCCAGAGAA	1200

Db	1141	CTGACATCAGGAGAGAGTCACAAAGGTTCAAAAGCAGTAAAAATACCCAGCCAGAGAAA	1200
Qy	1201	ATGCTCTCAAGAACCCAGAAAATTAATTAAGATGGTGAATGAGAGGTTGAAAGAAATGAG	1260
Db	1201	ATGCTCTCAAGAACCCAGAAAATTAATTAAGATGGTGAATGAGAGGTTGAAAGAAATGAG	1260
Qy	1261	AAGCATGAAGTAAATATGTGGGATTACTGAAAACTGACTAATGGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGTAAATATGTGGGATTACTGAAAACTGACTAATGGTGTCACTGTGGC	1320
Qy	1321	AATGGTGTAATGATTAATTTCTTCAAGAGAGGAGCAACCTGAAAAATTCAGCAATTT	1380
Db	1321	AATGGTGTAATGATTAATTTCTTCAAGAGAGGAGCAACCTGAAAAATTCAGCAATTT	1380
Qy	1381	CCTGACAAACGAAATGAAAGATACACAGAAATTTGGAAATTAAGTTTGTGACTCAAGAA	1440
Db	1381	CCTGACAAACGAAATGAAAGATACACAGAAATTTGGAAATTAAGTTTGTGACTCAAGAA	1440
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Db	1441	AAACAGATGCCCAAATTAATCTCTTCTGAAAGACGAAACCCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAGAGTCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTTGAATAAT	1560
Db	1501	TCAGAGAGAGTCACAAAGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTTGAATAAT	1560
Qy	1561	TTTATGGCTATCCGAAGAAATGAANAACACGGAAGTACTATGTCCGAAATTTCCAGAAAC	1620
Db	1561	TTTATGGCTATCCGAAGAAATGAANAACACGGAAGTACTATGTCCGAAATTTCCAGAAAC	1620
Qy	1621	CTGACTAATGGTGCACATGCTGCGCAATGATGATGATGAATTAATTTCTTCCAGGAAGAGC	1680
Db	1621	CTGACTAATGGTGCACATGCTGCGCAATGATGATGATGAATTAATTTCTTCCAGGAAGAGC	1680
Qy	1681	AGAACACCTGAAAGCCACGCAATTTCTTGACACTGGAATGAAGATATCAACATGACGAA	1740
Db	1681	AGAACACCTGAAAGCCACGCAATTTCTTGACACTGGAATGAAGATATCAACATGACGAA	1740
Qy	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG	1800
Db	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAAGAAAGACAGATGAAGTGGTTGAATAATGAAATTCGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGACAGATGAAGTGGTTGAATAATGAAATTCGAGCTTTCT	1860
Qy	1861	CTTAGTTGTAAGAAAGAAAGACATCTTTCAGTGAATAATGTAAGTTCGGGAAAGAAATTT	1920
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Qy	1921	GCCATGCTAAGACTGAGAGCTTGAACAATGAACATCAAGAGCCAGGCTTAAAAAATTTT	1980
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Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
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RESULT 8			
US-09-759-143-374			
Sequence 374: Application US/09759143			
Patent No. 6800746			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Devin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan L.			
APPLICANT: Jiang, Yuqun			
APPLICANT: Henderson, Robert A.			
APPLICANT: Kalos, Michael D.			
APPLICANT: Panger, Gary R.			

APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGGTGAAGTTGATTCATGCGCGGCTCTTCTGTGAAGAAGCCATTGGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCCGTTGCTTCCCTGTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCCGTTGCTTCCCTGTGCAAGGAGCGGCAAG 120
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DB 121 AACCAAGTGGGCACTTCTGAGACCAAGCACTCTGCTATGAAGACATTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGCG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGCG 240
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DB 301 TGGTGTGCACTGCTTCCCTGTGCAAGGAGGAGTGGCAAGCAAGTGGCAAG 360
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DB 361 GGAAGACTAGATGACAGTGGCTTCAATGAGGCCAAGTACAGTCCGTGGAGAAAGTC 420
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DB 481 CTCAGAGGACATGACGTGAACAAGAAAGCAAGCAAAAGAGATCTGCTTCAATCTGGCC 540
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DB 541 TCTGCAATGGGAATTCAGAGTAAATCTCGTGTGACAGACGATGATCAATCTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGCCGTACATGCCAGGAAGATGA 660
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DB 661 TGTGCTTATGTTGCTGGAACATGGCACTGATCAATATTCAGATGATGGAAT 720

QY 721 ACCACTGCACTAGCCTATGATTAAGTAATTAATGGCCAAAGCACTGCTTGA 780
DB 721 ACCACTGCACTAGCCTATGATTAAGTAATTAATGGCCAAAGCACTGCTTGA 780
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DB 1501 TCAGAGGAAGTCAACAAAGCTTGAAGGCAAGTGAATGGCCAGCAGAGCTAGAAAT 1560
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DB 1561 TTTATGCTATGAGAAATGAAGAGCAGGAATCTCATGTGGATTTCCAGAAAG 1620
QY 1621 CTGACTAATGGTGCAGCTGCTGGCAATGGTGAATGAATTAATCTTCCAGAAAG 1680
DB 1621 CTGACTAATGGTGCAGCTGCTGGCAATGGTGAATGAATTAATCTTCCAGAAAG 1680
QY 1681 AGAACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAAGATATCACAGTACGA 1740
DB 1681 AGAACCTGAAAGCAGCAATTTCTGCACTGAGAAATGAAGATATCACAGTACGA 1740
QY 1741 CAAATGATCTCAGAGCAATTTTGTGAAGACGAACACTGGAATATTAACAGATGAG 1800
DB 1741 CAAATGATCTCAGAGCAATTTTGTGAAGACGAACACTGGAATATTAACAGATGAG 1800


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Db      1321 AATGTGATTAATGATTTAAATTCCTCAAGAGAGACGAAACCTGAAATCAGCAATTT 1380
QY      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTGTTCTGATCAAGAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTGTTCTGATCAAGAAAGAA 1440
QY      1441 AAACAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAACCAAGACTTTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAACCAAGACTTTAAAGCTGACA 1500
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Db      1501 TCAGAGAAAGAGTCAACAAAGGCTTGAAGGCAAGTAAATGCGCAAGCAGAGCTAGAAAT 1560
QY      1561 TTTATGGCTATGCAAGAAATGAAGAGCAAGCAAGTATCTGATGGAATTTCCAGAAAC 1620
Db      1561 TTTATGGCTATGCAAGAAATGAAGAGCAAGCAAGTATCTGATGGAATTTCCAGAAAC 1620
QY      1621 CTGACTTAATGCTGCACTGCTGCAATGCTGATGATGATTAATCTCCCAAGAGAGAGC 1680
Db      1621 CTGACTTAATGCTGCACTGCTGCAATGCTGATGATGATTAATCTCCCAAGAGAGAGC 1680
QY      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAAGAGATGACAGTGAAGAA 1740
Db      1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAAGAGATGACAGTGAAGAA 1740
QY      1741 CAAAAATGATTAATGAGAGCAATTTGTGAAGACAGAACTGGAATATTAACAGATGAG 1800
Db      1741 CAAAAATGATTAATGAGAGCAATTTGTGAAGACAGAACTGGAATATTAACAGATGAG 1800
QY      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAAGAAATGAAATCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAAGAAATGAAATCTGAGCTTTCT 1860
QY      1861 CTTAGCTTTGAAGAAAGAAAGCAGATCTTGCATGAAATGTAAGTTGGGAGAAAT 1920
Db      1861 CTTAGCTTTGAAGAAAGAAAGCAGATCTTGCATGAAATGTAAGTTGGGAGAAAT 1920
QY      1921 GCCATGCTAGAGCTGAGAGTACAGATGAAACATCAGAGCGCTAAGAAAAA 1980
Db      1921 GCCATGCTAGAGCTGAGAGTACAGATGAAACATCAGAGCGCTAAGAAAAA 1980
QY      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-699-295-302
; Sequence 302, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Frudakie, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda B.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelley, Yaelir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-302

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Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGTGTGAGGTGATTCATATGCGCGGTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db      1 ATGGTGTGAGGTGATTCATATGCGCGGTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY      121 AGCAACGTGGGCACTTTCTGAGAGCAAGCAAGCTGCTGATGAAGCACTCAGAGGCAAG 180
Db      121 AGCAACGTGGGCACTTTCTGAGAGCAAGCAAGCTGCTGATGAAGCACTCAGAGGCAAG 180
QY      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY      241 GCGGCTTTGAGAGACCAAGCAAGCTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
Db      241 GCGGCTTTGAGAGACCAAGCAAGCTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
Db      301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
QY      361 GAGAGCTAGATGACAGTGCCTTCAATGAGGCCAGGTATCACGTCGTGAGAGAAATCTG 420
Db      361 GAGAGCTAGATGACAGTGCCTTCAATGAGGCCAGGTATCACGTCGTGAGAGAAATCTG 420
QY      421 GACAAAGCTTCAAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
Db      421 GACAAAGCTTCAAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
QY      481 CTCAGAGGACACTGAGAGTGAAGAAAGCAAGCAAGAAAGAGGACTGCTTAATCTGCGCC 540
Db      481 CTCAGAGGACACTGAGAGTGAAGAAAGCAAGCAAGAAAGAGGACTGCTTAATCTGCGCC 540
QY      541 TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGCAGAGCATGTCAACTTAAT 600
Db      541 TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGCAGAGCATGTCAACTTAAT 600
QY      601 GTCTTTGACAAAGAAAGAGCAGCTGTGATTAAGGCGGTCAATGCCAGAAAGATGAA 660
Db      601 GTCTTTGACAAAGAAAGAGCAGCTGTGATTAAGGCGGTCAATGCCAGAAAGATGAA 660
QY      661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTTCCAGATGATGGAAT 720
Db      661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTTCCAGATGATGGAAT 720
QY      721 ACCACTCTGCACTAGCTATCTAATATGAAGTAAATTAATGAGCAAGCACTGCTCTTA 780
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RESULT 11
US-09-534-825A-302
; Sequence 302, Application US/09534825A
; Patent No. 6861506

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534,825A
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FaestSeq For Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-534-825A-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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181 ATGAGCAATGAGTGTGCGGCACTGCTTCCTCTGCTGAGAGAGAGAGAGAGAGAGAG 240
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RESULT 12
US-09-657-279-374
; Sequence 374, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepner, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-10-012-896-374
Sequence 374 Application US/10012896
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Huzel, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Baseols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro

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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  ATGGTGGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60

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QY      181  ATGGGCAAGTGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
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DB      481  CTCAGGGAACATGACGTGAACAGAAAGAACAGCAAAAGAGACTGCTCTACATCTGGCC 540

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QY      1381  CCTGCAACGAAAGGAAAGATATCAAGAAATTTGCAATTTGTTCTGACATCAAGAA 1440
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QY      1441  AAACAGATGCCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
DB      1441  AAACAGATGCCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500

QY      1501  TCAAGAGAAAGATCACAAAGCTTGAAGGCACTGAAATGGCCAGCAGAGCTAAGAAAT 1560
DB      1501  TCAAGAGAAAGATCACAAAGCTTGAAGGCACTGAAATGGCCAGCAGAGCTAAGAAAT 1560

QY      1561  TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAC 1620
DB      1561  TTTATGGCTATGGAAGAAATGAAGAGCAGGAAGTACTCATGTGGATTTCCAGAAAAC 1620

QY      1621  CTGACTAATGATGCACTGCTGCAATGCTGATGAATTAATTTCTTCCAGAAAGAC 1680
DB      1621  CTGACTAATGATGCACTGCTGCAATGCTGATGAATTAATTTCTTCCAGAAAGAC 1680

QY      1681  AGAACACTGAAAGCCAGCAATTTCTCTGACACTGAGATGAAGAGTATCAAGTACGAA 1740
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QY      1741  CAAATGATATCTCAGAAAGATTTTGTGAAGAACGAACCTGGAATATTAACAGATGAG 1800
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QY      1801  ATTCTGATTCATGAGAAAAAGAGATAGAAAGTGTGAAAAATGAAATCTGAGCTTCT 1860
DB      1801  ATTCTGATTCATGAGAAAAAGAGATAGAAAGTGTGAAAAATGAAATCTGAGCTTCT 1860

QY      1861  CTTAGTTGTAAGAAAAAGAAAGACATCTTGACATGAATAATGTAAGTTGCGGGAAGAAAT 1920
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RESULT 14			
US-09-439-313-375			
/ Sequence 375, Application US/09439313			
/ Patent No. 6329505			
GENERAL INFORMATION:			
/ APPLICANT: Xu, Jiangchun			
/ APPLICANT: Dillon, Davin C.			
/ APPLICANT: Mitcham, Jennifer L.			
/ APPLICANT: Harlocker, Susan Louise			
/ APPLICANT: Jiang Yuqul			
/ APPLICANT: Reed, Steven G.			
/ APPLICANT: Kaios, Michael			
/ APPLICANT: Fanger, Gary			
/ APPLICANT: Retter, Mark			
/ APPLICANT: Solk, John			
/ APPLICANT: Day, Craig			
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
/ FILE REFERENCE: 210121.427C9			
/ CURRENT APPLICATION NUMBER: US/09/439,313			
/ CURRENT FILING DATE: 1999-11-12			
/ NUMBER OF SEQ ID NOS: 575			
/ SOFTWARE: FastSeq for Windows Version 3.0			
/ SEQ ID NO 375			
/ LENGTH: 2040			
/ TYPE: DNA			
/ ORGANISM: Homo sapien			
US-09-439-313-375			
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Best Local Similarity 97.8%; Pred. No. 0;			
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;			
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Db	1	ATGTTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAAGAACCAATTTGTCTC	60
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Db	61	AGGAGCAAGATGGGCAAGTGGTGTGCTGCCGTTGCTCCCTGCTCAGAGGAGTGGCAAGCGCAAG	120
QY	121	AGCAACGTGGGCACTTCTGAGAGCAACGACGACTCTGCTATGAAAGACACTCAGGAGCAAG	180
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QY	301	TGGTGTGGCCACTGTCCCTGCTGCGCAAGGGGAGCGGCAAGAGCAAGTGGGGCTTGG	360
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Db	421	GACAAAGCTTCCACAAAGCTGCTGTGGGGGTAAAGTCCCAAGAAAGATCTCATGTGCATG	480

QY	481	CTCAGGGGCACTGACGCTGAACAAGAGACAGGAGAAAGAGACTGCTCTCATCTGACC	540
Db	481	CTCAGGGGCACTGACGCTGAACAAGAGACAGGAGAAAGAGACTGCTCTCATCTGACC	540
QY	541	TCGCGCAATGGGAAATTCAGAAATGTAATACTCCTGCTGACAGACGATGTCAACTTAAT	600
Db	541	TCGCGCAATGGGAAATTCAGAAATGTAATACTCCTGCTGACAGACGATGTCAACTTAAT	600
QY	601	GTCCCTTGACAAACAAAAGAGGACAGCTCTGTATAAGCCGTACAAATGCAAGAAAGATGAA	660
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Db	901	CTGATATGATATGGAAGGACTGCTCTCATCTTCTGCTGATGTTGATGATCAGCAAGTATA	960
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Db	1081	AAAAAAGAAACAGATGCTTAAAAATCTCTTCTGAAACAGCAATCAGAACAAAGACTTAAG	1140
QY	1141	CTGACATCAGAGGAAGTCAACAAAGTTCAAGGCAAGTGAATAATAGCCAGCCAGAGAA	1200
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Db	1321	AATGATGATATATGGAATTAATTCCTCAAGAGGAGAGCAACACTGTAATAATCAGCAATTT	1380
QY	1381	CTGACAAACGAAGTGAAGAGTATCACAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA	1440
Db	1381	CTGACAAACGAAGTGAAGAGTATCACAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA	1440
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QY	1501	TCAGAGGAAGATCACAAAGCTTGAGGCGCACTGTAATAATGCCCAAGC-----	1547
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QY 1576 GAAATGAAAGACAGAAAGTACTCATGTGCAATTTCCAGAAAACCTGACTAATGTGTCC 1635
DB 1621 GAAATGAAAGACAGAAAGTACTCATGTGCAATTTCCAGAAAACCTGACTAATGTGTCC 1680
QY 1636 ACTGCTGGCAATGTATGATGATTAATTTCTCCAGAAAGAGCAAGAACACTGAAAGC 1695
DB 1681 ACTGCTGGCAATGTATGATGATTAATTTCTCCAGAAAGAGCAAGAACACTGAAAGC 1740
QY 1696 CAGCAATTTCTGCACTGAGATGAAAGATATCAGATGACAGAAACAAATGATCTGAC 1755
DB 1741 CAGCAATTTCTGCACTGAGATGAAAGATATCAGATGACAGAAACAAATGATCTGAC 1800
QY 1756 AAGCAATTTTGTGAAGACAGAACTGGAATTTAAGATGATGATTTGATTCATGAA 1815
DB 1801 AAGCAATTTTGTGAAGACAGAACTGGAATTTAAGATGATGATTTGATTCATGAA 1860
QY 1816 GAAAGACATAGAGTGGTTGAAATGAAATTTCTGAGCTTTCTTGTGTTAGAA 1875
DB 1861 GAAAGACATAGAGTGGTTGAAATGAAATTTCTGAGCTTTCTTGTGTTAGAA 1920
QY 1876 GAAAAAGACATCTTGATGATGAAATAGTACGTTGCGGAGAAATTCATGCTAAGAC 1935
DB 1921 GAAAAAGACATCTTGATGATGAAATAGTACGTTGCGGAGAAATTCATGCTAAGAC 1980
QY 1936 GAGCTTGACAAATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAA 1995
DB 1981 GAGCTTGACAAATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAA 2040

RESULT 15

US-09-352-616A-375
Sequence 375, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillion, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-375

Query Match 97.0%; Score 1940; DB 3; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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DB 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTCTGTGAAAGACATTTGTCTC 60
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Db 1261 AAGCATGAAAGTAATATATGTGGATTACTAGAAAACTGATATATGTGTGACTGTGGC 1320
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Db 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGAGCAAAACACCTGAAAGC 1740
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QY 1816 GAAAAAGCATGATGAGTGTGTAATAATGAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1875
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QY 1876 GAAAAAGCATGATGAGTGTGTAATAATGAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1935
Db 1921 GAAAAAGCATGATGAGTGTGTAATAATGAATTTCTGAGCTTTCTTTAGTTGTAGAAA 1980
QY 1936 GAGCTAGACACATGAGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 1995
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Scoring table: IDENTITY_NUC
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4	2000	100.0	2000	US-09-810-936-302	Sequence 302, App
5	2000	100.0	2000	US-09-822-827-374	Sequence 374, App
6	2000	100.0	2000	US-09-429-755-302	Sequence 302, App
7	2000	100.0	2000	US-09-924-400-302	Sequence 302, App
8	2000	100.0	2000	US-09-793-374	Sequence 374, App
9	2000	100.0	2000	US-09-895-814-374	Sequence 374, App
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13	2000	100.0	2000	US-10-144-678A-374	Sequence 374, App
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37	1147.6	57.4	1853	3	US-09-822-827-369	Sequence 369, App
38	1147.6	57.4	1853	3	US-09-429-755-295	Sequence 295, App
39	1147.6	57.4	1853	3	US-09-924-400-295	Sequence 295, App
40	1147.6	57.4	1853	3	US-09-895-793-369	Sequence 369, App
41	1147.6	57.4	1853	5	US-09-895-814-369	Sequence 369, App
42	1147.6	57.4	1853	5	US-10-012-896-369	Sequence 369, App
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ALIGNMENTS

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RESULT 1
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; Sequence 6, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molese, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Petersen, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-6

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTTGAGTTGATTCATGCGGCTCTTCTGTGAAGCAAGCAATTGGTCTC 60
        1 ATGTGTTGAGTTGATTCATGCGGCTCTTCTGTGAAGCAAGCAATTGGTCTC 60
DB      1 ATGTGTTGAGTTGATTCATGCGGCTCTTCTGTGAAGCAAGCAATTGGTCTC 60
QY      61 AAGAGCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGCTGCGAGGAGCGGCAAG 120
        61 AAGAGCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGCTGCGAGGAGCGGCAAG 120
DB      61 AAGAGCAAGATGGGCAAGTGTGCTGCTTCTTCCCTGCTGCGAGGAGCGGCAAG 120
QY      121 ACGAAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGACACTGAGAGCAAG 180
        121 ACGAAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGACACTGAGAGCAAG 180
DB      121 ACGAAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGACACTGAGAGCAAG 180
QY      181 ATGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
        181 ATGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
DB      181 ATGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
QY      241 GGGCGTTTGGAGACAGACGACTGCTAAGAGACACTGAGAGCAAGTGGCAAG 300
        241 GGGCGTTTGGAGACAGACGACTGCTAAGAGACACTGAGAGCAAGTGGCAAG 300

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Db 241 GGGCGCTTGTGAGACCAAGCACTGTCTATGAAAGCACTCAGGAACAAGATGGGCAAG 300
Qy 301 TGGTCTGTGCACTGCTTCCCTGCTGCGAGGGGAGGGGCAAGAGCAAGTGGGCGTTGG 360
Db 301 TGGTCTGTGCACTGCTTCCCTGCTGCGAGGGGAGGGGCAAGAGCAAGTGGGCGTTGG 360
Qy 361 GGAAGCTACAGATGACAGTGTCTTCACTGAGAGCCAGGATACCAAGTCCGTTGGAAGATCTG 420
Db 361 GGAAGCTACAGATGACAGTGTCTTCACTGAGAGCCAGGATACCAAGTCCGTTGGAAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGTGGTGGTAAAGTCCCAAGAAAGATCTCATCTGCGC 480
Db 421 GACAGCTCCACAGAGCTGCTGTGGTGGTAAAGTCCCAAGAAAGATCTCATCTGCGC 480
Qy 481 CTCAGGAGCACTGACCTGTGAACAAGAGCAAGCAAAAGAGATCTCTTCACTGCGC 540
Db 481 CTCAGGAGCACTGACCTGTGAACAAGAGCAAGCAAAAGAGATCTCTTCACTGCGC 540
Qy 541 TCTGCAATGGGAATTCAGAAAGTAAAGCTCTGCGAGCAAGATGCTCACTTAAT 600
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Qy 601 GTCTTGTGACAAACAAAAGAGAGCAAGCTGTGATTAAGGCGGTACAATGCGAGAGATGA 660
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Qy 661 TGTGCGTTATGTGTGTGGAACAATGGCACTGATCCAAATATTCAGATGAGATGGAAT 720
Db 661 TGTGCGTTATGTGTGTGGAACAATGGCACTGATCCAAATATTCAGATGAGATGGAAT 720
Qy 721 ACCACTGTGACACTACGCTATCTTAATGAAGATTAATGAGCCAAAGCACTGCTTGA 780
Db 721 ACCACTGTGACACTACGCTATCTTAATGAAGATTAATGAGCCAAAGCACTGCTTGA 780
Qy 781 TATGTGTGTGATATGCAATCAAAAACAAAGATGCGCTCAACACATGTTACTGTGTGA 840
Db 781 TATGTGTGTGATATGCAATCAAAAACAAAGATGCGCTCAACACATGTTACTGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCCGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTCCGTGAATTTTAAATCAAGAAAAGCGAATTTAAATGA 900
Qy 901 CTGATATGATATGAGAGAGCTGCTCATATCTGTATGTTGTGATCAGCAAGATTA 960
Db 901 CTGATATGATATGAGAGAGCTGCTCATATCTGTATGTTGTGATCAGCAAGATTA 960
Qy 961 GTGAGCTTCTAATTGAGCAAAAATATGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTAATTGAGCAAAAATATGATGTAATCTTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCGAGAGATATGCTGCTTCTATGATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
Db 1021 GCGAGAGATATGCTGCTTCTATGATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
Qy 1081 AAAAGAAAACAGATGCTAAATAATCTCTTCTGAAAACAGCAATCAGAACTTAAG 1140
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Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGTGAATAATAGCCAGCAAGAAA 1200
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Db 1201 ATGTCTCAAGAACCAAAATTAATGATGCTGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1261 AAGCATGAAGATTAATGAGGATTAAGAAAACCTGACTAATGCTGCTGAGC 1320
Qy 1321 AATGTGATTAATGATTAATCTTCAAGAGAGAGAGCAACTGTAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTTCAAGAGAGAGAGCAACTGTAATCAGCAATTT 1380

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Db 1441 AAAAGATGCGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA 1500
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Db 1681 AGAACAACCTGAAAGCGCAGCAATTTCTGCACTGAGAAATGAAGATATCAAGTACGAA 1740
Qy 1741 CAAAATGATATCTCAGAAAGCAATTTGTGAAGAAACAGCACTGGAATTAACAGATGAG 1800
Db 1741 CAAAATGATATCTCAGAAAGCAATTTGTGAAGAAACAGCACTGGAATTAACAGATGAG 1800
Qy 1801 ATTTGATTCATGAGAAAGAGAGATGAGATGTTGAAAAATTAATTTCTGAGCTTTCT 1860
Db 1801 ATTTGATTCATGAGAAAGAGAGATGAGATGTTGAAAAATTAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGCTTGGGAGAAATTT 1920
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATATGATGCTTGGGAGAAATTT 1920
Qy 1921 GCGATGCTTAAGCTGAGAGTACACAAATGAAACATCAGAGCAGCTTAATAAAAA 1980
Db 1921 GCGATGCTTAAGCTGAGAGTACACAAATGAAACATCAGAGCAGCTTAATAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-759-143-374
; Sequence 374, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepner, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12


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; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGTGGTGAAGGTGAATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGCTC 60
DB      1  ATGGTGGTGAAGGTGAATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGCTC 60
QY      61  AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
DB      61  AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
QY      121  AGCAACGTGGGCACTTCTGAGACAACAGCACTGTGTAAGACACTCAGAGCAAG 180
DB      121  AGCAACGTGGGCACTTCTGAGACAACAGCACTGTGTAAGACACTCAGAGCAAG 180
QY      181  ATGGGCAAGTGGTGGGCGCCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAAG 240
DB      181  ATGGGCAAGTGGTGGGCGCCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAAG 240
QY      241  GGGCTTCTGAGAGACCAAGCACTGCTGTAAGACACTCAGAGCAAGATGGGCAAG 300
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QY      301  TGGTGTCCCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB      301  TGGTGTCCCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
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DB      361  GGAAGATTAGAGACAGTGGCTTCAATGAGCCCAAGGTACCACTCCGTGGAAGATCTG 420
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DB      421  GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGCAAGAAAGATCTCATGCTATG 480
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DB      481  CTCAGGAGACATGACCTGAAACAAGAAAGACAAAGCAAGCTCTTCAACTCTGGCC 540
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DB      541  TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGAACAGAGATGCAATTTAAT 600
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DB      601  GTCTCTGACAAACAAAAGAGAGACAGCTGTAAGCGGTAAAGCCAGAGAAAGATGAA 660
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DB      901  CTGGATAGATATGGAAGAGACTGCTCATATCTTGCTGATGTTGTGATCAGCAAGTATA 960
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DB      1021  GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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DB      1261  AAGCATGAAGATTAATATGTTGGATTAATGAAAAACCTGACTAATGCTGCTGGC 1320
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DB      1321  AATGTGATATATGATTAATTCCTCAAGAGAGAGAGAAACCTGAAATGCAATTT 1380
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DB      1921  GCCATGCTTAAGACTGAGAGCTAGACACAATGAATAATCAGAGCAGCTTAATAAAAAA 1980
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Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374

/ Sequence 374, Application US/09780669

/ Patent No. US2002005197A1

/ GENERAL INFORMATION:

/ APPLICANT: Xu, Jiangchun

/ APPLICANT: Dillon, Davin C.

/ APPLICANT: Mitcham, Jennifer L.

/ APPLICANT: Harlocker, Susan L.

/ APPLICANT: Jiang, Yuqiu

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Kalos, Michael D.

/ APPLICANT: Fanger, Gary R.

/ APPLICANT: Retter, Marc W.

/ APPLICANT: Stolk, John A.

/ APPLICANT: Day, Craig H.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Carter, Darrick

/ APPLICANT: Li, Samuel

/ APPLICANT: Wang, Aijun

/ APPLICANT: Skelley, Yaelir A.W.

/ APPLICANT: Hepley, William

/ APPLICANT: Hural, John

/ APPLICANT: McNeill, Patricia D.

/ APPLICANT: Houghton, Raymond L.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

/ FILE REFERENCE: 210121.427C24

/ CURRENT APPLICATION NUMBER: US/09/780,669

/ CURRENT FILING DATE: 2001-02-09

/ NUMBER OF SEQ ID NOS: 943

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 374

/ LENGTH: 2000

/ TYPE: DNA

/ ORGANISM: Homo sapien

US-09-780-669-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCAGTCCGCGCTCTCTTGTGAAGGCAATTTGCTTC 60

DB 1 ATGGTGGTTGAGGTGATTCAGTCCGCGCTCTCTTGTGAAGGCAATTTGCTTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

DB 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

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QY 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGAGGAGGAGCAAGGCTGGGCGCTTGG 360

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QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGGAAAT 720

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Db 1501 TCGAGGAGAGTCAAGAGGCTTGGAGGCAATGCGCAAGCAAGCTAGAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAAGAAGCAAGAGTACTCATGCGATTTCCAGAAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAAGCAAGAGTACTCATGCGATTTCCAGAAAAC 1620
Qy 1621 CTGACTTAATGTCCTGCTGCGCATGCTGATGATGATTAATTTCTCCAGAGAAAGC 1680
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Qy 1741 CAAATGATGATCTGAGAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAG 1800
Db 1741 CAAATGATGATCTGAGAGCAATTTTGTGAAGAACAGAACCTGGAATTTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAGAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTCT 1860
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Db 1861 CTTAGTTGTAAGAGAGAAAGACATCTGCAATGAAATAGTACGTTGCGGAGAGAAAT 1920
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Db 1921 GCCATGCTAAGAGTGGAGCTAGACATGATGAAACATCAGAGCCAGCTAAATTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 4
US-09-810-936-302
Sequence 302, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/09/810,936
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGTGATGAGTTCATGCGCGGCTCTTCTGTGAGAGCAATTTGCTTC 60
Db 1 ATGGTGTGATGAGTTCATGCGCGGCTCTTCTGTGAGAGCAATTTGCTTC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGTGGCACTTCTGAGAGCAAGCAAGCTCTGATGAGAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGTGGCACTTCTGAGAGCAAGCAAGCTCTGATGAGAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGGCCGCTGCTTCCCTGCTGAGGAGAGTGTGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGGCCGCTGCTTCCCTGCTGAGGAGAGTGTGCAAGCAAGCTG 240
Qy 241 GCGGCTTCTGAGAGCAAGCAAGCTCTGATGAGAGCACTCAGAGCAAGATGGCAAG 300
Db 241 GCGGCTTCTGAGAGCAAGCAAGCTCTGATGAGAGCACTCAGAGCAAGATGGCAAG 300
Qy 301 TGTGCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGTGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGTGGCGCTTGG 360
Qy 361 GAGAGCTACAGATGACAGTGTCTTCAATGAGGCCAGGTACACGTCCTGAGAGATCTG 420
Db 361 GAGAGCTACAGATGACAGTGTCTTCAATGAGGCCAGGTACACGTCCTGAGAGATCTG 420
Qy 421 GACAGCTTCCAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATTCGATG 480
Db 421 GACAGCTTCCAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATTCGATG 480
Qy 481 CTGAGGAGCACTGAGCTGAGCAAGAGAGCAAGCAAGAGAGAGCTCTTACATCTGAGCC 540
Db 481 CTGAGGAGCACTGAGCTGAGCAAGAGAGCAAGCAAGAGAGAGCTCTTACATCTGAGCC 540
Qy 541 TCTGCAATGAGGAAATTCAGAGTGTAAATCTCTGCTGAGAGAGATGTCACTTAAT 600
Db 541 TCTGCAATGAGGAAATTCAGAGTGTAAATCTCTGCTGAGAGAGATGTCACTTAAT 600
Qy 601 GTGCTTGAACAACAAAGAGGACAGCTCTGATGAAAGCCGCTACATGCGAGAGATGAA 660
Db 601 GTGCTTGAACAACAAAGAGGACAGCTCTGATGAAAGCCGCTACATGCGAGAGATGAA 660
Qy 661 TGTGCTTAATGTTCTGAGACATGAGCACTGATCCAAATATTCAGATGATGAGAAAT 720
Db 661 TGTGCTTAATGTTCTGAGACATGAGCACTGATCCAAATATTCAGATGATGAGAAAT 720
Qy 721 ACCACTTGCACATGATCTATTAATGAGATTAATTAAGCCAAAGCACTGCTTTA 780
Db 721 ACCACTTGCACATGATCTATTAATGAGATTAATTAAGCCAAAGCACTGCTTTA 780
Qy 781 TATGCTGCTGATGATGATCAAAACAAAGAGTGTGCTGACACAGCTGTACTGTGTGA 840
Db 781 TATGCTGCTGATGATGATCAAAACAAAGAGTGTGCTGACACAGCTGTACTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATGATGATGAGAGAGTGTCTCATCTTCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATGATGATGAGAGAGTGTCTCATCTTCTGATGTTGTGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTTCTGAGAGAAATTAATGATATCTTCAAGATCTAATCTGAGAGAG 1020
Db 961 GTGAGCTTCTTCTGAGAGAAATTAATGATATCTTCAAGATCTAATCTGAGAGAG 1020
Qy 1021 GCCAGAGATGATGCTTCTTCTGATCATCATGATTAATTTGCGAGTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTTCTTCTGATCATCATGATTAATTTGCGAGTACTTTCTGACTAC 1080
Qy 1081 AAGAGAAAAAGATGCTAAATCTCTGAAAAACAGAAATCCAGAAACAAATTTAAAG 1140
Db 1081 AAGAGAAAAAGATGCTAAATCTCTGAAAAACAGAAATCCAGAAACAAATTTAAAG 1140
Qy 1141 CTGATGATGAGAGAGTCAAGGTTCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1200

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Db      1141 CTGACATCAGAGAAAGTCAAAAGTTCAAAAGCAGTGAATAAGCCAGCAAGAAA 1200
Oy      1201 ATGTCTCAAGAACCGAATAATAAGATGTGTATAGAGATTTGGAATAAATAATGAAG 1260
Db      1201 ATGTCTCAAGAACCGAATAATAAGATGTGTATAGAGATTTGGAATAAATAATGAAG 1260
Oy      1261 AAGCATGAAGAATATATATGTGGATTTACTAGAAAACCTGACTTAATGTGTCTCTGTC 1320
Db      1261 AAGCATGAAGAATATATATGTGGATTTACTAGAAAACCTGACTTAATGTGTCTCTGTC 1320
Oy      1321 AATGTGTATATATATATTTCTCTCAAGAAAGACGAAACCTGAAAATCACAATTT 1380
Db      1321 AATGTGTATATATATATTTCTCTCAAGAAAGACGAAACCTGAAAATCACAATTT 1380
Oy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTTGGAATTTGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTTGGAATTTGTTCTGATCAAGAA 1440
Oy      1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGAC 1500
Db      1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGAC 1500
Oy      1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Db      1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Oy      1561 TTTATGTGCTATCGAAGAAATGAAGAACGAGAAAGTCTCATGTGGATTTCCCAAGAAAC 1620
Db      1561 TTTATGTGCTATCGAAGAAATGAAGAACGAGAAAGTCTCATGTGGATTTCCCAAGAAAC 1620
Oy      1621 CTGACTTAATGTGTCCTGTCGCAATGGTGTATGTATGATTTAATCTTCAAGAAAGAC 1680
Db      1621 CTGACTTAATGTGTCCTGTCGCAATGGTGTATGTATGATTTAATCTTCAAGAAAGAC 1680
Oy      1681 AAGAACCTGAAAGCCAGCAATTTCTGCACTGAGATGAAGAGTATCACTGTCGAA 1740
Db      1681 AAGAACCTGAAAGCCAGCAATTTCTGCACTGAGATGAAGAGTATCACTGTCGAA 1740
Oy      1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGACATCGAAATTAACAGATGAG 1800
Db      1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGACATCGAAATTAACAGATGAG 1800
Oy      1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAAGAAATGAATTTCTGAGCTTTCT 1860
Db      1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAAGAAATGAATTTCTGAGCTTTCT 1860
Oy      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATATGTCGTTGGGGAAGAAAT 1920
Db      1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATATGTCGTTGGGGAAGAAAT 1920
Oy      1921 GCATGCTAAGACTGAGGCTGAGACAAATGAACATCAGAGCCAGCTAAAAAATAA 1980
Db      1921 GCATGCTAAGACTGAGGCTGAGACAAATGAACATCAGAGCCAGCTAAAAAATAA 1980
Oy      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 5
US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
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; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

Query Match      100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ATGTGTGTGAAGTTGATTTCCATGCCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Db      1 ATGTGTGTGAAGTTGATTTCCATGCCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
Oy      61 AGGAGCAAGATGGGCAAGTGGTCCGCTTCCCTGCTGAGGGAGCGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGGTCCGCTTCCCTGCTGAGGGAGCGGCAAG 120
Oy      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
Oy      181 ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCACTG 240
Db      181 ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCACTG 240
Oy      241 GGGCTTCTGAGACCAAGCACTGCTATGAAGACACTGAGGAACAAGATGGGCAAG 300
Db      241 GGGCTTCTGAGACCAAGCACTGCTATGAAGACACTGAGGAACAAGATGGGCAAG 300
Oy      301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
Oy      361 GGAAGCTACGATGACAGTGCCTTCAATGAGGCCAGGTACACGTCCTGTGGAAGATCTG 420
Db      361 GGAAGCTACGATGACAGTGCCTTCAATGAGGCCAGGTACACGTCCTGTGGAAGATCTG 420
Oy      421 GACAACTCCACAGAGCTGCGTGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
Db      421 GACAACTCCACAGAGCTGCGTGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
Oy      481 CTCAGGGAACACTGACGTGAACAAGAAAGCAAGCAAAAGAGGACTGCTTCAATCTGCGC 540
Db      481 CTCAGGGAACACTGACGTGAACAAGAAAGCAAGCAAAAGAGGACTGCTTCAATCTGCGC 540
Oy      541 TCTGCAATGGGAATTCAGAAAGTGAATTAACCTGCTGAGACAGATGTCACCTTAAT 600
Db      541 TCTGCAATGGGAATTCAGAAAGTGAATTAACCTGCTGAGACAGATGTCACCTTAAT 600
Oy      601 GTCTTGAACAACAAAGAGGACAGCTCTGATTAAGGCGGTCAATGACAGGAAGATGA 660
Db      601 GTCTTGAACAACAAAGAGGACAGCTCTGATTAAGGCGGTCAATGACAGGAAGATGA 660
Oy      661 TGTGCTTAATGTGTCGGAACATGCACTGATCAATATTCAGATGATGGAAT 720
Db      661 TGTGCTTAATGTGTCGGAACATGCACTGATCAATATTCAGATGATGGAAT 720
Oy      721 ACCACTCTGCACTAAGCTATCTATATGAAGATAATTAATGAGCCAAAGCACTGCTTGA 780
Db      721 ACCACTCTGCACTAAGCTATCTATATGAAGATAATTAATGAGCCAAAGCACTGCTTGA 780
Oy      781 TATGTGTGATATGGAATCAAAAAAAGAGCTGCTCAACCACTGTTACTTGGTGA 840
Db      781 TATGTGTGATATGGAATCAAAAAAAGAGCTGCTCAACCACTGTTACTTGGTGA 840
Oy      841 CATGACAAAAACAGCAAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATGCA 900
Db      841 CATGACAAAAACAGCAAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATGCA 900
Oy      901 CTGATATGATATGGAAGAGCTGCTCTCATCTGCTGATATGTTGTGATACAGCAAGTATA 960
Db      901 CTGATATGATATGGAAGAGCTGCTCTCATCTGCTGATATGTTGTGATACAGCAAGTATA 960
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Db 661 TGGCCTTATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGGAAT 720
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Qy 781 TATGCTGATATCGAATCAAAAAAAGCATGCGCTCACACACTGTTACTTGCTGA 840
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Qy 841 CATGACAAAAAAGCATGCGCTGAAATTTTATCAAGAAAAAAGCGAATTTAAATGA 900
Db 841 CATGACAAAAAAGCATGCGCTGAAATTTTATCAAGAAAAAAGCGAATTTAAATGA 900
Qy 901 CTGATAGATATGGAAGGACTGCTCATCTGCTGATATGTTGATGATGACAGATTA 960
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Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAAAGAAAAAGATGCTAAATAATCTCTGAAAAAGCAATCCAAAGAACTTAAAG 1140
Db 1081 AAAAGAAAAAGATGCTAAATAATCTCTGAAAAAGCAATCCAAAGAACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGTGAATAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGTGAATAATAGCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAATAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAATAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
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Qy 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGCAACTGAATATGCAATTT 1380
Db 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGCAACTGAATATGCAATTT 1380
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Db 1381 CCTGACAGAGAGATGAGAGATATCAAGAAATTTGCGAATTTGTTCTGACTA 1440
Qy 1441 AAAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGCAACAACTTAAAGCT 1500
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Db 1621 CTGACTAATGATGCGCATGCTGCGCATGATGATGATGATTAATCTTCCAGAGAA 1680
Qy 1681 AGAACAAGAGAGAGAGAGATTTCTGACACTGAGAAATGAAGAGATCAAGTGCAG 1740
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Qy 1741 CAAATGATATCTGAGAGCAATTTTGTGAAGACAGACACTGGAATATTAACAGAT 1800
Db 1741 CAAATGATATCTGAGAGCAATTTTGTGAAGACAGACACTGGAATATTAACAGAT 1800
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Db 1741 CAAATGATATCTGAGAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGAT 1800
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Db 1861 CTTAGTTTGAAGAAAGAAAGACATCTTGATGAAAAATGATGCTTGCGGAGAAATTT 1920
Qy 1921 GCCATGCTAGAGCTGAGAGTGAACAATGAACATCAGAGCAGCTAAAAA 1980
Db 1921 GCCATGCTAGAGCTGAGAGTGAACAATGAACATCAGAGCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 7
US-09-924-400-302
; Sequence 302, Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yaelir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-302
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Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTTGATGATGATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGATTC 60
Db 1 ATGTGTTGATGATGATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGATTC 60
Qy 61 AGGAGCAAGATGAGGAGATGCTGCGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGAGGAGATGCTGCGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGAGCTTCTGAGAGACAGAGCACTGCTGATGAGAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGAGCTTCTGAGAGACAGAGCACTGCTGATGAGAGCACTCAGAGCAAG 180
Qy 181 ATGGCAAGTGTGCGGCACTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGGCACTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAAGCTG 240
Qy 241 GCGGCTTCTGAGAGACAGAGCACTGCTGATGAGAGCACTCAGAGCAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACAGAGCACTGCTGATGAGAGCACTCAGAGCAAGATGGGCAAG 300
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OY	301	TGTCGTCGCCAC	CTGCTTCCCTCTGCTGCA	GGGGGAGCGGCAC	AGAGCAAGTGGCGCTTGG	360
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OY	361	GGAGACTACGATG	ACATGCGCTCTCA	TGAGGCCAGGTAC	CAAGTCGCGGAGAAATCTG	420
Db	361	GGAGACTACGATG	ACATGCGCTCTCA	TGAGGCCAGGTAC	CAAGTCGCGGAGAAATCTG	420
OY	421	GACAAAGCTTCA	CAGAGCTGCTGTGGGGTAA	AGTCCACAGAAAGATCTCAT	CGTCATG	480
Db	421	GACAAAGCTTCA	CAGAGCTGCTGTGGGGTAA	AGTCCACAGAAAGATCTCAT	CGTCATG	480
OY	481	CTCAGGGACACTG	ACGTGATACAGAAAGCA	ACGAAAGAGACTGCTCTA	CATCTGCGC	540
Db	481	CTCAGGGACACTG	ACGTGATACAGAAAGCA	ACGAAAGAGACTGCTCTA	CATCTGCGC	540
OY	541	TCTGCGAATGGGA	ATTGAGAGTGTAAATCTCCGCTG	GCAGACGATGCACTTAAT		600
Db	541	TCTGCGAATGGGA	ATTGAGAGTGTAAATCTCCGCTG	GCAGACGATGCACTTAAT		600
OY	601	GTCTTTGACAA	CAAAAAGAGACAGCTCTGAT	TAAAGCCGTACATGCAAGTGA	AGTGA	660
Db	601	GTCTTTGACAA	CAAAAAGAGACAGCTCTGAT	TAAAGCCGTACATGCAAGTGA	AGTGA	660
OY	661	TGTGCGTTAAT	TGTTGCTGGAACATG	GCACCTGATCCAAATTTCCAGAT	GAGTATGAAAT	720
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OY	721	ACCACTGCGAC	CTACGGCTATCTATATG	ATGAATTAATATGGCCAAAGCA	CTGCTCTTA	780
Db	721	ACCACTGCGAC	CTACGGCTATCTATATG	ATGAATTAATATGGCCAAAGCA	CTGCTCTTA	780
OY	781	TATGTCGTGAT	TATCGAATCAAAAAACA	GATGGCTCACACCACTGTTACTTG	GTGTGA	840
Db	781	TATGTCGTGAT	TATCGAATCAAAAAACA	GATGGCTCACACCACTGTTACTTG	GTGTGA	840
OY	841	CATGAGCAAAA	ACAGCAAGTCGTGAATTTT	TATCAAGAAAAAGCGAATTT	TAATGCA	900
Db	841	CATGAGCAAAA	ACAGCAAGTCGTGAATTTT	TATCAAGAAAAAGCGAATTT	TAATGCA	900
OY	901	CTGATATGAT	TATGGAAGACCTGCTCTCA	TACTTGCTGATGTTGTGAT	TAAGCAATGA	960
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OY	1021	GCCAGAGATAT	GCTGTTTCTAGTCATCAT	GATGTAATTTGCSAGTTA	ACTTTCTGAC	1080
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Db	1141	CTGACATCAG	AGAAAGTGCACAAAGGTT	CAAGGCTGAATAATAG	CAGCAGAGAAA	1200
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Db	1201	ATGTCCTCA	AGAACCGAAATTAATAG	GATGCTGATAGAGGTT	GAAAGAAATGAG	1260
OY	1261	AAAGCATGA	AAATTAATGTTGGATTA	CTAGAAAACTGAC	TAATGCTGTCACTGCTGGC	1320
Db	1261	AAAGCATGA	AAATTAATGTTGGATTA	CTAGAAAACTGAC	TAATGCTGTCACTGCTGGC	1320
OY	1321	AATGGTGAAT	TATGATTAATCTCTCA	AAAGAGACAGACCTG	GAATAATCAGCAATTT	1380
Db	1321	AATGGTGAAT	TATGATTAATCTCTCA	AAAGAGAGACAGACCTG	GAATAATCAGCAATTT	1380
OY	1381	CCTGACAA	CGAAAGTGAAGATAT	CAAGAAATTTGCGAAT	TAGTTTCTGACTACAAAGAA	1440

Db	Sequence	Accession	Length
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Qy	1441 AAACGATGCGCAAAATATCTCTTCTGAAACAGCAACCCAGAACGACTTAACCTGCA	1500	1500
Db	1441 AAACGATGCGCAAAATATCTCTTCTGAAACAGCAACCCAGAACGACTTAACCTGCA	1500	1500
Qy	1501 TCAGAGGAGAGTCACAAAGGCTTGAGGCGCAGTGAATAAGCCAGCAGAGCTAGAAAT	1560	1560
Db	1501 TCAGAGGAGAGTCACAAAGGCTTGAGGCGCAGTGAATAAGCCAGCAGAGCTAGAAAT	1560	1560
Qy	1561 TTTATGGCTATCGAAGAAATGAAAGACCGAAGTCTCATGTGCGATTCCAGAAAC	1620	1620
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Db	1741 CAAATATGATCTCAGAGCAATTTTGTGAGACAGAACACTGGAATTTACAGATGAG	1800	1800
Qy	1801 ATTGCGATTCCTGAGAAAGGACAGATGAGTGGTGAATAAATGAAATTCGAGCTTCT	1860	1860
Db	1801 ATTGCGATTCCTGAGAAAGGACAGATGAGTGGTGAATAAATGAAATTCGAGCTTCT	1860	1860
Qy	1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATCGTTGCGGAGAAATTT	1920	1920
Db	1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATCGTTGCGGAGAAATTT	1920	1920
Qy	1921 GCCATGCTAAGACTGAGACTGACACATGAAACATGAGCCAGCTTAAAAA	1980	1980
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Qy	1981 AAAAAAAAAAAAAAAAAA	2000	2000
Db	1981 AAAAAAAAAAAAAAAAAA	2000	2000

FILE REFERENCE: 210121.534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 374
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-895-793-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTGAAGTTTATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTTTATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAACAACAAGACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAACAACAAGACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGGAATGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGATGGCAAGCACTG 240
DB 181 ATGGGGAATGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGATGGCAAGCACTG 240
QY 241 GCGGCTTCTGGAAGACCAAGCAAGCTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GCGGCTTCTGGAAGACCAAGCAAGCTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGTGGCGCTTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGTGGCGCTTGG 360
QY 361 GGAAGATGAAGTGAAGTGGCTTCTGATGAGGCCCAAGTACCAAGTCCGTGGAAGATCTG 420
DB 361 GGAAGATGAAGTGAAGTGGCTTCTGATGAGGCCCAAGTACCAAGTCCGTGGAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGGTGGGTTAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGGTGGGTTAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGAGCACTGACCTGAAACAAGAAAGACAAAGCAAGCAAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACCTGAAACAAGAAAGACAAAGCAAGCAAGCTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAAGAGTAAATCTCTGCTGCAAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAAGAGTAAATCTCTGCTGCAAGAGATGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCGAAGAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCGAAGAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAGAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAAGAT 720
QY 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAATGCGCAAGACCTGCTTGA 780
DB 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAATGCGCAAGACCTGCTTGA 780
QY 781 TATGTGCTGATATTCGAATCAAAAACAAGCATGGCTCACACACTGTTACTTGGATGA 840
DB 781 TATGTGCTGATATTCGAATCAAAAACAAGCATGGCTCACACACTGTTACTTGGATGA 840
QY 841 CATGACCAAAAACAGCAAGTGTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
DB 841 CATGACCAAAAACAGCAAGTGTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900

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DB 841 CATGACCAAAAACAGCAAGTGTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGCTGCTCTCATACTTGGCTGATATGTTGGATACAGCAATGA 960
DB 901 CTGATATGATATGGAAGAGCTGCTCTCATACTTGGCTGATATGTTGGATACAGCAATGA 960
QY 961 GTGACGCTTCTACTGAGCAAAAATATGATATCTTCTCAAGATCTATCTGAGCAGACG 1020
DB 961 GTGACGCTTCTACTGAGCAAAAATATGATATCTTCTCAAGATCTATCTGAGCAGACG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
DB 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATCTAAAAATCTCTGTAACAGAAATCCAGAACTTAATGAAG 1140
DB 1081 AAGAAAAACAGATCTAAAAATCTCTGTAACAGAAATCCAGAACTTAATGAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAGTGAATAATGCGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCAAAAAGTTCAAAAGCAGTGAATAATGCGCAGAGAAA 1200
QY 1201 ATGCTCAAGAACCAAGAAATTAATGAAGATGATGATAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAATGAAGATGATGATAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGATTAATCTGAAAACCTGACTTAATGATGATCTGCTG 1320
DB 1261 AAGCATGAAGATTAATGATGATTAATCTGAAAACCTGACTTAATGATGATCTGCTG 1320
QY 1321 AATGTTGAATATGATTAATCTCAGAAAGAGACAGAACCTGAAAATGCAAAATTT 1380
DB 1321 AATGTTGAATATGATTAATCTCAGAAAGAGACAGAACCTGAAAATGCAAAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAGCAATGCGCAAAATATCTTCTGAAAACAGCAACCCAGAACCAAGCTTAATGCTGANA 1500
DB 1441 AAGCAATGCGCAAAATATCTTCTGAAAACAGCAACCCAGAACCAAGCTTAATGCTGANA 1500
QY 1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCACTGAAAATGGCAGCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGGAAGAGTCAAAAAGCTTGAAGGCACTGAAAATGGCAGCAGAGCTAGAAAAT 1560
QY 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAATGATCTCATGTCGATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATGGAAGAAATGAAGAGCAGGAATGATCTCATGTCGATTTCCAGAAAAAC 1620
QY 1621 CTGACTAATGGTGCACATGCTGGCAATGCTGATGAATTAATCTCTCCAGAGAAAGGC 1680
DB 1621 CTGACTAATGGTGCACATGCTGGCAATGCTGATGAATTAATCTCTCCAGAGAAAGGC 1680
QY 1681 AAGAACCTGGAAGCAGCAATTTCTGCACTGAGATGAAGAGTATCAAGTGCAGAA 1740
DB 1681 AAGAACCTGGAAGCAGCAATTTCTGCACTGAGATGAAGAGTATCAAGTGCAGAA 1740
QY 1741 CAAAATGATACTCAGAAAGATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATACTCAGAAAGATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTTGATTTCAAGAAAGAAAGCAGATGAAGTGTGTAAGAAATGAATTTCTGAGCTTTCT 1860
DB 1801 ATTTGATTTCAAGAAAGAAAGCAGATGAAGTGTGTAAGAAATGAATTTCTGAGCTTTCT 1860
QY 1861 CTTAAGTTGTAAGAAAGAAAGACATCTTGCATGAATAATAGTACGTTGGGGAAGAAATTT 1920
DB 1861 CTTAAGTTGTAAGAAAGAAAGACATCTTGCATGAATAATAGTACGTTGGGGAAGAAATTT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAACATCAGAGCAGCTAATTAATTAATTAAT 1980
DB 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAACATCAGAGCAGCTAATTAATTAATTAAT 1980

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OY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 9
US-09-895-814-374
Sequence 374, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yashir A.W.
APPLICANT: Heppler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basbols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGTGTGAGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTGGTCTC 60
Db 1 ATGTGTGTGAGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTGGTCTC 60

OY 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120

OY 121 AGCAACGTGGGCACTTCTGAGAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180

OY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240

OY 241 GGCGCTTCTGAGAGCAAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAGTGG 300
Db 241 GGCGCTTCTGAGAGCAAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAGTGG 300

OY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360

OY 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGGTACCACTCCGTGGAAGATCTTG 420
Db 361 GGAGACTAGATGACAGTGCCTTCAATGAGAGCCAGGTACCACTCCGTGGAAGATCTTG 420

OY 421 GACAAAGCTCCAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCCGATG 480
Db 421 GACAAAGCTCCAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCCGATG 480

OY 481 CTCAGGAGCACTGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGCACTGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540

OY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGCAAGAGATGTCACTTAAT 600

OY 601 GTCTTGAACAACAAAGAGAGAGCACTGATTAAGGCGGTACAAATGCGAGGAAGTGA 660
Db 601 GTCTTGAACAACAAAGAGAGAGCACTGATTAAGGCGGTACAAATGCGAGGAAGTGA 660

OY 661 TGTGCTTAATGTTCTGGAAACATGCACTGATCCAAATATTCAGATGATGGAAAT 720
Db 661 TGTGCTTAATGTTCTGGAAACATGCACTGATCCAAATATTCAGATGATGGAAAT 720

OY 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATATGCGCAAGCACTGCTTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATATGCGCAAGCACTGCTTTA 780

OY 781 TATGTGTGATGATGATGATCAAAAGCAAGTGCCTCAAGCCACTGATCTGCTGTA 840
Db 781 TATGTGTGATGATGATGATCAAAAGCAAGTGCCTCAAGCCACTGATCTGCTGTA 840

OY 841 CATGACAAACAAACAGAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTAAATGA 900
Db 841 CATGACAAACAAACAGAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTAAATGA 900

OY 901 CTGATTAATGATGAGAGAGTGTCTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATTAATGATGAGAGAGTGTCTCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960

OY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020

OY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGGCACTTCTTCTGATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGGCACTTCTTCTGATAC 1080

OY 1081 AAAGAAAAACAGATCTAAAAATCTCTCTGAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTAAAAATCTCTCTGAAAACAGCAATCCAGAACAAAGCTTAAAG 1140

OY 1141 CTGATATCAAGAGAGATGCAAAAGTTTCAAGGCAATGAAAATAGCCAGCCAGAGAA 1200
Db 1141 CTGATATCAAGAGAGATGCAAAAGTTTCAAGGCAATGAAAATAGCCAGCCAGAGAA 1200

OY 1201 ATGTCTCAAGAACAGAAATATAAGATGTTGTAAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATATAAGATGTTGTAAGAGGTTGAAGAAATGAAG 1260

OY 1261 AAGCATGAAGATTAATATGTTGATTAAGAAACCTGACTAATGTTGTCATCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGTTGATTAAGAAACCTGACTAATGTTGTCATCTGGC 1320

OY 1321 AATGTGATTAATGATTAATCTTCAAGAGAGCAAGCAACCTGAAATATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTTCAAGAGAGCAAGCAACCTGAAATATCAGCAATTT 1380

OY 1381 CTTGACAAAGAAAGTGAAGATATCAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAAGTGAAGATATCAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440

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QY 1441 AACAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
DB 1441 AACAGATGCCAAATATCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATCAAAAGGCTTGGGCGATGAAAATGGCCAGCCAGCTAGAAAT 1560
DB 1501 TCAGAGGAAGATCAAAAGGCTTGGGCGATGAAAATGGCCAGCCAGCTAGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAAGACACGAAAGTACTCATGTGGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAAGACACGAAAGTACTCATGTGGATTTCCAGAAAC 1620
QY 1621 CTGACTAATGTGGCCACTGCTGGCAATGTGATGATTAATTCCTCCAGAGAGAGC 1680
DB 1621 CTGACTAATGTGGCCACTGCTGGCAATGTGATGATTAATTCCTCCAGAGAGAGC 1680
QY 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGAAATGAAAGATCAAGTACGAA 1740
DB 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGAGAAATGAAAGATCAAGTACGAA 1740
QY 1741 CAAATGATATCTGAAAGCAATTTGTGAAGAACAGAACTGGAAATTTACAGATGAG 1800
DB 1741 CAAATGATATCTGAAAGCAATTTGTGAAGAACAGAACTGGAAATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAATTTCTGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTTGTGAAGAAAGCAATCTTGATGAAATGTAAGTTGGGGAGAAAT 1920
DB 1861 CTTAGTTGTGAAGAAAGCAATCTTGATGAAATGTAAGTTGGGGAGAAAT 1920
QY 1921 GCCATCTAGAGCTGAGCTAGACATGAAATCATCAGAGCAGCTAAATAAAAA 1980
DB 1921 GCCATCTAGAGCTGAGCTAGACATGAAATCATCAGAGCAGCTAAATAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-10-012-896-374
; Sequence 374, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retzer, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yaser A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Measner, Madeline Joy
; APPLICANT: Measner, Madeline Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27

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; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-374

Query Match      100.0%; Score 2000; DB 5; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGTTGATTCATAGCCGGTGGCTCTTCGTGTAAGAGCATTTGGTCTC 60
DB 1 ATGGGTGTTGAGTTGATTCATAGCCGGTGGCTCTTCGTGTAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTTGAGAGCAAGCAAGCACTCTGTATGAAGACATTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTTGAGAGCAAGCAAGCACTCTGTATGAAGACATTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCGACCTGTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGCCGACCTGTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGT 240
QY 241 GCGGCTTCTGAGACCAAGCAGCACTCTGTATGAAGACATTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCAGCACTCTGTATGAAGACATTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAAGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTCTGCTGCACTGCTTCCCTGCTGCAAGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAGACTAGAGTACAGAGTCCCTCATGAGCCCAAGTACAGTCCGTGGAAAGATCTG 420
DB 361 GGAGACTAGAGTACAGAGTCCCTCATGAGCCCAAGTACAGTCCGTGGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGATGCTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGATGCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTAGTAATACTCCGTGCTGAGACAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAACTAGTAATACTCCGTGCTGAGACAGATGCACTTAAT 600
QY 601 GTCTTGAACAACAAGAGAGAGCAGCTGTATGAAGGCGGTCAATGGCAGAGATGAA 660
DB 601 GTCTTGAACAACAAGAGAGAGCAGCTGTATGAAGGCGGTCAATGGCAGAGATGAA 660
QY 661 TGTGCTTAATGTGCTGGACAATGCACTGATCAATATTTCCAGAGTATGTAAT 720
DB 661 TGTGCTTAATGTGCTGGACAATGCACTGATCAATATTTCCAGAGTATGTAAT 720
QY 721 ACCACTTGCATATAGCTATCTATATGAAGTAATTAATGGCCAAAGCATGCTCTTA 780
DB 721 ACCACTTGCATATAGCTATCTATATGAAGTAATTAATGGCCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATGAAATCAAAAAAAGATGAGCTCAGCACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATGAAATCAAAAAAAGATGAGCTCAGCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900

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QY	901	CTGGAATATAATGAGAGACCTGCTCTCTACTCTGCTGTAATGTTGGATTCAGCAAGTATA	960
Db	901	CTGGATTAATATGGAAGACGTGCTCTCACTTCTGTAATGTTGGATTCAGCAAGTATA	960
QY	961	GTCAAGCTTCTACTGTGAGCAAAATATTATGATGATCTTCTCAAGATCTATCTGACAGAGC	1020
Db	961	GTCAAGCTTCTACTGTGAGCAAAATATTATGATGATCTTCTCAAGATCTATCTGACAGAGC	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTTAGTCATCATCTGTAATTTGGCAATCTTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTTAGTCATCATCTGTAATTTGGCAATCTTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACACATCCAGAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACCAATCCAGAAACAAAGACTTAAG	1140
QY	1141	CTGACATCAGAGGAAGTCACTAAAGGTTCAAGGCACTGTAATAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCACTAAAGGTTCAAGGCACTGTAATAATAGCCAGCCAGAGAA	1200
QY	1201	ATGCTTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG	1260
Db	1201	ATGCTTCAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG	1260
QY	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGAATAGTGTCACCTGCTGAC	1320
Db	1261	AAGCATGAAAGTAAATATGTTGGGATTTACTAGAAAACCTGAATAGTGTCACCTGCTGAC	1320
QY	1321	AATGCTGATTAATGATTAATCTTCAAGAGAGCAGAACCACTGAATAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTAATCTTCAAGAGAGCAGAACCACTGAATAATCAGCAATTT	1380
QY	1381	CCTGACAAAGAAAGTAAGAGATCACAGAAATTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAAGAAAGTAAGAGATCACAGAAATTTGGCAATTAAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAAATTACTCTTCTGAAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATTACTCTTCTGAAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGAGTCACTAAAGGCTTGAGGCGACTGAAAATTGGCCAGCCAGACTGAAAAT	1560
Db	1501	TCAGAGGAAGAGTCACTAAAGGCTTGAGGCGACTGAAAATTGGCCAGCCAGACTGAAAAT	1560
QY	1561	TTTATGCGCTATCGAAGAAATGAAAGACCGGAATACTCAATGTCGATTCCTCCAGAAAAC	1620
Db	1561	TTTATGCGCTATCGAAGAAATGAAAGACCGGAATACTCAATGTCGATTCCTCCAGAAAAC	1620
QY	1621	CTGACTAATGCTGCGACTGCTGGCAATGATGATGATTAATTTCTCCAAAGAAAGAGC	1680
Db	1621	CTGACTAATGCTGCGACTGCTGGCAATGATGATGATTAATTTCTCCAAAGAAAGAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCTGCAACTGGAATGGAAGATACACAGTGAAGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGCAACTGGAATGGAAGATACACAGTGAAGAA	1740
QY	1741	CAAAATGATCTCAGAAACCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAG	1800
Db	1741	CAAAATGATCTCAGAAACCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAG	1800
QY	1801	ATTCTGATTTCAATGAAGAAAGCAGATAGAGTGTGAAAAATGAATTTCTGAGCTTCT	1860
Db	1801	ATTCTGATTTCAATGAAGAAAGCAGATAGAGTGTGAAAAATGAATTTCTGAGCTTCT	1860
QY	1861	CTTAGATTGAAGAAAGAAAGACATCTTGCAATGAATTAATAGTACCTTCCGGGAAGAAAT	1920
Db	1861	CTTAGATTGAAGAAAGAAAGACATCTTGCAATGAATTAATAGTACCTTCCGGGAAGAAAT	1920
QY	1921	GCCATGCTAAGCTGAGCTAGACCAATGAACATCAAGCCAGACTAAAAAAGAAAAA	1980
Db	1921	GCCATGCTAAGCTGAGCTAGACCAATGAACATCAAGCCAGACTAAAAAAGAAAAA	1980

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CY      1981  AAAAAAAAAAAAAAAAAAAAAA  2000
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Db      1981  AAAAAAAAAAAAAAAAAAAAAA  2000
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RESULT 11
US-10-010-940-374
: Sequence 374, Application US/10010940
: Publication No. US2003008062A1
GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Hitchcock, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuxin
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael
: APPLICANT: Fanger, Gary
: APPLICANT: Retter, Mark
: APPLICANT: Solk, John
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATITIS
: FILE REFERENCE: 210121.427D3
: CURRENT APPLICATION NUMBER: US/10/010,940
: CURRENT FILING DATE: 2001-12-05
: NUMBER OF SEQ IDS NOS: 575
: SOFTWARE: FASTSEQ for Windows Version 3.0.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-010-940-374

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Cy      1981  AAAAAAAAAAAAAAAAAA 2000
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Db      1981  AAAAAAAAAAAAAAAAAA 2000

RESULT 11
US-10-010-940-374
; Sequence 374, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: JIANG YuguI
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaios, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Recter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-374

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OY 541 TGTGCAATGGGAATTGAGAAAGTAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
DB 541 TGTGCAATGGGAATTGAGAAAGTAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
OY 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGA 660
DB 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGA 660
OY 661 TGTGCGCTTAATGTTGGTGGAAACATGGACATGATCCAAATATTTCCAAATGAGTGAAT 720
DB 661 TGTGCGCTTAATGTTGGTGGAAACATGGACATGATCCAAATATTTCCAAATGAGTGAAT 720
OY 721 ACCACTGTGCACTACGCTATCTTAATGAAGATTAATTAAGCCAAAGACCTGCTCTTA 780
DB 721 ACCACTGTGCACTACGCTATCTTAATGAAGATTAATTAAGCCAAAGACCTGCTCTTA 780
OY 781 TATGCTGTGATATGCAATCAAAAAACAGCATGGCTCACAACACTGTTACTTGGTGA 840
DB 781 TATGCTGTGATATGCAATCAAAAAACAGCATGGCTCACAACACTGTTACTTGGTGA 840
OY 841 CATGACCAAAAAACAGCAAGTCGGAATTTTAAATCAAGAAAAACGCAATTTAAATGCA 900
DB 841 CATGACCAAAAAACAGCAAGTCGGAATTTTAAATCAAGAAAAACGCAATTTAAATGCA 900
OY 901 CTGATAGATATGGAAGAGACTGCTCATCTGCTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATAGATATGGAAGAGACTGCTCATCTGCTGTATGTTGTGATCAGCAAGTATA 960
OY 961 GTGACGCTTCTACTTGACAAAAATATGATATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGACGCTTCTACTTGACAAAAATATGATATCTTCTCAAGATCTATCTGACAGAG 1020
OY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCAGTTACTTCTGACTAC 1080
OY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGATTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCAGAACAGATTAAG 1140
OY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATGACCAAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGAGTGAATAATGACCAAGAGAAA 1200
OY 1201 ATGCTCCAAGAACCAAAATTAATAGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCCAAGAACCAAAATTAATAGATGCTGATAGAGAGGTTGAAGAAATGAAG 1260
OY 1261 AAGCATGAAGATTAATATGTTGGAATTACTAGAAAACTGACTAATGCTGCTGAGC 1320
DB 1261 AAGCATGAAGATTAATATGTTGGAATTACTAGAAAACTGACTAATGCTGCTGAGC 1320
OY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGTAATTCAGCAATTT 1380
DB 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGTAATTCAGCAATTT 1380
OY 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
OY 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
DB 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGCTTAAGCTGACA 1500
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DB 1501 TCAGAGAAAGAGTCACAAAGGCTTGAAGGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
OY 1561 TTTATGCTATCGAAGAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAC 1620

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OY 1621 CTGACTAATGTTGGCCACTGCTGCAATGTTGATGATTAATTCCTCAAGAGAGAGC 1680
DB 1621 CTGACTAATGTTGGCCACTGCTGCAATGTTGATGATTAATTCCTCAAGAGAGAGC 1680
OY 1681 AGAACACCTGAAAGCCAGCAATTTCTGCACTGAGATGAAGAGATACAGTACGAA 1740
DB 1681 AGAACACCTGAAAGCCAGCAATTTCTGCACTGAGATGAAGAGATACAGTACGAA 1740
OY 1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACATGAG 1800
DB 1741 CAAAATGATATCTCAAGAGCAATTTTGTGAAGAACGAAACCTGGAATATTAACATGAG 1800
OY 1801 ATTCTGATTCATGAAGAAAAACAGATAGAAAGTGTGAAAAATGAATTCAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAAACAGATAGAAAGTGTGAAAAATGAATTCAGCTTTCT 1860
OY 1861 CTTAGTTGTAAAGAAAAAGAACATCTTGCATGAAAAATAGTACGTTGGGGAAGAAAT 1920
DB 1861 CTTAGTTGTAAAGAAAAAGAACATCTTGCATGAAAAATAGTACGTTGGGGAAGAAAT 1920
OY 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
DB 1921 GCCATGCTTAAGCTGAGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 12
US-10-212-679-302
; Sequence 302, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirsch, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302

Query Match      100.0%; Score 2000; DB 6; Length 2000,
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 2000; Conservative 0; Mismatches 0;

OY 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
DB 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGCTTC 60
OY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
OY 121 AGCAAGTGGGCACTTCTGAGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGAGCAACG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGTGCAAGAGCAACG 240

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QY 241 GGGGCTTTGAGAGACCAAGCACTCTGCTATGAAAGCACTCAAGAAACAAGATGGGCAAG 300
 Db 241 GGGGCTTTGAGAGACCAAGCACTCTGCTATGAAAGCACTCAAGAAACAAGATGGGCAAG 300
 QY 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGGAGCGCAAGAGCAAGATGGGCGCTTGG 360
 Db 301 TGGTGCTGCACTGCTTCCCTCTGCAAGGGGGAGCGCAAGAGCAAGATGGGCGCTTGG 360
 QY 361 GAGAGCTACGATGACAGTGCCTTCAATGAGCCCAAGATCCAGTCCGTGAGAAAGATCTG 420
 Db 361 GAGAGCTACGATGACAGTGCCTTCAATGAGCCCAAGATCCAGTCCGTGAGAAAGATCTG 420
 QY 421 GAAAGCTCCAGAGAGTGCCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCAATGCTGATG 480
 Db 421 GAAAGCTCCAGAGAGTGCCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCAATGCTGATG 480
 QY 481 CTCAGGGAACAATAACGGAACAAGAGGAACAAGAGGAAGTGCCTCAATCTGAGCC 540
 Db 481 CTCAGGGAACAATAACGGAACAAGAGGAACAAGAGGAAGTGCCTCAATCTGAGCC 540
 QY 541 TCTGCAATGGGAATTCAGAAATGATTAACAATCTCTGCTGAGACAGAGATGCTCAATTAAT 600
 Db 541 TCTGCAATGGGAATTCAGAAATGATTAACAATCTCTGCTGAGACAGAGATGCTCAATTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCCAGAAAGATGAA 660
 Db 601 GTCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCCAGAAAGATGAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATTTCTCAAGTGAATGGAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAATTTCTCAAGTGAATGGAAT 720
 QY 721 ACCACTCTGCACTACGCTATCTAATAAGATTAATTAAGGCAAGAGCACTGCTTAA 780
 Db 721 ACCACTCTGCACTACGCTATCTAATAAGATTAATTAAGGCAAGAGCACTGCTTAA 780
 QY 781 TATGCTGCTGATTCGATCAAAAACAGCATGGGCTCAACCATCTGTTACTTGGTGA 840
 Db 781 TATGCTGCTGATTCGATCAAAAACAGCATGGGCTCAACCATCTGTTACTTGGTGA 840
 QY 841 CATGACAAAAACAGCAAGTCTGGAATTTTAAACAAGAAAAAGGAATTTAAATGCA 900
 Db 841 CATGACAAAAACAGCAAGTCTGGAATTTTAAACAAGAAAAAGGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGGACTGCTCTCATCTTCTGATATGTTGGATCAGCAAGTATA 960
 Db 901 CTGGATAGATATGGAAGGACTGCTCTCATCTTCTGATATGTTGGATCAGCAAGTATA 960
 QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGACAGACG 1020
 Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGAGTATGCTTCTAGTCATCATCATGTAATTTGCAAGTATCTATCTGACAGACG 1080
 Db 1021 GCCAGAGAGTATGCTTCTAGTCATCATCATGTAATTTGCAAGTATCTATCTGACAGACG 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCTGAGAACTTAAG 1140
 Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCTGAGAACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGACAGTGAATAATGCCAGCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGACAGTGAATAATGCCAGCCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAAGAAAG 1260
 Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAAGAAAG 1260
 QY 1261 AAGCATGAAGATTAATATGAGGATTAATAGAAAACTGACTAATGGTGTCACTGCTGGC 1320
 Db 1261 AAGCATGAAGATTAATATGAGGATTAATAGAAAACTGACTAATGGTGTCACTGCTGGC 1320

QY 1321 AATGTGATTAATGATTTAATTCCTCAAGAAAGAGAGAAACCTGAAAAATCAGCAATTT 1380
 Db 1321 AATGTGATTAATGATTTAATTCCTCAAGAAAGAGAGAAACCTGAAAAATCAGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGAAATTTAGTTCTGACTCAAGAA 1440
 Db 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTTGGAAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AAAAGATGCCAAAATATCTTCTTGAAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
 Db 1441 AAAAGATGCCAAAATATCTTCTTGAAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
 QY 1501 TCAGAGAAAGATCAAAAAGGCTTGGAGGCACTGAAAAATGGCCAGCAAGCTTGAAGAAAT 1560
 Db 1501 TCAGAGAAAGATCAAAAAGGCTTGGAGGCACTGAAAAATGGCCAGCAAGCTTGAAGAAAT 1560
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 Db 1561 TTTATGGCTATCGAAGAAATGAAAGAGCAAGAAAGTACTCATGTCGGATTTCCAGAAAAAC 1620
 QY 1621 CTGACTTAATGTGCACTGCTGCAATGCTGCAATGATGATTAATTTCTCCAAAGAAAGAGC 1680
 Db 1621 CTGACTTAATGTGCACTGCTGCAATGCTGCAATGATGATTAATTTCTCCAAAGAAAGAGC 1680
 QY 1681 AGAACACTGAAAGCCAGCAATTTCTGACACTGAGATGAAAGATATCAAGTGAAGAA 1740
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 QY 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGCATGAG 1800
 Db 1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGCATGAG 1800
 QY 1801 ATTCTGATTCATGAAGAAAAAGAGATAGAGTGTGTAAGAAAAATGAAATTTCTGAGCTTCT 1860
 Db 1801 ATTCTGATTCATGAAGAAAAAGAGATAGAGTGTGTAAGAAAAATGAAATTTCTGAGCTTCT 1860
 QY 1861 CTTAGTTGTAAGAAAGAAAAAGACATCTTGATGAAAAATGATACGTTGGCGGAAAGAAAT 1920
 Db 1861 CTTAGTTGTAAGAAAGAAAAAGACATCTTGATGAAAAATGATACGTTGGCGGAAAGAAAT 1920
 QY 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAACATCAAGCCAGCTAAAAAAGAAAAA 1980
 Db 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAACATCAAGCCAGCTAAAAAAGAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 RESULT 13
 US-10-144-678A-374
 ; Sequence 374, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retzer, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.

```
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Bassols, Carlota
/ APPLICANT: Roy, Teresa M.
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-374

Query Match      100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTTGAGAGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTGCTTC 60
DB      1 ATGTGTTGAGAGTTGATTCATGCGGCTCTCTTCTGTGAAGAGCCATTGCTTC 60

QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120

QY      121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180

QY      181 ATGGGCAAGTGTGCGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGT 240
DB      181 ATGGGCAAGTGTGCGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGT 240

QY      241 GGGCTTCTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB      241 GGGCTTCTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY      301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGAGTGGGCTTGG 360
DB      301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGAGTGGGCTTGG 360

QY      361 GGAAGACTACGATACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAAGATCTG 420
DB      361 GGAAGACTACGATACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAAGATCTG 420

QY      421 GACAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG 480
DB      421 GACAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG 480

QY      481 CTGAGGAGACCTGACGTGAACAAAGAGACAAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540
DB      481 CTGAGGAGACCTGACGTGAACAAAGAGACAAAGCAAAAGAGAGCTGCTTCAATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGGAACAGAGATGTCAACTTAAT 600
DB      541 TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGGAACAGAGATGTCAACTTAAT 600

QY      601 GTCTTGAACAACAAAAGAGAGACAGCTGTAATAAGCGGTAAATGCGCAGAGAGATGAA 660
DB      601 GTCTTGAACAACAAAAGAGAGACAGCTGTAATAAGCGGTAAATGCGCAGAGAGATGAA 660

QY      661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB      661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720

QY      721 ACCACTCTGCACTACCGTATCTAATATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
DB      721 ACCACTCTGCACTACCGTATCTAATATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
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QY      781 TATGTTGCTGATATGGAATCAAAAAACAAGCATGGCTTCACACCACTGTTACTGTGTA 840
DB      781 TATGTTGCTGATATGGAATCAAAAAACAAGCATGGCTTCACACCACTGTTACTGTGTA 840

QY      841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
DB      841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900

QY      901 CTGATATGATATGAAGAGCTGCTCATCTTCTGTAATGTTGTGGATCAGCAAGTATA 960
DB      901 CTGATATGATATGAAGAGCTGCTCATCTTCTGTAATGTTGTGGATCAGCAAGTATA 960

QY      961 GTGAGCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGGAACAGAG 1020
DB      961 GTGAGCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGGAACAGAG 1020

QY      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTAATTTGCGAGTTACTTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTAATTTGCGAGTTACTTTCTGACTAC 1080

QY      1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
DB      1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140

QY      1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAGGACAGTAAATAGCCAGCAGAGAA 1200
DB      1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAGGACAGTAAATAGCCAGCAGAGAA 1200

QY      1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATAGAGGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAGATTAATATGTTGGATTTCTAGAAAACTGACTAATGTTGTCCTGTGGC 1320
DB      1261 AAGCATGAAGATTAATATGTTGGATTTCTAGAAAACTGACTAATGTTGTCCTGTGGC 1320

QY      1321 AATGGATTAATGAATTAATCTCTCAAGAAAGAGAGAGAACCTGAAATCAGCAATT 1380
DB      1321 AATGGATTAATGAATTAATCTCTCAAGAAAGAGAGAGAACCTGAAATCAGCAATT 1380

QY      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTTCAAGAA 1440
DB      1381 CCTGACAAAGAAAGTGAAGAGTATCAAGAAATTTGCGAATTAATGTTCTGACTTCAAGAA 1440

QY      1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACCTTAAAGCTGACA 1500
DB      1441 AAACAGATGCCAAAATTAATCTTCTGAAAAACAGCAACCCAGAACCTTAAAGCTGACA 1500

QY      1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATGAGCAGAGCTAGAAAT 1560
DB      1501 TCAGAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATGAGCAGAGCTAGAAAT 1560

QY      1561 TTTATGCTATGGAAGAAATGAAGAGCACGGAAGTACTCATGTGGAATTTCCAGAAAAAC 1620
DB      1561 TTTATGCTATGGAAGAAATGAAGAGCACGGAAGTACTCATGTGGAATTTCCAGAAAAAC 1620

QY      1621 CTGACTAATGTTGCTGCACTGCTGCAATGTTGATGATTAATCTTCTCAAGAGAGAGC 1680
DB      1621 CTGACTAATGTTGCTGCACTGCTGCAATGTTGATGATTAATCTTCTCAAGAGAGAGC 1680

QY      1681 AGAACACCTGAAAGGACAGCAATTTCTGCACTGAGAAATGAAGAGATGACAGTGCAGAA 1740
DB      1681 AGAACACCTGAAAGGACAGCAATTTCTGCACTGAGAAATGAAGAGATGACAGTGCAGAA 1740

QY      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800
DB      1741 CAAAAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAG 1800

QY      1801 AATTCGATTCATGAAGAAAGAGATGAGAGTGTGTTGAAAAATGAATTTGAGCTTTCT 1860
DB      1801 AATTCGATTCATGAAGAAAGAGATGAGAGTGTGTTGAAAAATGAATTTGAGCTTTCT 1860
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QY 1861 CTTAGTTGTAGAGAAAGAAAGACATCTTCATGATAAATAGTAGTTCGGGAGAAAT 1920
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Db 1861 CTTAGTTGTAGAGAAAGAAAGACATCTTCATGATAAATAGTAGTTCGGGAGAAAT 1920
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QY 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAA 1980
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Db 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAA 1980
|
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QY 1981 AAAAAAAAAAAAAAAAAA 2000
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Db 1981 AAAAAAAAAAAAAAAAAA 2000
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|

RESULT 14

US-10-033-527-6
Sequence 6, Application US/10033527
Publication No. US20030170631A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, Davin C.
APPLICANT: Moleah, David A.
APPLICANT: Xu, Jiangchun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
OF TITLE OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513C1
CURRENT APPLICATION NUMBER: US/10/033.527
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-10-033-527-6

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGTAAGAAGCCATTGGTTC 60
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|
|
Db 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGTAAGAAGCCATTGGTTC 60
|
|
|
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGCAAG 120
|
|
|
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGCAAG 120
|
|
|
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACACTTCTGTAAGACACTCAGAGCAAG 180
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|
|
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACACTTCTGTAAGACACTCAGAGCAAG 180
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|
|
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG 240
|
|
|
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG 240
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Db 241 GGGGCTTCTGAGACACAGACACTGCTGTAAGACACTCAGAAAGATGGCAAG 300
|
|
|
QY 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGCGCTTG 360
|
|
|
Db 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGCGCTTG 360
|
|
|
QY 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTAACAGTCCGTGGAGAAATCTG 420
|
|
|
Db 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTAACAGTCCGTGGAGAAATCTG 420
|
|
|
QY 421 GACAACTCCACAGAGCTGCTGTGGGGAAGTCCCGCAAGAAAGATCTCATGTCATG 480
|
|
|
Db 421 GACAACTCCACAGAGCTGCTGTGGGGAAGTCCCGCAAGAAAGATCTCATGTCATG 480
|
|
|

QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACGTGCTACACTGGCC 540
|
|
|
Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACGTGCTACACTGGCC 540
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|
QY 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGATGTCACCTTAAT 600
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Db 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGATGTCACCTTAAT 600
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QY 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACATGCCAGAAATGAA 660
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|
|
Db 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACATGCCAGAAATGAA 660
|
|
|
QY 661 TGTGCTTATGTTGTGGAACATGCGACATGATCCAAATTTCCAGATGATGGAAT 720
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Db 661 TGTGCTTATGTTGTGGAACATGCGACATGATCCAAATTTCCAGATGATGGAAT 720
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QY 721 ACCACTCTGACACTACGCTATCTAATAAGATTAATTAAGCCAAACACTGCTTTA 780
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Db 721 ACCACTCTGACACTACGCTATCTAATAAGATTAATTAAGCCAAACACTGCTTTA 780
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QY 781 TATGCTGATATGCAATCAAAAAACAAGCATGCGCTCACACACTGTTACTTGTGTA 840
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Db 781 TATGCTGATATGCAATCAAAAAACAAGCATGCGCTCACACACTGTTACTTGTGTA 840
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QY 841 CATGACCAAAAACAGCAATGCGTAATTTTAAATCAAAAAAGCCAAATTTAAATGCA 900
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Db 841 CATGACCAAAAACAGCAATGCGTAATTTTAAATCAAAAAAGCCAAATTTAAATGCA 900
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QY 901 CTGATATGATGAGAAAGACCTGCTCATACTTGTGTTGTTGATGATGCAAGTATA 960
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Db 901 CTGATATGATGAGAAAGACCTGCTCATACTTGTGTTGTTGATGATGCAAGTATA 960
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QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGCG 1020
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QY 1021 GGCAGAGATATGCTGTTCTGATCATCATGTAATTTGCACTTCTGCTAC 1080
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Db 1021 GGCAGAGATATGCTGTTCTGATCATCATGTAATTTGCACTTCTGCTAC 1080
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QY 1081 AAGAGAAACAGATGCTAAATACTCTGTAACAGCAATCCAGAACAGACTTAAG 1140
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Db 1081 AAGAGAAACAGATGCTAAATACTCTGTAACAGCAATCCAGAACAGACTTAAG 1140
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QY 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAGGACAGAAATGCGCAGAGAA 1200
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Db 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAGGACAGAAATGCGCAGAGAA 1200
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QY 1201 ATGTCTCAAGAACAGAAATTAATGAATGATGATGAGAGTTGAAAGAAATGAAG 1260
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Db 1201 ATGTCTCAAGAACAGAAATTAATGAATGATGATGAGAGTTGAAAGAAATGAAG 1260
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|
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QY 1261 AAGCATGAAGATTAATGATGGAATTAATGAGAAACCTGATTAATGATGCTGCTG 1320
|
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Db 1261 AAGCATGAAGATTAATGATGGAATTAATGAGAAACCTGATTAATGATGCTGCTG 1320
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QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGACAAATTT 1380
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Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGACAAATTT 1380
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QY 1381 CCTGACAAAGAGTGAAGATATCACAGAAATTTGGGAAATTTGTTCTGATCAAGAA 1440
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Db 1381 CCTGACAAAGAGTGAAGATATCACAGAAATTTGGGAAATTTGTTCTGATCAAGAA 1440
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Db 1441 AAAAGATGCAAAATTAATCTCTGTAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
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QY 1501 TCAAGAGAAAGTCAAAAAGCTTGAAGGCAAGTAAATGTCACAGAGCTAGAAAT 1560
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Db 1501 TCAAGAGAAAGTCAAAAAGCTTGAAGGCAAGTAAATGTCACAGAGCTAGAAAT 1560
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QY 1561 TTTATGCTATGAGAAATTAAGAAAGCAAGAGTACTATGTGGATTTCCAGAAAC 1620
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|

Db 1561 TTTATGGCTATCCAGAAATAAGAAAGACGGAAGTACTATGTCGGAATTCACAGAAAC 1620
QY 1621 CTGACCTAAATGATGCGCATCTGTCGCAATGATGATGATTAATTCCTCCAGAGAAAC 1680
Db 1621 CTGACCTAAATGATGCGCATCTGTCGCAATGATGATGATTAATTCCTCCAGAGAAAC 1680
QY 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAAATGAAGATGATCAAGTGAAGAA 1740
Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAAATGAAGATGATCAAGTGAAGAA 1740
QY 1741 CAAATGATGATCTGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Db 1741 CAAATGATGATCTGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CTTAGTTGTAAAGAAAGAAAGCAATCTTGATGAAATATGATCGTTGCGGAGAAATTT 1920
Db 1861 CTTAGTTGTAAAGAAAGAAAGCAATCTTGATGAAATATGATCGTTGCGGAGAAATTT 1920
QY 1921 GCCATGCTAAAGCTGAGCTGAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAAGCTGAGCTGAGACACATGAAACATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 15
US-10-294-025-374
Sequence 374, Application US/10294025
Publication No. US2003018530A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Skolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapiens
US-10-294-025-374

Query Match 100.0%; Score 2000; DB 6; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGATGTTGAGATTTGATTCATGCGGCTGCTTTCTGTGAAGAGCATTTGATTC 60
QY 61 AGGAGCAAGATGAGCAAGTGTGCTGCGGCTGCTTTCCCTGCTGAGGAGAGCGCAAG 120
Db 61 AGGAGCAAGATGAGCAAGTGTGCTGCGGCTGCTTTCCCTGCTGAGGAGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTTCTGAGACACAGCAAGCTTGTATGAAGACCTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTTCTGAGACACAGCAAGCTTGTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGAGCAAGCG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGAGCAAGCG 240

QY 241 GCGGCTTCTGAGACCAAGCAGACTCTGCTATGAAGACATCAGGAACAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGACCAAGCAGACTCTGCTATGAAGACATCAGGAACAAGATGGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
QY 361 GGAAGCTACATGACAGTGCCTTCATGAGGCCAGGTATCAGGTCGAGGAAGATCG 420
Db 361 GGAAGCTACATGACAGTGCCTTCATGAGGCCAGGTATCAGGTCGAGGAAGATCG 420
QY 421 GACAACTCCACAGAGCTGCTGTGTGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGTGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
QY 481 CTCAGGGAACCTGACGTGAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGACC 540
Db 481 CTCAGGGAACCTGACGTGAACAAGAGCAAGCAAGAAAGAGACTGCTTACATCTGACC 540
QY 541 TGTGCAATGGGAATTCAGAAATGATTAATCTGCTGGAACAGACATGCTAT 600
Db 541 TGTGCAATGGGAATTCAGAAATGATTAATCTGCTGGAACAGACATGCTAT 600
QY 541 TGTGCAATGGGAATTCAGAAATGATTAATCTGCTGGAACAGACATGCTAT 600
Db 541 TGTGCAATGGGAATTCAGAAATGATTAATCTGCTGGAACAGACATGCTAT 600
QY 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGAGCCGTAACAATGCCAGAAAGTGA 660
Db 601 GTCTTGAACAACAAAAGAGAGCAGCTCTGATTAAGAGCCGTAACAATGCCAGAAAGTGA 660
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Db 661 TGTGCTTAATGTGCTGGAACATGCGCTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCACTAGGCTATCTATAAGATTAATTAAGGCCAAAGCACTGCTCTA 780
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QY 781 TATGCTGATGATGATCAATCAAAAAGAGAGCTGCTCACACACTGTTACTTGGTGA 840
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QY 841 CATGACAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
Db 841 CATGACAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAGCGAATTTAAATGCA 900
QY 901 CTGATGATGATGAGAGAGCTGCTCATCTGCTGATGATGATGATGATGATGATGATGAT 960
Db 901 CTGATGATGATGAGAGAGCTGCTCATCTGCTGATGATGATGATGATGATGATGATGAT 960
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGAGAG 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGAGAG 1020
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Db 1021 GCGAAGATATGCTGTTTCTAGCATCATGTAATTTGCGAGTTACTTTCTGACTAC 1080
QY 1081 AAAAAAAAAAAGATGTAATAATCTCTGAAAACAGAAATCCAGAAACCTTAAG 1140
Db 1081 AAAAAAAAAAAGATGTAATAATCTCTGAAAACAGAAATCCAGAAACCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAGGAGTGAAGAAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAGGAGTGAAGAAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGAT 1260
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Db 1261 AAGCATGAAGATTAATGATGATGATTAATCAAGAAACCTGAATAGATGATGATGATGAT 1320
QY 1321 AATGATGATTAATGATTAATCTCCTCAAGAGAGAGCAAGAACCTGAAATCAGCAATTT 1380

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Db 1321 AATGGATATATGATTTAATTCCTCAAGAGAAAGCAAGAACCTGAAAATCAGCAATTT 1380
Qy 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
Qy 1441 AAAACGATGCCAAAATATCTTTCTGAAAACAGCAACCCGAAACAAAGACTTAAAGCTGACA 1500
Db 1441 AAAACGATGCCAAAATATCTTTCTGAAAACAGCAACCCGAAACAAAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATATGGCCAGGAGCTAGAAAAT 1560
Db 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATATGGCCAGGAGCTAGAAAAT 1560
Qy 1561 TTTATGGCTATCGAAGAAATGAAGAACACGAAAGTACTCATGTGCGATTTCCAGAAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAACACGAAAGTACTCATGTGCGATTTCCAGAAAAC 1620
Qy 1621 CTGACTAATGCTGCCACTGTGGCAATGGTGAATGATGATTAATTCCTCCAGAAAGAGC 1680
Db 1621 CTGACTAATGCTGCCACTGTGGCAATGGTGAATGATGATTAATTCCTCCAGAAAGAGC 1680
Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAA 1740
Qy 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG 1800
Db 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATATAGTACGTTGGCGGAGAAATTT 1920
Db 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATATAGTACGTTGGCGGAGAAATTT 1920
Qy 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAAAACATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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Search completed: December 18, 2005, 15:26:34
Job time : 1634.23 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:12:24 ; Search time 243.564 Seconds
(without alignments)
4025.047 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atggtggtggtgagtgatc.....aaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*
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2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
9: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170.6	8.5	1041	US-10-131-826A-21	Sequence 262, App
2	84.6	4.2	14770	US-10-821-234-268	Sequence 181, App
3	71.4	3.6	1870	US-10-750-185-34429	Sequence 4, App1
4	66	3.3	2048	US-10-955-054A-16	Sequence 489, App
5	61	3.0	3343	US-11-108-172-795	Sequence 75, App
6	60.2	3.0	4270	US-10-714-781A-54	Sequence 95, App
7	60.2	3.0	5004	US-10-714-781A-77	Sequence 54, App
8	58.8	2.9	6928	US-10-714-781A-60	Sequence 77, App
9	56	2.8	2505	US-11-186-283-9	Sequence 60, App
10	56	2.8	3026	US-11-186-283-7	Sequence 9, App
11	52	2.6	6549	US-11-186-284-92	Sequence 71, App
12	50.6	2.5	5054	US-10-821-234-123	Sequence 92, App
13	50.4	2.5	2505	US-11-186-283-3	Sequence 123, App
14	50.4	2.5	3025	US-11-186-283-1	Sequence 3, App
15	50	2.5	2487	US-10-689-742-165	Sequence 1, App
16	49.8	2.5	1790	US-11-000-463-671	Sequence 165, App
17	49.4	2.5	1926	US-10-750-185-55958	Sequence 671, App
18	46.4	2.3	1108	US-10-689-742-209	Sequence 5595, A
19	45	2.2	2668	US-10-131-826A-511	Sequence 209, App
20	44.4	2.2	3819	US-10-131-826A-405	Sequence 511, App
21	44	2.2	496	US-10-131-826A-533	Sequence 405, App
22	43.8	2.2	2036	US-10-996-217A-8	Sequence 533, App
23	43.6	2.2	755	US-10-131-826A-153	Sequence 8, App
					Sequence 153, App

24	43	2.1	398	US-11-123-896-262	Sequence 262, App
25	42.8	2.1	1524	US-10-131-826A-181	Sequence 181, App
26	42.8	2.1	2392	US-11-045-802-4	Sequence 4, App1
27	42.8	2.1	2476	US-10-131-826A-489	Sequence 489, App
28	42.8	2.1	2778	US-11-080-991-75	Sequence 75, App
29	42.8	2.1	4339	US-10-909-125-801	Sequence 801, App
30	42.8	2.1	28524	US-10-995-561-13292	Sequence 13292, A
31	42.6	2.1	1533	US-10-131-826A-217	Sequence 217, App
32	42.6	2.1	2933	US-10-131-826A-345	Sequence 345, App
33	42.4	2.1	373	US-10-986-501-106	Sequence 106, App
34	42.4	2.1	156297	US-11-121-086-65	Sequence 65, App
35	42.2	2.1	1441	US-11-080-991-57	Sequence 57, App
36	42.2	2.1	1658	US-11-102-240-59	Sequence 59, App
37	42.2	2.1	1668	US-10-955-054A-113	Sequence 113, App
38	42.2	2.1	2463	US-11-108-528-3	Sequence 3, App1
39	42	2.1	1454	US-10-750-185-57501	Sequence 57501, A
40	42	2.1	1904	US-10-131-826A-99	Sequence 99, App
41	41.8	2.1	693	US-10-131-826A-499	Sequence 499, App
42	41.8	2.1	1503	US-10-131-826A-363	Sequence 363, App
43	41.8	2.1	2846	US-11-102-240-37	Sequence 37, App
44	41.8	2.1	34000	US-11-102-978-3	Sequence 3, App1
45	41.6	2.1	201	US-10-995-561-46434	Sequence 46434, A

ALIGNMENTS

RESULT 1
US-10-131-826A-21
Sequence 21, Application US/10131826A
Publication No. US20050245750A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588

/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 21
/ LENGTH: 1041
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-131-826A-21

Query Match 8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 4.7e-29;

Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCCGAGTACCGTCCGTGAGAGAGATCTGAGCAAGCTCCAGAGC 437
DB 300 TGGCTTCGCAATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCAGAGC 359
QY 438 TGCCTGCTGGGTAAGATCCCGAGAAAGATCTCATGCTGATGCTGAGGACATGAGT 497
DB 360 TGTCTTACATGTAATCTAGAGAACTGAA--GTACCTTCTGCTCACGATATTATGACCG 416
QY 498 GAAACAAG 557
DB 417 CAATTAAG 476
QY 558 AGAAGTATGTAAG 617
DB 477 GGAATATGTAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
QY 618 GAGACAGCTCTGATTAAG 677
DB 537 CAGAGACAGCTCTGATCAAG 596
QY 678 GGAACATGAGCAGATCCAAATATTCAGATGAGTATGAGAAATACAGCTGAGTACAGC 737
DB 597 GCAAAATGGCGCAATCCAAATATTCAGATGAGTATGAGAAATACAGCTGAGTACAGC 656
QY 738 TATCTATATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 797
DB 657 TGTGTATATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 716
QY 798 ATCAAAAAACAG 810
DB 717 AGAATGACAGCAAG 729

RESULT 2

US-10-821-234-268
/ Sequence 268, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andertman, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 268
/ LENGTH: 14770
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-268

Query Match 4.2%; Score 84.6; DB 6; Length 14770;
Best Local Similarity 49.9%; Pred. No. 2.3e-09;
Matches 213; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 511 AAGCAAAAG 570
DB 1879 AAGAAAGATTTATCT 1938
QY 571 CTCTGCTGAG 630
DB 1939 CTCTGCTGAG 1998
QY 631 ATTAAGCCCTGTAATGCAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
DB 1999 CATGTAGCTGCAATTAATGCAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2058
QY 691 GATCCAAATATTTCCAGATAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
DB 2059 TCACCTCAG 2118
QY 751 GATTAATTAATGAG 810
DB 2119 CAGATGAGACATAG 2178
QY 811 CATGCTCAGACAG 870
DB 2179 CAG 2238
QY 871 TTAATCAAG 930
DB 2239 CTCTCTGAG 2298
QY 931 CTCTCTG 937
DB 2299 TTGGCTG 2305

RESULT 3

US-10-185-34429
/ Sequence 34429, Application US/10750185
/ Publication No. US2005026063A1
/ GENERAL INFORMATION:
/ APPLICANT: NMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM11100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 34429
/ LENGTH: 1870
/ TYPE: DNA
/ ORGANISM: Bovine 1986880438718
US-10-750-185-34429

Query Match 3.6%; Score 71.4; DB 6; Length 1870;
Best Local Similarity 72.1%; Pred. No. 9.2e-07;
Matches 93; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 916 AGAGCTGCTCTCACTACTGCTGATGTTGTGATCAGCAAGTATGTCAGCTTCTACTT 975
DB 1634 AGAAGAGCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1693
QY 976 GAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGCGGACAGAGATGCT 1035
DB 1694 CAGCAAGGTGTTGACATCTTTCTCAAGATGTTTGTGATGAGCTGCGAAGAAATGCT 1753
QY 1036 GTTCTAGT 1044

Db 1128 CTCCTCTGGAATGGCTGTATGTTCAAGAAATACCGAGGCTATPAAAAATCTTGATGAGT 1187
QY 584 GACGATGTCACTTAATATGTCCTTGACAAACAAAAGAGACGCTGTGATAAGCCGTAC 643
Db 1188 ATGAGACTAAACCTGTAGTACTGAATGACACA--ACTTCTGTCTGCATGATGCGGTG 1244
QY 644 AATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGGCAGCTATCCAAATATTC 703
Db 1245 TGAAGACGACTCAAAAATATGTGAATGATCTGTGAAGAAATTAATGTAACAAATGTC 1304
QY 704 CAGATGATATGAAAATACCACTCTGCACTACGCTATCTTAATGAAGATAAATTAATG 763
Db 1305 TTTACAGCGGAGGCTTACTCCCTTGTGTGTTGGCAGTTACCTTAACAAAGTTAATTTG 1364
QY 764 CCAAGACACTGCTCTTATATATGTCGTGATATCGAATCAAAAACAAGACATGCGCTCAC 823
Db 1365 TTTAACTTCTATTTGGCTCATTTCCGCGATGATGATATTTCAACAACGATCGTTAATC 1424
QY 824 CACTGTACTTGTGTATCATGACGAAAACAGACATCGTGAATTTTAAATCAAGAAA 883
Db 1425 CTCTACATATAGCCGATCAAAATTAATTAACAATGTTAACTTATATGAACAAAG 1484
QY 884 AAGCGAATTTAAATGACATGATGATGATGAAAGACTGCTCATACTGCTGATGTT 943
Db 1485 GTGCTGATATGACTGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1544
QY 944 GTGATTCAGCAAGTATATGTCAGCTTCTTACTGACAAATA 985
Db 1545 CTGAAATATTTGAATATGTAGCACACTTAAATAATA 1586

RESULT 9

US-11-186-283-9
; Sequence 9, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-9

Query Match 2.8%; Score 56; DB 7; Length 2505;
Best Local Similarity 46.3%; Pred. No. 0.0029;

Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;

QY 524 CTGCTTACATCTGCGCTCTGCGAATGGGAATTCAGAAGTAGTAAATCTCTGCTGACA 583
Db 308 CAGCTCTGACCTGGCGCTTTACAGAGACGCCGGAATTAATCACTTCACTGTTGACA 367
QY 584 GACGATGTCAACTTATATGCTTGTGACAAACAAAAGAGACAGCTGATTAAGCCGTAC 643

Db 368 GCGAGACAGATGTTTCAGCAAGTGGATACGCTGCTCACAGCCCTCCACATAGCTGCA 427
QY 644 AATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGCGACATGATCAAAATATTC 703
Db 428 TAGCTGAGACCCAGAGGCTGAGAAAGTGTCTGTACAAATGGGGCAATGTATGTTTC 487
QY 704 CAGATGATATGAAAATACCACTCTGCACTACGCTATCTTAATGAAGATAAATTAATG 763
Db 488 AATATCCGCTCTTCTTACCCCACTGCAATGACACTTACTTATGAGCGACAGCTAA 547
QY 764 CCAAGACACTGCTCTTATATATGTCGTGATATGATCAAAAACAAGACATGCGCTCAC 823
Db 548 CAGTGTCTTTTGAAGTTTGTGCTGATGTCATATGATGATGATGATGATGATGATGAT 607
QY 824 CACTGTACTTGTGTATCATGACGAAAACAGCAATCGTGAATTTTAAATCA----- 878
Db 608 CTCTGACCTGGCTCTGCAAAAGGCTTCTTCAACTTGTGAATCTCTGTGAAGAAAG 667
QY 879 -GAAAAAGCGAATTTAAATGACATGATGATGATGATGATGATGATGATGATGATGAT 937
Db 668 GGAGCAAGCAGATGTGAACGCTCAGACAAATGAACACACGTCCTGCACTTCTGTT 727
QY 938 TATGTTGTGATCAGCAAGTATATGTCAGCTTCTTACTTGAAGAAAATATGATATCTT 997
Db 728 CTGATTTGACACCAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 787
QY 998 CTCAG 1003
Db 788 CTCACG 793

RESULT 10

US-11-186-283-7
; Sequence 7, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3026
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(2565)
US-11-186-283-7

Query Match 2.8%; Score 56; DB 7; Length 3026;
Best Local Similarity 46.3%; Pred. No. 0.0011;

Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;

QY 524 CTGCTTACATCTGCGCTCTGCGAATGGGAATTCAGAAGTAGTAAATCTCTGCTGACA 583
Db 368 CAGCTCTGACCTGGCGCTTTACAGAGACGCCGGAATTAATCACTTCACTGTTGACA 427
QY 584 GACGATGTCAACTTATATGCTTGTGACAAACAAAAGAGACAGCTGATTAAGCCGTAC 643

Db 428 GCGAGCAGATGTCAGCAAGTGGATACGGTGGCTTCACAGCCCTCCACATAGCTGCAA 487
Qy 644 AATGCCAGAGATGAATGGGTTAATGTGCTGGAAATGACCTGATCCAAATATTC 703
Db 488 TAGCTGACACCCAGAGGCTGCAAGAGTCTGTACAAATGGGCAATGGAAATGTC 547
Qy 704 CAGATGATGATGAAATACCACTGCTGACCTAGCTATCTATATGAAGATTAATATG 763
Db 548 AAGATGCCCTCTTCTTACCCCACTGCAATGCAACCTACTATGGGCAAGAGCTAA 607
Qy 764 CCAAGACATGCTCTTATATATGCTGATGATGATCAAAAACCAAGATGCTTCAC 823
Db 608 CCAAGTCTCTTTTGAAGTGTGCTGATGATCAATGAACGGTGAAGTTGGGCAAG 667
Qy 824 CACTGTACTGTGTGATACATGAGCAAAAACAGAACTGGTGAATTTTAACTCA 878
Db 668 CTCTGACCTGGCTTTCGCAAAAGGCTTCTTCAACATGTGAAACTCTGTGAAAG 727
Qy 879 -GAAAAAGCGAATTTAAATGCACTGATGATGATGAAAGACTGCTCTCATACTT 937
Db 728 GGAGCAAGCAGATGTGAACGCTCAGAGACAAAGAACACAGTCCCTGCACTTCT 787
Qy 938 TATGTTGATGACGAGATATGTCAGCTTCTTACTTGAACAAAATATTGATGAT 997
Db 788 CTCGATTTGACACCAATATATGATGACTCTGCTCCAGAGTACTTGAAGTCCAG 847
Qy 998 CTCAG 1003
Db 848 CTCAG 853

RESULT 11
US-11-186-284-92
; Sequence 92, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-0292RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 6549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240) ..(4904)
US-11-186-284-92

Query Match 2.6%; Score 52; DB 7; Length 6549;
Best Local Similarity 46.8%; Pred. No. 0.033;
Matches 163; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy 491 CTGACGTGAACAAGAGCAAGCAAAAGAGACTGTCTACATCTGGCCTTGCCAAATG 550
Db 2626 CTGCTGTGTGGGCAAAACAGAGAGGGTTCCACTTTTGTGTCAGACGCCAG 2685
Qy 551 GGAATTCAGAAATAGTAAACTCTCTGACAGACATGTCAACTTAATGTCCTTGACA 610
Db 2686 GGCAATTGGCAGATTGTAGACTGTGTTGAACGGGCTGTGTATGAACTTAAGTGACA 2745
Qy 611 ACAAAGAGACACACTCTGATTAAGCCGCTGCAATGCCAGAAATGATATGCGTTAA 670
Db 2746 ACAAAGCCGAGCGCCCTCATGCTGCTGTGAAAGGCACTTGAGCACCGTGAAT 2805
Qy 671 TGTTCGGAACATGACGACTGATCCAAATATTCAGATGATGATGAATAACACTGTC 730
Db 2806 TCCCTCTTCAAAAGTGTGACGCCCTTCTCTTGAACAAAGAGGTCTGTACGATTAA 2865
Qy 731 ACTACGCTATCTATATGAAAGTAAATTAATGCGCAAAAGCACTGCTTTATATGTC 790
Db 2866 GCTGGGCTGTGTGAAAGGTCAACAGGCAAGTGTCCAGATCTGTGTAAGAGAGCTG 2925
Qy 791 AATAGCAATCAAAAACAGATGGCTCAGACCACTGTTACTTGTG 838
Db 2926 CAATAGACCAGACAGCAAGATGGCCGACACCCCTTGACCTGCTG 2973

RESULT 12
US-10-821-234-123
; Sequence 123, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andermani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 123
; LENGTH: 5054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-123

Query Match 2.5%; Score 50.6; DB 6; Length 5054;
Best Local Similarity 44.4%; Pred. No. 0.061;
Matches 203; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

Qy 526 GCTTACATCTGGCCTTGCCAAATGGAAATTCAGATGATGAATCTCTGCTGACAGA 585
Db 519 GCTTACATCTGGCAGCAAGAACGCCACATGATGATCAGAAAGCTGCTGATCT 578
Qy 586 CGATGCACTAATAGTCTCTGCAACAACAAAGAGACAGCTGTATTAAGCCGTCACA 645
Db 579 AATGCCAGCCGAAAGGTGTGACAGCTCTGGGAAAAACAGCTTTACATTATCCAGG 638
Qy 646 TGCAGAAAGATGATGTCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTC 705
Db 639 CAGGCTGCTTCAAGCTGTGTGCAATTTCTTCGCAACACAGAGCCCTTAACCTCAA 698
Qy 706 GATGATGAAATACCACTTGCACCTAAGCTATCTATATGAAGATTAATGAATG 765
Db 699 GATTGATGGAATATACCGCTGCTGCTGTGTAACAAATGTCACAGTGAATCTGT 758
Qy 766 AAGACCTGCTTATATGCTGTATGATGCAATCAAAAAACAGATGCTCACACA 825
Db 759 CACTTCTCTGATGATGAGACAGATGCAATTCAGGAAACAAAGTGAAGAACTGCT 818
Qy 826 CTGTACTTGTGTATGATGACAAACAGCAAGTGTGAAATTTTATCAAGAAAAA 885

Db 819 CTCATCTGCGCTGTGAGATTGGACGCTTAAGCTGTGGAGCCTTAATTAAGGGT 878
Qy 886 GCGAATTTAAATGCACTGTAGATATGAGAGACGCTCTCATCTGTGTATGTGT 945
Db 879 GCAGACCTTAACCTTGTGATTTCTTGTGATACAAAGCCTTACATTATTCAAACTCTCA 938
Qy 946 GGATCAGCAAGTATAGTACGCTTCTTACTTACAGCAAA 982
Db 939 GAAATGCGAGAAATTCAAAGCCTTCTTATTCAAAA 975

RESULT 13

US-11-186-283-3
; Sequence 3, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNT-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-3

Query Match 2.5%; Score 50.4; DB 7; Length 2505;
Best Local Similarity 44.0%; Pred. No. 0.051;
Matches 213; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

Qy 523 ACTGCTCTACATCTGCGCTGTGAGATTGGAAATTCAGAGTAGTAATACTCCTGTGAC 582
Db 307 ACAGCCTTGATTTAGCACTTTACAGAGATTAAGATGCAAGAAATGATCACTTCTGTCTTAC 366
Qy 583 AGACGATGCACTTATATGCTCTTGACAACAAAAAGAGAGACGCTGTGATAAGGCCGTA 642
Db 367 AGTGAAGCTGATATAGAGAGGTGATACGGTGGCTCACTCCCTCATATGTGTACA 426
Qy 643 CAATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATT 702
Db 427 ATATGCTGCGACCTAGAGGCTGTGATGCTGTGTGCAACATGAGACTATATGCAATATT 486
Qy 703 CCAAGATGATGGAATTAACAATCTGCACTAGCTATCTATATATAAATAATTAATG 762
Db 487 CAAGATGCAAGTTTTTTCATCTCATTTGCAATTTGACGCGTACTATGAGATGAACAGTA 546
Qy 763 GCCAAGACACTGCTTTATATGCTGATATGATCAAAATAAACAAGATGGCTCACA 822
Db 547 ACTGCGCTCTTTTGAATTTGCTGTGATTAATGTAAGTGAAGTGAAGTGA 606
Qy 823 CCACTGTACTTGTGTATGATGAGCAAAAACAGCAAGCGTGAATTTTAAATCAAGAA 882
Db 607 CCCCTCACCTAGCATCTGCAAAAAGATTTCTGAATATGCAAACTCTTATGAGAA 666
Qy 883 AAAGCAATTTAATGCACTGTATATGATATGAAAGACGCTCTCATACTTGTGTATGT 942

Db 667 GCGAAGACGAGATGTGATGATGTAAGTAAAGACCATGCTCCACTTTCTGT 726
Qy 943 TGTGATCAGCAAGTATAGTACGCTTCTTACTTACAGCAAAATATGATATCTTCA 1002
Db 727 TCTGATTTGGAACACCATGATATAGTATCTGCTCAAAAGTATTTGAAATTCAA 786
Qy 1003 GATC 1006
Db 787 CCTC 790

RESULT 14

US-11-186-283-1
; Sequence 1, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNT-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48)..(2552)
US-11-186-283-1

Query Match 2.5%; Score 50.4; DB 7; Length 3025;
Best Local Similarity 44.0%; Pred. No. 0.055;
Matches 213; Conservative 0; Mismatches 271; Indels 0; Gaps 0;

Qy 523 ACTGCTCTACATCTGCGCTGTGAGATTGGAAATTCAGAGTAGTAATACTCCTGTGAC 582
Db 354 ACAGCCTTGATTTAGCACTTTTACAGAGATTAAGATGCAAGAAATGATCACTTCTGTCTTAC 413
Qy 583 AGACGATGCACTTATATGCTCTTGACAACAAAAAGAGAGACGCTGTGATAAGGCCGTA 642
Db 414 AGTGAAGCTGATATAGAGAGGTGATACGGTGGCTCACTCCCTCATATGTGTACA 473
Qy 643 CAATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATT 702
Db 474 ATATGCTGCGACCTAGAGGCTGTGATGCTGTGTGCAACATGAGACTATATGCAATATT 533
Qy 703 CCAAGATGATGGAATTAACAATCTGCACTAGCTATCTATATATAAATAATTAATG 762
Db 534 CAAGATGCAAGTTTTTTCATCTCATTTGCAATTTGACGCGTACTATGAGATGAACAGTA 593
Qy 763 GCCAAGACACTGCTTTATATGCTGATATGATCAAAATAAACAAGATGGCTCACA 822
Db 594 ACTGCGCTCTTTTGAATTTGCTGTGATTAATGTAAGTGAAGTGAAGTGA 653
Qy 823 CCACTGTACTTGTGTATGATGAGCAAAAACAGCAAGCGTGAATTTTAAATCAAGAA 882
Db 654 CCCCTCACCTAGCATCTGCAAAAAGATTTCTGAATATGCAAACTCTTATGAGAA 713
Qy 883 AAAGCAATTTAATGCACTGTATATGATATGAAAGACGCTCTCATACTTGTGTATGT 942

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Db      714 GCAGCAAGCAGATGTGATGCTCAAGATAATGAAGACCATGTCCTCCATTTCTGT 773
QY      943 TGTGATCAGCAGATATAGTCAAGCTTCTACTTGAGCAAAATATGATATCTCTCA 1002
Db      774 TCTCGATTTTGACACCATATATAGTTAAGTATCTGTCGCAAGATGATTTGGAAGTTCA 833
QY      1003 GATC 1006
Db      834 CTC 837
```

RESULT 15

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US-10-689-742-165
; Sequence 165, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallee, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 165
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-689-742-165
```

Query Match 2.5%; Score 50; DB 6; Length 2487;

Best Local Similarity 56.8%; Pred. No. 0.063;

Matches 92; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY      1839 AAAAAATGATCTGAGCTTCTCTAGTTGTAAGAAAAAGACATCTTGATGAATA 1898
Db      2267 AATTTTGTTCACGATGATGTCATGTTTAAATGGCGATTAAATACTCTGCTGTATA 2326
QY      1899 TAGTACGTTGCGGAGAAATTGCCATGCTAAAGACTGAGCTAGACACAATGAAACATCA 1958
Db      2327 TAGTAGTTTGTAGTAAATATTGCAATAAAAAATCTGCCCGAATTAATAAAAAAAA 2386
QY      1959 GAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2000
Db      2387 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2428
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Search completed: December 18, 2005, 07:36:38
Job time : 246.564 secs

Query Match	Score	DB	Length
55.2%;	1105;	4;	6098;
Best Local Similarity	88.2%;	Pred. No. 3.4e-255;	

Matches 1243; Conservative 0; Mismatches 95; Indels 71; Gaps 1;

```

OY 1 ATGGTGTTGAGGTGATTCATGCGGGTGCCTTCTGTGAAGAGCATTTGGTCTC 60
    |||||
Db 441 ATGGTACATGAGTTTGTTCATATGCGGCTGCTCTGTGTGAAGAGCATTCGATCTC 500
OY 61 AGGAGCAAGATGGGCAAGTGTGTCCGTTGTCTCCCTGTGTGAGGAGAGCGGCAAG 120
    |||||
Db 501 AGGAGCAAGATGGGCAAGTGTGTTCACACCGCTCCCTGTGTGAGGAGAGCGGCAAG 560
OY 121 AGCAAGTGTGGGCTTCTGTGAAGCAAGACATCTGTGATGAAGACATCAGAGCAAG 180
    |||||
Db 561 AGCAAGTGTGGGCTTCTGTGAAGCAAGACATCTGTGATGAAGATGTCTCAGAGCAAG 620
OY 181 ATGGCAAGTGTGGGCTGCTCTCCCTGTGTGAGGAGGAGTGTGCAAGAGCAAGTGT 240
    |||||
Db 621 ATGGCAAGTGTGGGCTGCTCTCCCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 680
OY 241 GAGGCTTCTGTGAAGCAAGCAAGCTGTGTATGAAGACATCAGAGCAAGATGGGCAAG 300
    |||||
Db 681 GGCATCTTGTGAAGCAAGCAAGCTCTTATGAAGAGCTCAAGAGCAAGATGGGCAAG 740
OY 301 TGGTGTGCTGCACTGTCTCCCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
    |||||
Db 741 TGGTGTGCTGCACTGTCTCCCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800
OY 361 GGAGACTAGATGATGAGTGTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTG 420
    |||||
Db 801 GGAGACTAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860
OY 421 GACCAAGCTTCAAGAGCTGTGTGTGGGAGTAAATGCCAGAAAGAGATCTCATCTGTGAG 480
    |||||
Db 861 GACCAAGCTTCAAGAGCTGTGTGTGGGAGTAAATGCCAGAAAGAGATCTCATCTGTGAG 920
OY 481 CTCAGAGGACATGAGCTGTGAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
    |||||
Db 921 CTCAGAGGACATGAGCTGTGAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 980
OY 541 TCTGCAATGGGAAATTCAGAGTGTGAAGTCTCTGTGTGAGGAGGAGGAGGAGGAGGAGT 600
    |||||
Db 981 TCTGCAATGGGAAATTCAGAGTGTGAAGTCTCTGTGTGAGGAGGAGGAGGAGGAGGAGT 1040
OY 601 GTCTCTTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
    |||||
Db 1041 GTCTCTTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
OY 661 TGTGCTTATGTGTGTGTGAAGCTGTGACATGACCAATTTTCAAGATGATGTGAAGT 720
    |||||
Db 1101 TGTGCTTATGTGTGTGTGAAGCTGTGACATGACCAATTTTCAAGATGATGTGAAGT 1160
OY 721 ACCACTCTGCACTAGCTATCTTATATGAAGATTAATGAGGCAAGAGCATGCTCTTA 780
    |||||
Db 1161 ACCACTCTGCACTAGCTATCTTATATGAAGATTAATGAGGCAAGAGCATGCTCTTA 1220
OY 781 TATGTGCTGATATTCGAATCAAAAAAAGAGATGAGGCTCAACCATGTTACTTGTGTGA 840
    |||||
Db 1221 TATGTGCTGATATTCGAATCAAAAAAAGAGATGAGGCTCAACCATGTTACTTGTGTGA 1280
OY 841 CATGAGCAAAAAAGAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
    |||||
Db 1281 CATGAGCAAAAAAGAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 1340
OY 901 CTGAGATGATATGAAGAGGAGTGTCTCATATCTTGTGTATGTTGTGTGATCAGCAATTA 960
    |||||
Db 1341 CTGAGATGATATGAAGAGGAGTGTCTCATATCTTGTGTATGTTGTGTGATCAGCAATTA 1400
OY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGTGACAGAG 1020
    |||||
Db 1401 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGTGACAGAG 1460
OY 1021 GCCAGAGATATGCTGTTCTTATGATCATCATGATTAATTTCCAGTTACTTTCTGACTAC 1080
    |||||
Db 1461 GCCAGAGATATGCTGTTCTTATGATCATCATGATTAATTTCCAGTTACTTTCTGACTAT 1520

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OY 1081 AAGAGAAAAAGATGTAAATCTTCTGAAAAAGCAATCCAGAACAGACTTAAAG 1140
    |||||
Db 1521 AAGAGAAAAAGATGTAAATCTTCTGAAAAAGCAATCC----- 1564
OY 1141 CTGACATCAGAGAAAGATCAGAAAGGTTCAAAAGCAGTGAATAATGCCAGCAGAGAA 1200
    |||||
Db 1565 -----AGAAA 1569
OY 1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
    |||||
Db 1570 ATGTCTCAAGAACAGAAATTAATGAAGCTGTGATGAGAGGTTGAAGAAATTAAG 1629
OY 1261 AAGCATGAAAGTAAATATGTGGGATTAATCTAGAAAACTGACATATGATGTGACTGTGAC 1320
    |||||
Db 1630 AAGCATGAAAGTAAATCTGTGTGGATTAATCCAGAAAACTGACATATGATGTGACTGTGAC 1689
OY 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGAGCAGAACCTGAAATATGACAAATTT 1380
    |||||
Db 1690 AATGTGATTAATGATTAATTTCTCAAGAAAGAGCAGAACCTGAAATATGACAAATTT 1749
OY 1381 CCTGACAAAGAAAGTGAAGATATCACAG 1409
    |||||
Db 1750 CCTGACAAAGAAAGTGAAGATATCACAG 1778

```

RESULT 2
 BM763453
 LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5', mRNA sequence.
 DEFINITION
 ACCESSION BM763453
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
 1 (bases 1 to 633)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 High quality sequence stop: 633.
 Location/Qualifiers
 1..633
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /issue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_lib="S13KMS5"
 /note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tobacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E.

QY 930 ACTTGTGTATGTTGTGATCAGCAAGTATAGTCAGCTTCTACTTGAGCAAAATATATGA 989
DB 421 ACTGCTGTATGTTGTGATCAGCAAGTATAGTCAGCTTCTACTTGAGCAAAATATATGA 480
QY 990 TGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATAGTCTGTTTCTAGTCATCA 1049
DB 481 TGTATCTTCTCAAG-----ATCTGAAAAGACGGCCAGAGATAGTCTGTTTCTAGTCATCA 536
QY 1050 TCAATGTAATTTGGCAGTACTTCTCTGATCACTAAGAAAAGAAAGAACTCTAAAATCTCTTC 1109
DB 537 TCAATGTAATTTGGCAGTACTTCTCTGATCACTAAGAAAAGAAAGAAAGATGTTAAAATCTCTTC 596
QY 1110 TGAACAACGCAATCCAGAACCAAGC 1134
DB 597 TGAACAACGCAATCCAGAACCAAGC 621

RESULT 4
BU930826 729 bp mRNA linear EST 18-OCT-2002
LOCUS AGENCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
DEFINITION 5' mRNA sequence.
ACCESSION BU930826
VERSION BU930826.1 GI:24119645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 729)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapdb-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM2943 row: 0 column: 04
High quality sequence stop: 555.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6668956"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDMN-LIB (Clontech);
Site 1: SfiI (ggcgccgcgcgcgc); Site 2: SfiI
(ggccatcattggcc); 5' and 3' adaptor were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN
Query Match 25.4%; Score 508; DB 5; Length 729;
Best Local Similarity 94.8%; Pred. No. 2.6e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
QY 579 GGCACAGCATGTCTCACTTATGTCTTGACAAACAAAGAGACAGCTCTGATAAG-- 636
DB 3 GGCACAGCATGTCTCACTTATGTCTTGACAAACAAAGAGAGACAGCTCTGATAAGGT 62

QY 637 -----GCCGTACAAAGCCAGGAAGATGTCGCTT 668
DB 63 ATGCAATGCCACACTATATACAGATGAGGCCCTTACAAATGCCAGGAAGATGTCGCTT 122
QY 669 AATGTTGCTGAAACATGAGCATGATCAATCAATATTCAGATGATATGAAATACACATCT 728
DB 123 AATGTTGCTGAAACATGAGCATGATCAATCAATATTCAGATGATATGAAATACACATCT 182
QY 729 GCACATACGCTATCTATATGATGATTAATTAATGCAAGACATGCTCTTATATGTCG 788
DB 183 GCACATACGCTATCTATATGATGATTAATTAATGCAAGACATGCTCTTATATGTCG 242
QY 789 TGAATTCGAATCAAAAAACAAGCATGCGCTCACACATGCTACTTGGTGATCAGAGGA 848
DB 243 TGAATTCGAATCAAAAAACAAGCATGCGCTCACACATGCTACTTGGTGATCAGAGGA 302
QY 849 AAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTAATGCACTGATAG 908
DB 303 AAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGCAATTTAATGCACTGATAG 362
QY 909 ATATGAAAGACTGCTCTCATATCTTGTATATGTTGTGATCAGCAAGTATATGTCAGCTT 968
DB 363 ATATGAAAGACTGCTCTCATATCTTGTATATGTTGTGATCAGCAAGTATATGTCAGCTT 422
QY 969 TCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACAGCGCAGAGA 1028
DB 423 TCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACAGCGCAGAGA 482
QY 1029 GTATGCTGTTTGTAGTCATCATCATGATATTTGCCAGTTACTTCTGACTCAAGAAAA 1088
DB 483 GTATGCTGTTTGTAGTCATCATCATGATATTTGCCAGTTACTTCTGACTCAAGAAAA 542
QY 1089 ACAGATGCTTAAATCTCTTCTGAAAAACGCAATCCG 1126
DB 543 ACAGATGCTTAAATCTCTTCTGAAAAACGCAATCCG 580

RESULT 5
AL703938 544 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP68681728.r1 686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKFP68681728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 544)
REFERENCE Olsenweider,B., Obermaier,B., Mewes,W., Mewes,H.W., Weill,B. and
Wiemann,S.
EST (Olsenweider,B., Obermaier,B., Mewes,H.W., Weill,B. and
Wiemann,S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neubherg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German genome Project. No 81 sequence
available.
This clone (DKFP68681728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..544
/organism="Homo sapiens"
/mol_type="mRNA"


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/db_xref="taxon:9606"
/clone="DKFZp686E1728"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="686 (synonym: hicc3)"
/notes="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIB;
cDNA-collection"

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ORIGIN

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Query Match      23.9%; Score 478.6; DB 1; Length 544;
Best Local Similarity 93.6%; Pred. No. 3e-104;
Matches 510; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

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QY 649 CAGGAAGATGATGTCGCTTAATGTCGGAAACATGCGATCCAAATATTCAGAT 708
DB 1 CAGGAAGATGATGTCGCTTAATGTCGGAAACATGCGCGCATGAAATATTCAGAT 60
QY 709 GAGTATGAAATACCACTGCACTACGCTATCTATATGAGATTAATTAATGCGCAA 768
DB 61 GAGTATGAAATACCGCTCTACCTA-TCTATCTACATGAGATTAATTAATGCGCAA 119
QY 769 GCACTGCTCTTATATGTCGCTGATTCGAATCAAAAAACAAGCATGCTCACACCACTG 828
DB 120 GCACTGCTCTTATATGTCGCTGATTCGAATCAAAAAACAAGTCGCTCACACCACTT 179
QY 829 TTAATGTCGTCATAGCAAAAAACAAGTCGCTGAAATTTTATATCAAAAAAGCG 888
DB 180 TTGCTTGGCGTCATGAACAAAAACAAGTCGCTGAAATTTTATCAAAAAAGCT 239
QY 889 AATTTAATGCACTGATGATATGAGAAAGCACTGCTCTCACTTCTGTATGTTGGA 948
DB 240 AATTTAATGCACTGATGATATGAGAAAGCACTGCTCTCTGTATGTTGGA 299
QY 949 TCAGCAAGTATAGTCAGCTTCTTACTTGAACAAATATGATGATCTTCTCAAGATCTA 1008
DB 300 TCAGCAAGTATAGTCAGCTTCTTACTTGAACAAATATGATGATCTTCTCAAGATCTA 359
QY 1009 TCTGACACAGCGCCAGAGATGATGCTGTTCTAGTCATCATCATTAATTTGCCAGTTA 1068
DB 360 TCTGACACAGCGCCAGAGATGATGCTGTTCTAGTCATCATCATTAATTTGTAATTA 419
QY 1069 CTTTCTGATCAAAAGAAAAGAGATGCTAAATATCTTCTGAAAAGCAATCCAGAA 1128
DB 420 CTTTCTGATCAAAAGAAAAGAGATGCTAAATATCTTCTGAAAAGCAATCCAGAA 479
QY 1129 CAAGACTTAAGCTGACATCAGAGAAAGTCACAAAGGTTCAAAAGCAGTAAATATAC 1188
DB 480 CAAGACTTAAGCTGACATCAGAGAAAGTCACAAAGGCTTAAGTCACTGTAATATAC 539
QY 1189 CAGCC 1193
DB 540 CAGCC 544

```

RESULT 6

```

LOCUS BF676987 865 bp mRNA linear EST 21-DEC-2000
DEFINITION 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
mRNA sequence.
ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 865)
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

```

FEATURES

source

Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM1067 row: m column: 03
 High quality sequence stop: 642.
 Location/Qualifiers

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1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH MGC 83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccggcgcc); Site_2: SfiI
(ggcattcagcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCGCAGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
```

ORIGIN

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Query Match      23.6%; Score 472.8; DB 2; Length 865;
Best Local Similarity 97.4%; Pred. No. 8.3e-103;
Matches 491; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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QY 635 AGCGGTCAATATCCAGAAAGATGATGTCGCTTAATGTCGAAACATGCGCATGATC 694
DB 69 AGCGGTCAATATCCAGAAAGATGATGTCGCTTAATGTCGAAACATGCGCATGATC 128
QY 695 CAAATATTCAGATGATGATGAAATACCACTTCTGCACTAGCTATCTTAATGAAGATA 754
DB 129 CAAATATTCAGATGATGATGAAATACCACTTCTGCACTAGCTATCTTAATGAAGATA 188
QY 755 AATTAATGCGCCAAAGCATGCTCTTATATGTCGATATGCAATCAAAAAACAAGATG 814
DB 189 AATTAATGCGCCAAAGCATGCTCTTATATGTCGATATGCAATCAAAAAACAAGATG 248
QY 815 GCCTCACACCTGTTACTGTTGATGATGACCAAAAAACAAGTCGGAATTTTAA 874
DB 249 GCCTCACACCTGTTACTGTTGATGATGACCAAAAAACAAGTCGGAATTTTAA 308
QY 875 TCAGAAAAAAGCGAATTTAAATGCACTGATATGAGAAAGCATGCTCTCATACTTG 934
DB 309 TCAGAAAAAAGCGAATTTAAATGCGCTGATATGAGAAAGCATGCTCTCATACTTG 368
QY 935 CTGTATGTTGTCATCAGCAAGTATAGTCAGCTTCTTACTTGAACAAATATGATGAT 994
DB 489 TAA-TTGCAGTTACTTTCTGACTCAAAAGAAAAACAAGTCGTAATAAATCTCTTGAAA 547
QY 1115 ACAGCAATCCAGAAACACTTAA 1138
DB 548 ACAGCAATCCAGAAATGCTCAA 571

```

RESULT 7

BX492731

LOCUS BX492731 505 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZP781C0523 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
 DKFZP781C0523 5', mRNA sequence.
 ACCESSION BX492731
 VERSION BX492731.1 GI:32004516
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 505)
 Bloeker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Oanger, A.,
 Podo, G., Han, M., and Wiemann, S.
 EST (Bioecker, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)
 Unpublished (2003)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@kfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No s1 sequence available.
 This clone (DKFZP781C0523) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
 Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZP781C0523"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="781 (synonym: hlcc4)"
 /note="Vector: pSport1_sfl; Site_1: sflIA; Site_2: sflIB;
 cDNA-collection"

ORIGIN
 Query Match 18.8%; Score 376.4; DB 5; Length 505;
 Best Local Similarity 92.7%; Pred. No. 1.4e-79;
 Matches 395; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 325 TCGAGGGGAGGCGGCAAGCAAGTGGCGCTTGGGAGACTACATACAGTGCCTTC 384
 DB 80 TGGCTGGGAGGCGGCAAGCAAGTGGCGCTTGGGAGACTACATACAGCGGCTTC 139
 QY 385 ATGAGCCAGGATACCAAGTCCGTGGAGAAATCTGGAGCAAGTCCAGAGCTGCTGG 444
 DB 140 ATGAGCCAGGATACCAAGTCCGTGGAGAAATCTGGAGCAAGTCCAGAGCTGCTGG 199
 QY 445 TGGGTAAGTCCCGGAGAAAGATCTCATGTCATGCTGAGGAGACTGACGTTGAACAAG 504
 DB 200 TGGGTAAGTCCCGGAGAAAGATCTCATGTCATGCTGAGGAGACTGACGTTGAACAAG 259
 QY 505 AAGGACAGCAAAAGAGAGCTGCTCACTTGGCTTGGCAATGGGAATTCAGAAATTA 564
 DB 260 AAGGACAGCAAAAGAGAGCTGCTCACTTGGCTTGGCAATGGGAATTCAGAAATTA 319
 QY 565 GTTAAATCTGCTGGAGAGAGTGTCACTTAATGTCCTTGAACAACAAAAGAGAA 624
 DB 320 GTTAAATCTGCTGGAGAGAGTGTCACTTAATGTCCTTGAACAACAAAAGAGAA 379
 QY 625 GCTGTGATAAAGCCGTGACATGTCAGAGAAATGTAATGTCGTTAATGTTGCTGAACAT 684
 DB 380 GCTGTGATAAAGCCGTGACATGTCAGAGAAATGTAATGTCGTTAATGTTGCTGAACAT 439
 QY 685 GGCATGATCAAAATTTCCAGATGAGTATGGAATATCACTTGCATACGCTATCTAT 744
 DB 440 GGCATGATGAAATTTCCAGATGAGTATGGAATATCACTTGCATACGCTATCTATC 499

QY BX437445 745 AATGAA 750
 DB 500 AATGAA 505

RESULT 8
 LOCUS BX437445
 DEFINITION BX437445 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006YL04
 5-PRIME, mRNA sequence.
 ACCESSION BX437445
 VERSION BX437445.2 GI:46959477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 910)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30771569.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5500.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0CAP006Df02QPlc=5500.r.
 Location/Qualifiers
 1..910
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0CAP006YL04"
 /issue_type="THYMUS"
 /clone_1ib="Homo sapiens THYMUS"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and EcoRV sites of the
 pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
 Query Match 17.9%; Score 357.2; DB 5; Length 910;
 Best Local Similarity 69.6%; Pred. No. 6.7e-75;
 Matches 501; Conservative 1; Mismatches 209; Indels 9; Gaps 1;

QY 223 AGTGGAGAGCAAGTGGGCGCTTCTGGAGACCAAGAGCTGCTGTAAGACATCC 282
 DB 100 AGAGCCGAGAGCAATGAGTGTCTGTAAGCCCGATGCTGGGCCATGTAAGATTT 159
 QY 283 AGGAACAAGATGGGAGAGTGTGCTGCCACTTCCCTGCTGAGAGGGGAGCGGCAAG 342
 DB 160 TTTAGTAAGAAAGGAGAGTGCCTTGGGCTCTTGGCGGCGCGGAGAGAGCAGC---- 216
 QY 343 AGCAAGTGGGCGCTTGGGAGAGTACATGACAGTGCCTTACATGAGGCCAGTACAC 402
 DB 217 -----GGGGAGAGGGGGGCGAGCGGGGAGGGGCGCTTACTGACGCCCGCTACAC 270
 QY 403 GTCCGTGAGAGAGATCTGGAGCAAGTCCACAGAGTGCCTGATGGGGTAAAGTCCCA 462
 DB 271 GTCCGAGACCGAGATCTCGGCAAGATCCACAAAGCTGCCAGGCGGGGTATGTGGTAA 330
 QY 463 AAGATTCATGCTGATGCTGACGAGCACTGACGTGAACAAGAGCAAGCAAGAGAG 522

Db 331 GTGACAGACATCTTTTGTCTCAGAGAAATGGCTTGACGATAGACAAAGTGAACAGG 390
 QY 523 ACTGCTTTCATCTGCGCTCTGCTCCATATGGAAATTCAGAAATGTAATACTCTGCTGAC 582
 Db 391 AGGGCTTTCATATTTGGCCCTGTGCGCAATGGTCAATCCGAAAGTAGTAATCTCTCCGTGGAC 450
 QY 583 AACAGATGCACTTAATGCTCTGCAACAAANAAGAGACGCTGTGAATAAGGCGTA 642
 Db 451 AGAAAATGCACTCAATGCTGTGACAAAGAAACAGACGCTGTGAATAAGGCGTA 510
 QY 643 CAATGCAAGAAAGATGAATGTGCGTAATGTTGCTGGAACATGCACTGATCCAAATATT 702
 Db 511 CAATGCAAGAAAGATGAATGTGCACTATTTCTGTAACATGCTGATCCAAATCTT 570
 QY 703 CCAATGATATGGAATATCCACTCTGCACTACGCTATCTATATGAATTAATTAATG 762
 Db 571 GGGGATGTCATGCGCAACACTGCTCTTCACTATGCTGTATATAGACATATACATG 630
 QY 763 GCCAAGCACTGCTTATATGCTGCTGATGATGATGATGATGATGATGATGATGATG 822
 Db 631 GCAACAAAGCTGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 690
 QY 823 CCAGTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
 Db 691 CCAGTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 750
 QY 883 AAAGCAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 942
 Db 751 AAAGCAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 810

RESULT 9

AUI20666 843 bp mRNA linear EST 01-AUG-2002
 LOCUS AUI20666 HEMBB1 Homo sapiens cDNA clone HEMBB1001175 5', mRNA
 DEFINITION sequence.

ACCESSION AUI20666
 VERSION AUI20666
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 843)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.

TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp

REFERENCE HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source Location/Qualifiers

1..843
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBB1001175"
 /rissue_type="whole embryo, mainly body"
 /dev_stage="embryo, 10 weeks"
 /clone_lib="HEMBB1"
 /note="Vector: pME18SFJ3"

ORIGIN

Query Match 17.4%; Score 348.8; DB 1; Length 843;
 Best Local Similarity 69.2%; Pred. No. 7, 1e-73;
 Matches 492; Conservative 0; Mismatches 210; Indels 9; Gaps 1;

QY 223 AGTGCAGAGAGCAAGTGGGCGCTTCTGAGACCAAGCACTGCTATGAAGACATC 282
 Db 119 AAGCGAGAGAGACATAGAGTGTCTCTGAACCCCGTCTGCTGCGCCATGAAGAGATT 178
 QY 283 AGGAACAGATGGGCAAGTGTGCTGCCACTCTTCCCTGCTGCAAGGAGAGCGCAAG 342
 Db 179 TTATAGTGAAGAGGCGAGAGTGGCTTGGGCTCTTCTGCGCGGCGGAGAGCAGC--- 235
 QY 343 AGCAAGTGGGCGCTTGGGAGACTACATGACATGACATGACATGACATGACATGACAT 402
 Db 236 -----GCGGAGGCGGCGGCGAGCGGAGGCGGCTTCTGCGAGCTCGCTACAC 289
 QY 403 GTCCGTGAGAGAGATCTGAGCAAGCTCCACAGAGCTCTGCTGGGGTAAAGTCCCA 462
 Db 290 GTCCGAGACCGAGATCTCGGCAAGATCCACAAAGCTCCAGCGCGGTATGTGGGAAA 349
 QY 463 AAGATCTCATGCTCATGCTCAGGACACTGACGTGAACAGAGCAAGCAAGAAAGG 522
 Db 350 GTGACAGAGATCTTTTGTCTCAGAAAGATGCTTGAACGATAGAGCAAGATGAACAG 409
 QY 523 ACTGCTTTCATCTGCGCTCTGCGCAATGGAAATTCAGAAATGTAATACTCTGCTGAC 582
 Db 410 AGGCTCTTCACTTTGGCTGTGCAATGCTATCCAGAAATGTAACTCTCTGCTGAC 469
 QY 583 AGACATGCACTTAATGCTCTTGAACAACAANAAGAGACGCTGTAAAGGCGTA 642
 Db 470 AGAAAATGCGAGCTCAATGTCTGTGACAAAGAAACAGACAGCTGTGTAAGGCTGTA 529
 QY 643 CAATGCCAGAAAGATGAATGCTGTTAATGTTGCTGGAACATGCACTGATCCAAATATT 702
 Db 530 CAATGCCAGAAAGATGAATGCTCAATATTCTGTAGAACATGCTGATCCAAATCTT 589
 QY 703 CCAGATGATATGAAATATCCACTCTGCACTACGCTATATTAATGAATTAATTAAG 762
 Db 590 GCGGATGTCATGAGGCAACACTGCTCTTCACTATGCTGTATTAAGAGACATATCAGTA 649
 QY 763 GCCAAGCACTGCTCTTATATGCTGCTGATATGATGATGATGATGATGATGATGATG 822
 Db 650 GCAACAAAGCTCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATG 709
 QY 823 CCAGTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 882
 Db 710 CCAGTCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 769
 QY 883 AAAGCAATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 933
 Db 770 AAAGCAATTTAATGCTTANATTAATTAATTAATTAATTAATTAATTAATTAATTA 820

RESULT 10

LOCUS CR860726 2677 bp mRNA linear HTC 12-NOV-2004
 DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp459P0427 (from clone DKFZp459P0427).
 ACCESSION CR860726
 VERSION CR860726.1 GI:55732274
 KEYWORDS HTC.

SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pongo.
 1 (bases 1 to 2677)

AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Well,B., Amid,C.,
 Obanger,A., Fobo,G., Han,M. and Wiemann,S.
 TITLE The German cDNA Consortium
 JOURNAL Direct Submission
 Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by GSF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp459F0427) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: <http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459F0427> Further information about the clone and the sequencing project is available at <http://mipe.gsf.de/projects/cdna/>.

FEATURES

source

1..2677

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp459F0427"

/issue_type="cortex"

/clone_id="459 (synonym: pcor1). Vector pSport1_Sfi; host

DH10B; sites SfiI + SfiIb"

/dev_stage="adult"

/note="hypothetical protein (Homo sapiens), differentially

spliced"

gene

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/gene="DKFZp459F0427"

/gene="DKFZp459F0427"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAH92841.1"

/db_xref="GI:55732275"

/translation="MGVRSFLAACRRMATWRKNRDKDPSNGSYRQKDLGMIHK

AATADVNKLLESILGLNDVDRDKRRTALHCAHGRPGVADLVARKRLMTD

SENRTALKAQCOEAVNCASILEHGGDPAVDGNTALHYATINENISMGKLLAY

GADIRASGCHTSLILAVNRKEEMVAFLKKKPDTRIDRPGTALILAAKNSSTS

VYQILQHNIDVFCODISGWTBMDYAAASKFOATLKRDIRAKKA"

ORIGIN

Query Match

Best Local Similarity

Matches

17.4%; Score 347.2; DB 4; Length 2677;

69.4%; Pred. No. 2,3e-72;

0; Mismatches 208; Indels 0; Gaps 0;

472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

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472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

472; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

858 AGTCGTGAATTTTAACTCAAGAAAAAGCAATTTAAATGACGTAGATATGGAAG 917
 730 AATGTGCACTTTTGTGGAAGAAAAACAGATTTAACTGCAATAGATATTTGGAG 789
 918 GACTGCTCTCACTTGTGTAATGTTGGATGACCAAGATATGTCAGCTTCTACTGA 977
 790 AACAGCCCTCACTTGTGCTGCTGTAAGGATCAACAGTATGATCTACAGCTTCTCA 849
 978 GCAAAATTTGATATGATCTTCTCAAGATCTATCTGACAGAGCCAGAGATAGCTGT 1037
 850 GCACATATGACGCTTTTGGCAAGATATATCTGATGACTGACAGAAAGTACGCTGC 909
 1038 TTCTAGTCATCATCATGTAA 1057
 910 TGCTTCTAAGTTTCAAGCA 929

RESULT 11

DQ053800

LOCUS

DEFINITION

Homo sapiens KIAA1074 gene, VIRTUAL TRANSCRIPT, partial sequence.

ACCESSION

DQ053800

VERSION

DQ053800.1 GI:66899747

KEYWORDS

SSS.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo.

REFERENCE

1 (bases 1 to 5130)

Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,

White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(ex) PLOS Biol. 3 (6), E170 (2005)

JOURNAL

PUBMED

15869325

2 (bases 1 to 5130)

Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,

White,T.J., Shtinsky,J.J., Adams,M.D. and Cargill,M.

Direct Substitution

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering

them based on alignment. Translation starts at the beginning of

alignment.

FEATURES

source

1..5130

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="10"

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/gene="KIAA1074"

/locus_tag="HCL4399"

ORIGIN

Query Match

Best Local Similarity

Matches

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71.4%; Pred. No. 5,8e-72;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

Db 122 ACCTCCGAGACCGAGATCTCGCAAGATCCACAAAGCTGGCAGCGGGTAATGATG9CGCA 181

Qy 461 GAAGAGATCTCATCCGATCTCTAGGAGACCTCACTGTAACAAAGAGACAAAGAAAGA 520

Db 182 AAGTGAAGAGATCTCTTTGGCTCAGAGAAAGATGGCTTGAACGATAGACAAAGATGACCA 241

Qy 521 GGACTGCTTACATCTGGGCTCTGGCAATGGAAATTCAGAAAGTAAATCTCTGCTGG 580

Db 242 GAGCGGCTCTACATCTTTGGCTCTGGCAATGGTATCCAGAAAGTAAATCTCTGCTGG 301

Qy 581 ACAGAGATGTCATCTTAATGTCCTTGAACAAACAAAGAGACGCTGATTAAGGCGC 640

Db 302 ACAGAAATGCGAGCTCAATGTCGTGAGCAACAAAGAGACGCTGATTAAGGCGC 361

Qy 641 TACATGCGCAGAAAGATGATGTCCTTAATGTTGCTGGAACATGGCATGATCCAAAT 700

Db 362 TACAAATGCCAGAGAAAGATGTCATTAATCTGCTAGAACATGGTGTGATCCAAATC 421

Qy 701 TTCCAGATGATGTAAGAAATACCACTGTCAGCTACGCTAATCTTAATGAAGATTAATTA 760

Db 422 TTGCGGATGTCATGCGACACATGCTCTTCACTATGCTGTATTAATGAGACATATCAG 481

Qy 761 TGCGCAAGACATGCTCTTAATGTCGTGATGTCATGATCAATCAAAACAAAGCATGCTCA 820

Db 482 TAGCAACAAAGCTGCTTTTGTATGATGCAAAATTTGAGCAAAACAAAGATGACCTCA 541

Qy 821 CACCATGTTACTTGTGTATCATGACGCAAAACAGCAAGTGTGAATTTTATCAAGA 880

Db 542 CACCATTTTACTTGTGTATGATGAGCAAAACAGCAAGTGTGAATTTTATCAAGA 601

Qy 881 AAAAGCGAATTTAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 917

Db 602 AAAAGCGAATTTAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATG 638

RESULT 12

CR994478 909 bp mRNA linear EST 28-JUN-2005

LOCUS CR994478 RZPD no. 9016 Homo sapiens cDNA clone RZPD9016M101 5',

DEFINITION mRNA sequence.

ACCESSION CR994478

VERSION CR994478.1 GI:68288363

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 909)

AUTHORS Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D. and Korn, B.

TITLE Human T-Lymphocytes library

JOURNAL Unpublished (2005)

COMMENT Contact: Inge Airlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

RZPD: RZPD9016M101.

RZPDLIB: (Human T-Lymphocytes) RZPD LIB No. 9016

http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016 Contact:

Inge Airlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

FEATURES

source

1..909

/organism="Homo sapiens"

This clone is available from RZPD:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD9016M101

Contact RZPD (product-support@rzpd.de) for further information.

Primer name: qe3_4, primer sequence: CGGATTAACAATTCACACAG.

Location/Qualifiers

ORIGIN

Query Match 17.2%; Score 343.4; DB 7; Length 909;

Best Local Similarity 69.3%; Pred. No. 1.4e-71;

Matches 500; Conservative 0; Mismatches 211; Indels 10; Gaps 2;

Qy 223 AGTGGCAAGACGACGTCGCGCTCTGAGACCAAGACCTGCTGTAAGACACTC 282

Db 92 AAGCCGAGAGAGACATGAGTGTCTCTGAAGCCGCTGCTGGCCATGAAGAGATT 151

Qy 283 AGGAACAAAGTGGGCAAGTGTGTGTCGACCTGCTCCCTGCTGACGGGGAGCGGCAAG 342

Db 152 TTTAGTAAGAAAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208

Qy 343 AGCAAGTGTGGGCTGTTGGGAGACATGACATGACATGACATGACATGACATGACATGAC 402

Db 209 -----GCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 262

Qy 403 GTCCGTGAGAGATCTGGAACAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCGACAG 462

Db 263 GTCCGAGACCGAGATCTCGGCAAGATCCCAAGCTGCCAGCGGGTAAATGTGGGAGAA 322

Qy 463 AAGATCTCATGCTCATGCTCAAGGACACTGACGTGACAGAAAGAGACAAAGAGAGAG 522

Db 323 GTGACAGAGATCTTTGCTCAAGAAAGATGCTGGAACGATGAGACAAAGATGAGACAG 382

Qy 523 ACTGCTCATGCTGCGCTCTGCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAC 582

Db 383 AGGCTCTACATTTGGCTGTGCAATGTGTATCCAGAAAGTAAATCTCTGCTGAGAC 442

Qy 583 AGACGATGCACTTAATGTCCTTGAACAAAGAGAGACAGCTCTGATTAAGGCGCTA 642

Db 443 AGAAATGCCAGCTCAATGTCTGTGACAAAGAAACAGACAGCTCTGATTAAGGCGCTA 502

Qy 643 CAATGCGAAGAGATGATGTCGTTAATGTTGCTGGAACATGACCTGATCCAAATATT 702

Db 503 CAATGCGAAGAGAGATGATGTCGTTAATGTTGCTGGAACATGACCTGATCCAAATATT 562

Qy 703 CCAATGATGATGAAATTCACCTGCACTACGCTATCTTAATTAATGAATTAATTAAG 762

Db 563 GCGGATGTCATGCAACACCTCTCTTCACTATGCTGTATTAATTAATGAATTAATTAAG 622

Qy 763 GCCAAAGACCTCTCTTAATGATGTCGATATGATGATGATGATGATGATGATGATGATGAT 821

Db 623 GCAACAAAGCTCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 682

Qy 822 ACCACTGTTACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 881

Db 683 ACCACTTACTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742

Qy 882 AAAAGCGAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 941

Db 743 AAAAGCGAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802

Qy 942 T 942

Db 803 T 803

FEATURES
source

Location/Qualifiers
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/clone="IMAGE:30389199"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 16.2%; Score 324; DB 6; Length 874;
Best Local Similarity 91.7%; Pred. No. 6.9e-67;

Matches 354; Conservative 0; Mismatches 30; Indels 2; Gaps 1;

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QY 1614 AGAAGACCTGACTTAATGTCCTGCTGCAATGATGATGATTAATTCCTCCAG 1673
DB 1 AGAAGACCTGACTTAATGTCCTGCTGCAATGATGATGATTAATTCCTCCAG 60
QY 1674 GAAAGACGAGACCTGAAAGCCAGCAATTCCTGACATGAAATGAAAGATGACAG 1733
DB 61 GAAAGACGAGACCTGAAAGCCAGCAATTCCTGACATGAAATGAAAGATGACAG 120
QY 1734 TGAAGACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1793
DB 121 TGAAGACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 1794 CGATGAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1853
DB 181 AGATGAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
QY 1854 GCTTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1913
DB 239 GCTTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
QY 1914 AGAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973
DB 299 AGAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 358
QY 1974 AAAAAAAAAAAAAAAAAAAAAAAAAA 1999
DB 359 AAAAAAAAAAAAAAAAAAAAAAAAAA 384
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RESULT 15.

BM469654 1020 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT 6444673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
DEFINITION 5', mRNA sequence.

ACCESSION BM469654
VERSION BM469654.1 GI:18518696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1020)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Place: LNL12351 row: m column: 06
High quality sequence stop: 680.
Location/Qualifiers
1. 1020
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5585453"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 16.2%; Score 323.2; DB 3; Length 1020;
Best Local Similarity 74.6%; Pred. No. 1.1e-66;

Matches 406; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

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QY 399 CCAGCTCCCTGAGAAAGATCTGACCAAGCTCCACAGAGCTGCTGGGTAAATCCC 458
DB 1 CCAGCTCCCAAGCCGAGATCTGGCAAGATCCACAAAGTGCAGGCGGTAAATGTCG 60
QY 459 CAGAAAGATCTCATGTCATGCTGATGAGGACACTGACGTAACAAGAACAGCAAGCA 518
DB 61 GAAAGTGCAGCAGATCTCTTCTGCTGAGAAAGATGCTTGAACGATGAGACAAAGTAA 120
QY 519 GAGAGCTGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
DB 121 CAGAGCGGCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 579 GAGAGCGATGCTCACTTAATGCTCTTGAACAACAAAGAGAGACGCTCTGTAAGGC 638
DB 181 GAGAGCGAAATCCAGCTCAATGCTGTGACAAAGCAAGACAGCTCTGATGAAAGC 240
QY 639 CGTACATGCTCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
DB 241 TGTACATGCTCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 699 TATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 758
DB 301 TCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 759 AATGCGCAAGACCTGCTTTATATGCTGCTGATATGATGATGATGATGATGATGAT 818
DB 361 ACTAGCAACAAAGCTGCTTTTATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 819 CACACCACTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
DB 421 CACACCACTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 879 GAAAAAGGGAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
DB 481 GAAAAAGGGAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 939 ATGT 942
DB 541 ATAT 544
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Search completed: December 19, 2005, 01:38:35
Job time : 8066.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:05:29 ; Search time 10314.1 Seconds
(without alignments)
11242.903 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atcgctgctgagctgctgctc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11752642

Minimum DB seq length: 10

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBank:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_ses:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	6	BD242273 Compounds
2	2040	100.0	2040	6	AR278480 Sequence
3	2040	100.0	2040	6	AR350944 Sequence
4	2040	100.0	2040	6	AR367176 Sequence
5	2040	100.0	2040	6	AR371072 Sequence
6	2040	100.0	2040	6	AR400212 Sequence
7	2040	100.0	2040	6	AR405479 Sequence
8	2040	100.0	2040	6	AR433320 Sequence
9	2040	100.0	2040	6	AR563859 Sequence
10	2040	100.0	2040	6	AR588845 Sequence
11	2040	100.0	2040	6	AR605665 Sequence
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13	2040	100.0	2040	6	AR642106 Sequence
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DEFINITION	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.				
ACCESSION	BD242273.1	GI:33052043			
KEYWORDS	JP 2002520054-A/360.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2040)				
AUTHORS	Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.				
TITLE	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use				
JOURNAL	Patent: JP 2002520054-A 360 09-JUL-2002;				
COMMENT	CORIXA CORP				
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JIANGCHUN XU, PI					
PI	JENNIFER LYNN MITCHAM				
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CC	and methods				
CC	for their use				
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ORIGIN

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LOCUS Sequence 375 from patent US 6512094.
DEFINITION AR278480
ACCESSION AR278480
VERSION AR278480.1 GI:29712726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Recter,M.W., Stolk,J.A., Day,C.H.,
Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skelly,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 375 28-JAN-2003;
Corixa Corporation; Seattle, WA
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RESULT 3	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM
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		PAT 17-AUG-2003				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1 (bases 1 to 2040)	Prudakis, T.N., Reed, S.G., Smith, J.M. and Misher, L.	Compositions and methods for the treatment and diagnosis of breast cancer	Patent: US 6586570-A 303 01-JUN-2003;	
			Corixa Corporation; Seattle, WA	
			Location/Qualifiers	

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Db	1141	CTGACATCAGAGGAAGTCACAAAAGGTTCAAAGGACAGTGAATTAACCGCCAGAGAAA	1200
OY	1201	ATGTCCTCAGAACCCAGAAATTAATTAAGATGTGTATAGAGAGTTTGAAGAAATATGAG	1260
Db	1201	ATGTCCTCAGAACCCAGAAATTAATTAAGATGTGTATAGAGAGTTTGAAGAAATATGAG	1260
OY	1261	AAGCATGAAGTAAATATATGTGGGATTCTAGAAAACTGACTAATGTGTGTACCTGTGGC	1320
Db	1261	AAGCATGAAGTAAATATATGTGGGATTCTAGAAAACTGACTAATGTGTGTACCTGTGGC	1320
OY	1321	AATGTGTATATGGAATTAAATCCCAAGGAAGAGCAAGAACCTGAAATAATAGCAATTT	1380
Db	1321	AATGTGTATATGGAATTAAATCCCAAGGAAGAGCAAGAACCTGAAATAATAGCAATTT	1380
OY	1381	CCTGACAAACGAATGGAAGATATCACGAATTTGGCAATTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAATGGAAGATATCACGAATTTGGCAATTAGTTTCTGACTACAAAGAA	1440
OY	1441	AAACGATGCCAAATAATCTTTCTGAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA	1500

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RESULT 4
LOCUS AR367176 2040 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 375 from patent US 6339505.
ACCESSION AR367176
VERSION AR367176.1 GI:34600151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yudin,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6339505-A 375 11-DEC-2001;
FEATURES
source location/Qualifiers
1..2040
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 5
 AR371072 2040 bp DNA linear PART 12-SBP-2003
 LOCUS AR371072 Sequence 375 from patent US 6395278.
 DEFINITION AR371072
 ACCESSION AR371072
 VERSION AR371072.1 GI:34607965
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 2040)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yugu,J.
 TITLE Prostate specific fusion protein compositions
 JOURNAL Patent: US 6395278-A 375 28-MAY-2002;
 Corixa Corporation; Seattle, WA

FEATURES
 source Location/Qualifiers
 1..2040
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 100.0%; Score 2040; DB 6; Length 2040;
 Best Local Similarity 100.0%; Pred.No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
AR400212 2040 bp DNA linear PAT 18-DEC-2003
LOCUS AR400212
DEFINITION Sequence 375 from patent US 6620922.
ACCESSION AR400212
VERSION AR400212.1 GI:40143377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kales M.D., Fanger G.R., Reiter M.W., Stolk J.A., Day C.H.,
Vedvyk T.S., Carter D., Li S.X., Wang A., Skelley Y.A.W.,
Hepler W.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 375 16-SEP-2003;
Corixa Corporation; Seattle, WA
FEATURES
source
Location/Qualifiers
1..2040
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCTGAGAGTATGATTCATATGCGGCTGCTCTTCTGTGAAGAAAGCAATTTGCTTC 60
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LOCUS AR405479
DEFINITION Sequence 375 from patent US 6630305.
ACCESSION AR405479
VERSION AR405479.1 GI:40154316
KEYWORDS
SOURCE
ORGANISM
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Unclassified.

REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y., Kalos M.D., Fanger G.R., Reiter M.W., Stolk J.A., Day C.H., Vedick T.S., Carter D., Li S.X., Wang A., Skelky Y.A.W., Hepler W.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 375 07-OCT-2003;
Corixa Corporation; Seattle, WA;
BOX;

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AR433320 2040 bp DNA linear part 18-DEC-2003
LOCUS AR433320
DEFINITION Sequence 303 from patent US 6656480.
ACCESSION AR433320
VERSION AR433320.1 GI:40196102
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2040)
Rettner M.W. and Dillon D.C.
TITLE
Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL
Patent: US 6656480-A 303 02-DEC-2003;
Corixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS AR563859
DEFINITION Sequence 375 from patent US 6759515.
ACCESSION AR563859
VERSION AR563859.1 GI:53978910
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Retter,M.W., Skolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,

Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6759515-A 375 06-JUL-2004;
Corixa Corporation; Seattle, WA
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RESULT 11
AR605665
LOCUS AR605665 2040 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 375 from patent US 6818751.
ACCESSION AR605665
VERSION AR605665.1 GI:56657329
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,T., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kados,M.D., Fanger,G.R., Reister,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeily,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6818751-A 375 16-NOV-2004;
Corixa Corporation; Seattle, WA
FEATURES
source 1. 2040
/organism="Unknown"
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ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
AR615064
LOCUS AR615064 2040 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 303 from patent US 6828431.
ACCESSION AR615064
VERSION AR615064.1 GI:56671468
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Frudek, T.N., Reed, S.G., Smith, J.M., Misher, L.E., Dillon, D.C.,
Retter, M.W., Wang, A., Skeiky, Y.A.W., and Harlocker, S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: US 6828431-A 303 07-DEC-2004;
Corixa Corporation; Seattle, WA
FEATURES
source
1. 2040
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

LOCUS AR642106 2040 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 303 from patent US 6861506.
ACCESSION AR642106
VERSION AR642106.1 GI:62778254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Fridakis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6861506-A 303 01-MAR-2005;
FEATURES
source Corixa Corporation; Seattle, WA
Location/Qualifiers
1..2040
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 RESULT 14
 AR657004
 LOCUS AR657004 2040 bp DNA linear PART 13-JUN-2005
 DEFINITION Sequence 375 from patent US 6894146.
 ACCESSION AR657004
 VERSION AR657004.1 GI:67590124
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H., Vedvik,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepner,W.T. and Henderson,R.A.
 TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
 JOURNAL Patent: US 6894146-A 375 17-MAY-2005;
 FEATURES
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 /organism="Unknown"
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 Query Match 100.0%; Score 2040; DB 6; Length 2040;
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 DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
 QY 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
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 QY 241 GCGGCTTCTGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
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 DB 361 GGAAGTACAGTACAGTGGCTTCAATGAGCCCAAGTACCAAGTCCGTGGAAGAACTTG 420
 QY 421 GACAACTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
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 QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGATGCTTACATCTGGCC 540
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 QY 361 GGAAGCTAGTGAAGAGGCTTCAATGAGCCAGGTAACAAGTCCGTTGGAAGATCTG 420
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Search completed: December 19, 2005, 15:33:38
 Job time : 10320.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: December 19, 2005, 01:50:48 ; Search time 1218.45 Seconds
(without alignment)
11158.458 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atcgctggtcgcaggtcgtatcc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9978348

Minimum DB seq length: 10

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
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9: geneseqn2003bs: *
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12: geneseqn2004as: *
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14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2040	100.0	2040	3 AAC81013	AAC81013 Human B11
2	2040	100.0	2040	4 AAH93716	Aah93716 Human pro
3	2040	100.0	2040	4 AAI67213	Aai67213 B305D iso
4	2040	100.0	2040	4 AAH63809	Aaah63809 Human pro
5	2040	100.0	2040	4 AAH02781	Aah02781 Prostate
6	2040	100.0	2040	4 AAH85030	Aaah85030 Human pro
7	2040	100.0	2040	5 ACA59617	Acas59617 Prostate
8	2040	100.0	2040	6 AB195178	Ab195178 Human B30
9	2040	100.0	2040	6 AAS99857	Aaas99857 Breast tu
10	2040	100.0	2040	8 ACC95344	Acc95344 Prostate
11	2040	100.0	2040	8 ADA11382	Ada11382 Human bre
12	2040	100.0	2040	10 ADC15355	Adc15355 Human bre
13	2040	100.0	2040	10 ADB13825	Adb13825 Human pro
14	2040	100.0	2040	10 ADG26241	Adg26241 Human pro
15	1989	97.5	2040	3 AAH06600	Aaah06600 Human imm
16	1551	76.0	2000	3 AAC81012	Aac81012 Human B11
17	1551	76.0	2000	4 AAH93715	Aah93715 Human pro
18	1551	76.0	2000	4 AAI67212	Aai67212 B305D iso
19	1551	76.0	2000	4 AAH63808	Aaah63808 Human pro

20	1551	76.0	2000	4 AAH02780	Aah02780 Prostate
21	1551	76.0	2000	4 AAH85029	Aaah85029 Human pro
22	1551	76.0	2000	5 ACA59616	Acas59616 Prostate
23	1551	76.0	2000	6 AB195179	Ab195179 Human B30
24	1551	76.0	2000	6 AAS99858	Aaas99858 Breast tu
25	1551	76.0	2000	8 ACC95343	Acc95343 Prostate
26	1551	76.0	2000	8 ADA11381	Ada11381 Human bre
27	1551	76.0	2000	10 ADC15354	Adc15354 Human bre
28	1551	76.0	2000	10 ADB13824	Adb13824 Human pro
29	1551	76.0	2000	10 ADG26240	Adg26240 Human pro
30	1500	73.5	2000	3 AAH06599	Aaah06599 Human imm
31	1128	55.3	1155	3 AAH06598	Aaah06598 Human imm
32	1128	55.3	1155	3 AAC81011	Aac81011 Human B11
33	1128	55.3	1155	4 AAH93714	Aah93714 Human pro
34	1128	55.3	1155	4 AAI67211	Aai67211 B305D iso
35	1128	55.3	1155	4 AAH63807	Aaah63807 Human pro
36	1128	55.3	1155	4 AAH02779	Aah02779 Prostate
37	1128	55.3	1155	4 AAH85028	Aaah85028 Human pro
38	1128	55.3	1155	5 ACA59615	Acas59615 Prostate
39	1128	55.3	1155	6 AB195178	Ab195178 Human B30
40	1128	55.3	1155	6 AAS99857	Aaas99857 Breast tu
41	1128	55.3	1155	8 ACC95342	Acc95342 Prostate
42	1128	55.3	1155	8 ADA11380	Ada11380 Human bre
43	1128	55.3	1155	10 ADC15353	Adc15353 Human bre
44	1128	55.3	1155	10 ADB13823	Adb13823 Human pro
45	1128	55.3	1155	10 ADG26239	Adg26239 Human pro

ALIGNMENTS

RESULT 1	
AAC81013	AAC81013 standard; cDNA; 2040 BP.
XX	XX
XX	AAC81013;
XX	13-FEB-2001 (first entry)
XX	XX
DE	Human B11a91 antigen splice isoform B11C-9-16 cDNA.
KW	Human; breast tumour-specific antigen; cytostatic; vaccine;
XX	breast cancer; B18a91; B11a91; B15a91; B5.
OS	Homo sapiens.
PN	WO200061753-A2.
XX	XX
PD	19-OCT-2000.
XX	XX
PF	07-APR-2000; 2000WO-US009312.
XX	XX
PR	09-APR-1999; 99US-00289198.
PR	28-OCT-1999; 99US-00429755.
PR	23-MAR-2000; 2000US-00534825.
XX	XX
PA	(COR1-) CORIXA CORP.
PI	Frudakis TN, Smith JM, Reed SG, Misher LB, Retter MW, Dillon DC;
DR	WPI, 2000-628403/60.
DR	F-PSDB; AAB28630.
PT	An isolated polypeptide comprising an immunogenic portion of a breast
PT	tumor protein used for inhibiting the development of cancer, especially
XX	breast cancer, and monitoring cancer progression in a patient.
XX	XX
PS	Claim 4, Page 178; 187pp; English.
XX	XX
CC	The present sequence is given in a specification relating to compositions
CC	and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC	sequences that are preferentially expressed in breast tumor tissue, and
CC	the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
XX
XX Sequence 2040 BP, 716 A, 392 C, 500 G, 432 T, 0 U, 0 Other:

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGCTTGAAGTATTCATCCGCGTCCCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGTGCTTGAAGTATTCATCCGCGTCCCTCTTCTGTGAAGAAGCATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTTCTGGAAGCAACGACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTTCTGGAAGCAACGACTCTGTATGAAGCACTCAGAGCAAG 180
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QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGAGTACAGTGTCTTCAATGAGCCCAAGTACACGTCCTGTGAGAAATCTG 420
DB 361 GGAGACTAGAGTACAGTGTCTTCAATGAGCCCAAGTACACGTCCTGTGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCGCATG 480
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QY 1921 GAAAAAGAGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 GAAAAAGAGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
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RESULT 3
AA167213
ID AA167213 standard; cDNA; 2040 BP.
AC AA167213;
DT 11-FEB-2002 (first entry)
DE B305D isoform C splice variant 3 encoding cDNA.
XX Genetic substructure; DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..2016
XX FT /*tag= a

FT /product= "B305D isoform C splice variant"
XX MO200175171-A2.
XX 11-OCT-2001.
XX 02-APR-2001; 2001WO-US010631.
XX 03-APR-2000; 2000US-0194241P.
XX 20-JUL-2000; 2000US-0219862P.
XX 27-JUL-2000; 2000US-0221300P.
XX 18-DEC-2000; 2000US-0256592P.
XX (CORI-) CORIXA CORP.
XX Houghton RL, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;
XX WPI; 2001-626449/72.
XX P-PsDB; AAG65978.
XX Identifying tissue (tumor)-specific polynucleotides overexpressed in
XX tissue of interest as compared to control tissue, for detecting cancer
XX cells in patient, comprises DNA microarray analysis or quantitative
XX polymerase chain reaction.
XX Claim 4; Page 94-95; 127pp; English.
XX The invention relates to identifying tissue-specific polynucleotides (P)
XX that involves performing a genetic substructure to identify pool of (P)
XX from tissue of interest (TI), performing DNA microarray analysis to
XX identify first subset of polynucleotides (SP1) at least 2-fold over
XX expressed in TI, and performing quantitative polymerase chain reaction
XX (PCR) analysis on SP1 to identify second subset of (P). The method is
XX useful for determining the presence or absence of a cancer cell in a
XX patient, monitoring the progression of cancer in a patient using a
XX biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX urine or a tumour biopsy sample. The methods are useful for determining
XX the presence or absence of or monitoring progression of prostate, breast,
XX colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
XX gastric, kidney, bladder, pancreatic or endometrial cancer. The present
XX sequence represents a cDNA encoding a B305D isoform C splice variant
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2040; DB 4; Length 2040;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGCGT 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACAGCGT 240
QY 241 GCGGCTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACCAAGCACTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
QY 361 GGAAGCTAGATGACAGTGTCTTATGAGAGCCAGGTACCAAGTCCGTGGAAGATCTG 420

Db 361 GGAGACTAGATGACGTGCTTCAATGAGCCAGGATCCAGCTCCGTGGAGAAATCTG 420
QY 421 GACAACTCCACGAGCTGCTGTGGGTAAAGTCCCGCAAGAAAGATCTCATGTCATG 480
Db 421 GACAACTCCACGAGCTGCTGTGGGTAAAGTCCCGCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGACATGACGTGAACAGAAAGGACAAAGAAAGGAGCTGCTCATGCTGGCC 540
Db 481 CTCAGGAGACATGACGTGAACAGAAAGGACAAAGAAAGGAGCTGCTCATGCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTCGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTCGACAGAGATGCACTTAAT 600
QY 601 GTCTTTGACACAAAGAGGACAGCTGTGATTAAGCCGTACATGCGAGAAATGAA 660
Db 601 GTCTTTGACACAAAGAGGACAGCTGTGATTAAGCCGTACATGCGAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAAACATGGCACTGATCCAAATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAAACATGGCACTGATCCAAATTTCCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGSCAAAGCATGCTCTTA 780
Db 721 ACCACTCTGCACTACCTATCTATTAATGAAGATTAATTAATGSCAAAGCATGCTCTTA 780
QY 781 TATGTGCTGATATTCGAATCAAAACAGACATGSCCTCACACACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATTCGAATCAAAACAGACATGSCCTCACACACTGTTACTTGGTGA 840
QY 841 CATGACAAAAACAGAAAGTCGTGAATTTTAAATCAAGAAAAACCGAATTTAAATGCA 900
Db 841 CATGACAAAAACAGAAAGTCGTGAATTTTAAATCAAGAAAAACCGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGCTGCTCATATCTGTATGTTGTTGATGAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATATCTGTATGTTGTTGATGAGCAAGTATA 960
QY 961 GTTACGCTTCTACTTGGAGCAAAATATGATATCTTCTCAAGATCTATCTGGACAGC 1020
Db 961 GTTACGCTTCTACTTGGAGCAAAATATGATATCTTCTCAAGATCTATCTGGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAAAGCTTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAAGTTCAAGGAGTGAATTAATGAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAAGTTCAAGGAGTGAATTAATGAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGAGAGGTTGAAGAAAGAAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGAGAGGTTGAAGAAAGAAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGATTACTAGAAAACTGACTAATGCTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGTTGGATTACTAGAAAACTGACTAATGCTGCTGGC 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGTAATGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACTGTAATGCAATTT 1380
QY 1381 CTTGAAGAAAGATGAAGATATCAAGAAATTTGGGAATTTGCTGATCAAAAGAA 1440
Db 1381 CTTGAAGAAAGATGAAGATATCAAGAAATTTGGGAATTTGCTGATCAAAAGAA 1440
QY 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500

Db 1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
QY 1501 TCAAGAAAGAGTCAACAAAGGCTTTGAGGCACTGAAATGSCCAGCAGAGAAAGATCT 1560
Db 1501 TCAAGAAAGAGTCAACAAAGGCTTTGAGGCACTGAAATGSCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCGAAATTAATTAAGATGTTAGAGAGCTGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCGAAATTAATTAAGATGTTAGAGAGCTGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAACACAGAGAGTACTATGTCGGAATCCGAAATCCGACTAATGCTGACC 1680
Db 1621 GAAATGAAGAACACAGAGAGTACTATGTCGGAATCCGAAATCCGACTAATGCTGACC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGGTATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACATGAGATGAAGATATCACAGTGAAGAACAAATGATACTGAG 1800
Db 1741 CAGCAATTTCTGACACATGAGATGAAGATATCACAGTGAAGAACAAATGATACTGAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAGCAGATGAAGTGTGAAAAATGAATTTCTGACCTTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGTGAAAAATGAATTTCTGACCTTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCATCTTGCATGAAAAATGATAGTTGCCGGAAGAAATGCCATGCTAAGACAG 1980
Db 1921 GAAAAAGCATCTTGCATGAAAAATGATAGTTGCCGGAAGAAATGCCATGCTAAGACAG 1980
QY 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAATTAATTAATTAATTAATTAATTAAT 2040

RESULT 4
AAS63809
ID AAS63809 strand: cDNA; 2040 BP.
XX
AC AAS63809;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #10.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX

PI Xu J, Dillon DC, Metcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Reter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX WPI, 2001-639232/73.
XX P-PSDB; AA069779.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX
XX Claim 1; Page 350; 579p; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGAATTCATGCCGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTGAATTCATGCCGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGCAAGCACTGCTATGAAGCACTCAGAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGAGCAAGCACTGCTATGAAGCACTCAGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
DB 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 240
QY 241 GGGGCTTTGAGAGCAAGCACTGCTATGAAGCACTCAGAGAGCAAGTGTGCAAG 300
DB 241 GGGGCTTTGAGAGCAAGCACTGCTATGAAGCACTCAGAGAGCAAGTGTGCAAG 300
QY 301 TGGTGTGCAAGTGTGCTTCCCTGCTGCAAGGAGAGGCAAGCAAGTGTGCGCTTGG 360
DB 301 TGGTGTGCAAGTGTGCTTCCCTGCTGCAAGGAGAGGCAAGCAAGTGTGCGCTTGG 360
QY 361 GGAAGTGAAGTGAAGTGTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 420
DB 361 GGAAGTGAAGTGAAGTGTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGAGAGCACTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTGT 540
DB 481 CTCAGAGAGCACTGAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTGT 540
QY 541 TCTGCAATGGGAATTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600
DB 541 TCTGCAATGGGAATTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600
QY 601 GTCTTTGACAAAG 660
DB 601 GTCTTTGACAAAG 660

DB 601 GTCTTTGACAAAG 660
QY 661 TGTGGTTAATGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TGTGGTTAATGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACCACTGCACTAGCTATCTATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
DB 721 ACCACTGCACTAGCTATCTATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
QY 781 TATGTGCTGATATGATCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGTGCTGATATGATCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 CATGAGCAAAAACAGAGTGTGGAATTTTAACTCAAGAAAAGAGAGAGAGAGAGAGAG 900
DB 841 CATGAGCAAAAACAGAGTGTGGAATTTTAACTCAAGAAAAGAGAGAGAGAGAGAGAG 900
QY 901 CTGATATGATATGAG 960
DB 901 CTGATATGATATGAG 960
QY 961 GTGAGCTTCTACTGAGCAAAAATATGATGATCTTCAAGATCTATCTGAGAGAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAAATATGATGATCTTCAAGATCTATCTGAGAGAGAG 1020
QY 1021 GGCAGAGATATGCTGTTTCTGATCATCATGATATGATGATGATGATGATGATGATG 1080
DB 1021 GGCAGAGATATGCTGTTTCTGATCATCATGATATGATGATGATGATGATGATGATG 1080
QY 1081 AAGAGAAAACAGATCTAAAATCTCTCTGAAAACAGCAATCCAGAACCAAGCTTAAAG 1140
DB 1081 AAGAGAAAACAGATCTAAAATCTCTCTGAAAACAGCAATCCAGAACCAAGCTTAAAG 1140
QY 1141 CTGATCATGAG 1200
DB 1141 CTGATCATGAG 1200
QY 1201 ATGTCTCAAGAACAG 1260
DB 1201 ATGTCTCAAGAACAG 1260
QY 1261 AAGCATGAAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
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QY 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGCAAG 1440
DB 1381 CCTGCAAG 1440
QY 1441 AAAAGATGCAAGATTAATCTCTCTGAAAACAGCAATCCAGAACCAAGCTTAAAGTGA 1500
DB 1441 AAAAGATGCAAGATTAATCTCTCTGAAAACAGCAATCCAGAACCAAGCTTAAAGTGA 1500
QY 1501 TCGAG 1560
DB 1501 TCGAG 1560
QY 1561 CAAAGAACAGAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 CAAAGAACAGAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GAAATGAG 1680
DB 1621 GAAATGAG 1680
QY 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740

OY	1741	AAGCAATTTCTGACACTGAAATGAAGAATATCACTGACGAAACAAATGATATCTCAG	1800
Db	1741	CAGCAATTTCTGACACTGAAATGAAGAATATCACTGACGAAACAAATGATATCTCAG	1800
OY	1801	AAGCAATTTTGAAGAACAGACACTGGAATATTACACGATGAGATTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGAAGAACAGACACTGGAATATTACACGATGAGATTCTGATTCATGAA	1860
OY	1861	GAAAAAGCATATGAAATGAAATTTGAAATTTCTGATTTCTCTTAATTTGTAAGAA	1920
Db	1861	GAAAAAGCATATGAAATGAAATTTGAAATTTCTGATTTCTCTTAATTTGTAAGAA	1920
OY	1921	GAAAAAGCATCTTGATCATGAAATATGATCGATGCGGAAAGAAATTCGATGCTAAAGCTG	1980
Db	1921	GAAAAAGCATCTTGATCATGAAATATGATCGATGCGGAAAGAAATTCGATGCTAAAGCTG	1980
OY	1981	GAGCTAGACAAATGAAATCATCAGAGCCAGCTTAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAGACAAATGAAATCATCAGAGCCAGCTTAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 5
AAH02781
ID AAH02781 standard; cDNA; 2040 BP.

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen determined cDNA splice variant of B305D #10.

KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.

Homo sapiens.

PN WO200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US027464.

PR 04-OCT-1999; 99US-0157455P.

PA (CORI-) CORIXA CORP.

Pi Xu J, Skeiky YAW, Reed SG, Cheever MA;

DR WPI; 2001-245062/25.
DB P-POND; 2001-245062/25.

DT	XX	Probate & Succession
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98	98	98
99	99	99
100	100	100

XX
FI
XX
treatment and diagnosis of prostate

CS 144M 50; Page 233; 2/6/99; English.

least an immunogenic portion of a prostatic tumour antigen protein or its

production. (I), prostate tumour polynucleotides, an antigen

pharmaceutical composition containing (I) are useful for inhibiting the

CC specific proteins and oligonucleotides that hybridise to a polynucleotide

CC presence or absence of a cancer or monitoring the progression the

CC AAB74798 to AAB74821 and AAB74830 are sequences used in the

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2040;	DB 4;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2040; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ATGGAGTGAAGTGAATTCATGCCCGGCTGCCTTCTGGAAGAAAGCCATTTGCTGC	60
Db	1	ATGGAGTGAAGTGAATTCATGCCCGGCTGCCTTCTGGAAGAAAGCCATTTGCTGC	60
QY	61	AGAGCAAGATGGGCAAGTGTGTGCTGTCTTCCCTGCTGCAGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGTGTGCTGTCTTCCCTGCTGCAGGAGAGCGGCAAG	120
QY	121	AGCAAGTGGGCACTTCTGAGAACAGAGCACTCTGTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGAGAACAGAGCACTCTGTATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGCAAGCTG	240
QY	241	GGCGCTTCTGAGAACAGAGCACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG	300
Db	241	GGCGCTTCTGAGAACAGAGCACTCTGTATGAAGACACTCAGAGCAAGATGGGCAAG	300
QY	301	TGTGTGTGCCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGTGGGCGCTTGG	360
Db	301	TGTGTGTGCCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGGAGTACACAGTCCGCTGGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGGAGTACACAGTCCGCTGGAGAAAGATCTG	420
QY	421	GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTTCATGCTCATG	480
Db	421	GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTTCATGCTCATG	480
QY	481	CTCAGGGACACTGACGTGAACAAGAGAGCAAGAGAAAGAGCACTGCTTCATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGAACAAGAGAGCAAGAGAAAGAGCACTGCTTCATCTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAAGTGTAAAACTCCGTGTCGACAGACGATGCAACTTAT	600
Db	541	TCTGCCAATGGGAATTCAGAAAGTGTAAAACTCCGTGTCGACAGACGATGCAACTTAT	600
QY	601	GTCCTTGAACAACAAAAGAGGACAGCTCTGTATAAGGCGTTCATATGCCAGAAAGATGA	660
Db	601	GTCCTTGAACAACAAAAGAGGACAGCTCTGTATAAGGCGTTCATATGCCAGAAAGATGA	660
QY	661	TGTGCGTTAATGTGTGTGAACAATGGGACATGATCAATATTTCCAGATGAGTATGGAAT	720
Db	661	TGTGCGTTAATGTGTGTGAACAATGGGACATGATCAATATTTCCAGATGAGTATGGAAT	720
QY	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTAATGGCAAGCACTGCTCTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTAATGGCAAGCACTGCTCTTA	780
QY	781	TATGTGTGTGATATCGAATCAAAAAACAAGCATGGCTCCACACACTGTACTTGGTGTGA	840
Db	781	TATGTGTGTGATATCGAATCAAAAAACAAGCATGGCTCCACACACTGTACTTGGTGTGA	840
QY	841	CATAGGCAAAAACAGCAAGTGTGAATAATTTTATCAAGAAAAAAGGAAATTTAATGCA	900
Db	841	CATAGGCAAAAACAGCAAGTGTGAATAATTTTATCAAGAAAAAAGGAAATTTAATGCA	900
QY	901	CTGATAGATATGGAAGGACTGCTCATATCTTGTATGTTTGTGATCAGCAAGATATA	960
Db	901	CTGATAGATATGGAAGGACTGCTCATATCTTGTATGTTTGTGATCAGCAAGATATA	960
QY	961	GTCAGCCTTCAACTTGAAGCAAAAATATGATGTAATCTTCAAGATCTATCTGACACAGC	1020
Db	961	GTCAGCCTTCAACTTGAAGCAAAAATATGATGTAATCTTCAAGATCTATCTGACACAGC	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATCATTAATTTGGCCAGTTACTTTCAGACTAC	1080

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Db 1021 GCCAGAGATGCTCTTCTAGTCATCATCATGATTAATTGTCAGTTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAG 1140
Db 1081 AAGAGAAAAAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCTGAATAATATGAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCTGAATAATATGAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGAGGAGTTACTAGAAAACCTGACTAATGCTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATATGAGGAGTTACTAGAAAACCTGACTAATGCTGCTGCG 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAAACCTGAAATCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATTTCTGATCAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATTTCTGATCAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTCTGAAAACAGCAATCCAGAAACAAGCTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAGAGGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAGAGGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
QY 1561 CAGAAACCAAGAAATAATTAAGATGTGATAGAGCTAGAAATTTTAATGCTATCGAA 1620
Db 1561 CAGAAACCAAGAAATAATTAAGATGTGATAGAGCTAGAAATTTTAATGCTATCGAA 1620
QY 1621 GAAATGAAGAGACGAGAGTACTCATGTCGAGTTCCCGAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAGACGAGAGTACTCATGTCGAGTTCCCGAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGTGATGATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGCAATGTGATGATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGAAGAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAAAGAGCACTGAAATTAACAGATGAATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGAAGAAAGAGCACTGAAATTAACAGATGAATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAAATGTGTTGAAAAATGAATTTCTGAGCTTCTCTTAATGTAAGAA 1920
Db 1861 GAAAGCAGATAGAAATGTGTTGAAAAATGAATTTCTGAGCTTCTCTTAATGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGAATGAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGAATGAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTGAGACATGAAATCACTGAGACCGAGCTAAAAAATGCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 GAGCTGAGACATGAAATCACTGAGACCGAGCTAAAAAATGCTGCTGCTGCTGCTGCTGCTG 2040
```

RESULT 6
AAH85030
ID AAH85030 standard; cDNA; 2040 BP.
XX
AC AAH85030;

```
XX 25-SEP-2001 (first entry)
DT Human prostate-specific CDNA sequence B305D splice variant #10.
XX
DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
XX chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030904.
XX
PR 12-NOV-1999; 99US-00439313.
XX
PR 18-NOV-1999; 99US-00443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Retter MW, Stolk JA, Day CR, Skeiky YAW, Wang A,
XX WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX
PS Claim 31; Page 248; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712B, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
QY 61 AAGAGCAGATGAGGAGAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AAGAGCAGATGAGGAGAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTAATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTAATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGCTTCTGAGACCAAGCACTCTGTAATGAAGCACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGACCAAGCACTCTGTAATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGCAAGTGGGCGCTTGG 360
```

Db 301 TGTGCTGCACGCTTCCCTGCTGCAAGGGAGGGGCAAGAGCAAGTGGGCGCTTGG 360
Qy 361 GGAAGCTAAGATACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGGAAGAAATCTG 420
Db 361 GGAAGCTAAGATACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGGAAGAAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAAGAGATCTCATGCTCAG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGGTAAAGTCCCGAAGAGATCTCATGCTCAG 480
Qy 481 CTCAGGAGACCTGACCTGGAACAAGAGACAAAGAGAGAGCTGCTCTACATCTGACC 540
Db 481 CTCAGGAGACCTGACCTGGAACAAGAGACAAAGAGAGAGCTGCTCTACATCTGACC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGATGTAATCTCTGCTGGAAGAGAGATGCTCAATTA 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATGTAATCTCTGCTGGAAGAGAGATGCTCAATTA 600
Qy 601 GTGCTTGAACAACAAAAGAGAGACAGCTCTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
Db 601 GTGCTTGAACAACAAAAGAGAGACAGCTCTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
Qy 661 TGTGCTTAATGTTGCTGGAACATGAGCACTGATCCAAATTTCCAGATGATGGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGAGCACTGATCCAAATTTCCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
Db 721 ACCACTCTGCACTACGCTATCTTAATGAAGATTAATTAAGCCAAAGCACTGCTTAA 780
Qy 781 TATGAGCTGATATCGAATTAATAAACAAGATGAGCTCAGACATGTTACTTGGTGA 840
Db 781 TATGAGCTGATATCGAATTAATAAACAAGATGAGCTCAGACATGTTACTTGGTGA 840
Qy 841 CATGACAAAAACAGCAAGCTGGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
Db 841 CATGACAAAAACAGCAAGCTGGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
Qy 901 CTGGATAGATAGGAAGAGCTGCTCATATCTTGTGATGTTGTGATCAGCAAGTAA 960
Db 901 CTGGATAGATAGGAAGAGCTGCTCATATCTTGTGATGTTGTGATCAGCAAGTAA 960
Qy 961 GTCAAGCTTCTACTTGAAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACGAG 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACGAG 1020
Qy 1021 GGCAGAGATAGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GGCAGAGATAGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATCTCTTGTGAAAAACGCAATCTCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATCTCTTGTGAAAAACGCAATCTCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCGAAGAAAGTCAAAAGTTCAAAAGCAAGTGAATTTGCCAGCCAGAGAA 1200
Db 1141 CTGACATCGAAGAAAGTCAAAAGTTCAAAAGCAAGTGAATTTGCCAGCCAGAGAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGATGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATAGATGATGATGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATGAGGATTAAGAAAACCTGACTAATGCTGCTGCTG 1320
Db 1261 AAGCATGAAAGTAAATGAGGATTAAGAAAACCTGACTAATGCTGCTGCTGCTG 1320
Qy 1321 AATGATGATTAATGATTAATCTTCAAGAGAAAGCAAGCACTGAAATTCGCAATTT 1380
Db 1321 AATGATGATTAATGATTAATCTTCAAGAGAAAGCAAGCACTGAAATTCGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATTCACAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440

Db 1381 CCTGACAAAGAAAGTAAAGATTAATCAAGAAATTTGGAATTTAGTTCTGACTCAAGAA 1440
Qy 1441 AAAAGATCCAAATACTCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAAAGATCCAAATACTCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGATTCAAAGGCTTGAAGGCACTGAGAAATTTGAGCAAGAGAAATGATCT 1560
Db 1501 TCAGAGAAAGATTCAAAGGCTTGAAGGCACTGAGAAATTTGAGCAAGAGAAATGATCT 1560
Qy 1561 CAAGAACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 CAAGAACCAAGATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 GAAATGAAGACACGAAAGTACTCATGTCGATTTCCAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGACACGAAAGTACTCATGTCGATTTCCAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATGATGATGATGATGATGATGATGATGATGAT 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTTACAGATGATGATGATGATGATG 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTTTACAGATGATGATGATGATGATG 1860
Qy 1861 GAAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Db 1861 GAAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Qy 1921 GAAAAAGCATCTTCATGATGAATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAAGCATCTTCATGATGAATGATGATGATGATGATGATGATGATGATGATGATG 1980
Qy 1981 GAGCTGACACATGATGAAGACAGCCAGCTTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTGACACATGATGAAGACAGCCAGCTTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 7
ACAS9617
ID ACAS9617 standard; cDNA; 2040 BP.
XX
AC ACAS9617;
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #360.
XX
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSM; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.
PA (JIANG/) JIANG Y.
PA (KALOS/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEIK/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
DR MPI; 2001-245062/25.
XX P-PSDB; ABU71670.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
PS Example 11; SEQ ID NO 375; 85bp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 3 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated CDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGTTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTTCCCTGTGCGAGGAGAGCGGCAAG 120
DB 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTTCCCTGTGCGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACAGAGCACTGTGTAAGAACAATCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGACAGAGCACTGTGTAAGAACAATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTGCGAGGAGAGTGGCAAGCAAGT 240
QY 241 GGGGCTTTGGAGAACCAAGCACTGTGTAAGAACAATCAGAGCAAGTGGCAAG 300
DB 241 GGGGCTTTGGAGAACCAAGCACTGTGTAAGAACAATCAGAGCAAGTGGCAAG 300

QY 301 TGGTGTGCACTGCTCCCTGTGTCAGAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTCCCTGTGTCAGAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGTCTTCATGAGGCCCAAGTACCAAGTCCGTGAGAGATCTG 420
DB 361 GGAGACTAGATGACAGTGTCTTCATGAGGCCCAAGTACCAAGTCCGTGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCGGCTGTGAGGAGTAAAGTCCCAAGAAAGATCTACGTCAG 480
DB 421 GACAGCTCCACAGAGCTGCGGCTGTGAGGAGTAAAGTCCCAAGAAAGATCTACGTCAG 480
QY 481 CTCAGGGACACTGAGGTGAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGAGCC 540
DB 481 CTCAGGGACACTGAGGTGAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGAGCC 540
QY 541 TTGTCGAATGGGAATTGAGAGTGAATAAATCTCTGTGAGACAGACGATGTCACTTAAT 600
DB 541 TTGTCGAATGGGAATTGAGAGTGAATAAATCTCTGTGAGACAGACGATGTCACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGGACAGCTGTGAATAAAGCCGTACATGCGCAAGATGAA 660
DB 601 GTCCCTGACAAACAAAAGAGGACAGCTGTGAATAAAGCCGTACATGCGCAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGACATGACATGATCCAAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGACATGACATGATCCAAATATTCAGATGATGAGAAAT 720
QY 721 ACCACTGTGACATGCTATCTATATATGAAATTAATGAGCCAAAGACTGCTCTTA 780
DB 721 ACCACTGTGACATGCTATCTATATGAAATTAATGAGCCAAAGACTGCTCTTA 780
QY 781 TATGTCGTGATATGGAATCAAAAACAAAGATGCGCTCACACACTGTACTTGGTGA 840
DB 781 TATGTCGTGATATGGAATCAAAAACAAAGATGCGCTCACACACTGTACTTGGTGA 840
QY 841 CATGACAAAACACAGCAAGTGTGAATTTTAAATCAAGAAAAGAGCAATTTAAATGCA 900
DB 841 CATGACAAAACACAGCAAGTGTGAATTTTAAATCAAGAAAAGAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGTAATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAGAGAGCTGCTCATCTTGTGTAATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTATCTGAGGAAAATTAATGATATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTATCTGAGGAAAATTAATGATATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACCAATTTAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACCAATTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGCAAGTAAATATGCCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGCAAGTAAATATGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAAGATGTGATAGAGAGTTGAAGAAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAAGATGTGATAGAGAGTTGAAGAAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGGAAATTAAGAAAATCTGACTAATGTGTCACTGTGAC 1320
DB 1261 AAGCATGAAAGTAAATATGATGGAAATTAAGAAAATCTGACTAATGTGTCACTGTGAC 1320
QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAGACAGAACCTGAAATATGACAAATTT 1380
DB 1321 AATGTGATATATGATTAATTTCTCAAGAGAGACAGAACCTGAAATATGACAAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAATTAATTTCTGACTACAAAGAA 1440

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Db      1381 CCGACAGAGAAAGTGAAGGTATCACAGAAATTTGGAAATTTCTGACTACAGAGAA 1440
Qy      1441 AAACAGATGCCAAATACTCTTGTAAAAACAGAACCCAGAACCAAGATTAAAGCTGACA 1500
Db      1441 AAACAGATGCCAAATACTCTTGTAAAAACAGAACCCAGAACCAAGATTAAAGCTGACA 1500
Qy      1501 TCAGAGGAAGAGTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGAGAGAAAGATCT 1560
Db      1501 TCAGAGGAAGAGTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGAGAGAAAGATCT 1560
Qy      1561 CAGAGAACCAATAATAATAGATGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Db      1561 CAGAGAACCAATAATAATAGATGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAAGAGACGAGAGTACTCATGTGCAATTCACAGAAACCTGACTAAATGGTGCC 1680
Db      1621 GAAATGAAGAGACGAGAGTACTCATGTGCAATTCACAGAAACCTGACTAAATGGTGCC 1680
Qy      1681 ACTGCTGGCAATGCTGATATGATTAATTTCTCCAGAGAGAGAGCACTGTAAGC 1740
Db      1681 ACTGCTGGCAATGCTGATATGATTAATTTCTCCAGAGAGAGAGCACTGTAAGC 1740
Qy      1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTGAAGAGCAAAATGATCTCAG 1800
Db      1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTGAAGAGCAAAATGATCTCAG 1800
Qy      1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATATTAACAGATGATGCTGATTCAGAA 1860
Db      1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATATTAACAGATGATGCTGATTCAGAA 1860
Qy      1861 GAAAAGCAGATGAGATGTTGAAAAAATGAATTCGAGCTTCTCTTGTGTTAAGAA 1920
Db      1861 GAAAAGCAGATGAGATGTTGAAAAAATGAATTCGAGCTTCTCTTGTGTTAAGAA 1920
Qy      1921 GAAAAAGCATCTTGATGATGAAAAATAGATGTTGCGGAGAGAAATGGCATTGAAGCTG 1980
Db      1921 GAAAAAGCATCTTGATGATGAAAAATAGATGTTGCGGAGAGAAATGGCATTGAAGCTG 1980
Qy      1981 GAGCTAGACACATGAAACATCGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db      1981 GAGCTAGACACATGAAACATCGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 8
ABL95180
ID      ABL95180 standard; cDNA; 2040 BP.
XX
AC      ABL95180;
XX
DT      19-JUL-2002 (first entry)
XX
DE      Human B305D splice variant cDNA sequence SEQ ID NO 375.
XX
KW      Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW      gene therapy; gene; ss.
XX
OS      Homo sapiens.
XX
PN      US200202248-A1.
XX
PD      21-FEB-2002.
XX
PF      12-JAN-2001; 2001US-00759143.
XX
PR      25-FEB-1997; 97US-00806099.
PR      01-AUG-1997; 97US-00904804.
PR      10-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.

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PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00443686.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-00568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      10-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651236.
PR      06-SEP-2000; 2000US-00657279.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
XX
PA      (XUJU/) XU J.
PA      (DILL/) DILLON D C.
PA      (MITC/) MITCHAM J L.
PA      (HARL/) HARLOCKER S L.
PA      (JIAN/) JIANG Y.
PA      (KALO/) KALOS M D.
PA      (FANG/) FANGER G R.
PA      (RETT/) RETTER M W.
PA      (STOL/) STOLK J A.
PA      (DAYC/) DAY C H.
PA      (VEDV/) VEDVICK T S.
PA      (CART/) CARTER D.
PA      (LISX/) LI S X.
PA      (WANG/) WANG A.
PA      (SKER/) SKERKY Y A W.
PA      (HEPL/) HEPLER W T.
PA      (HEND/) HENDERSON R A.
XX
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
PI      Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR      WPI; 2002-255649/30.
XX
PT      New prostate-specific polynucleotides for diagnosing and treating
PT      diseases, in particular prostate cancer, and as markers for the
PT      progression of cancer.
XX
PS      Claim 1; SEQ ID NO 375; 87bp; English.
XX
CC      The present invention provides prostate-specific coding sequences and
CC      their encoded proteins. These can be used in the diagnosis and treatment
CC      of cancers, particularly prostate cancer. The present sequence is a cDNA
CC      described in the invention
XX
SQ      Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match      100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGTGTTGAGGTTGATTCATGCGGCTGCTCTTGTGAAGAGCAATTTGGTCTC 60
Db      1 ATGGTGTTGAGGTTGATTCATGCGGCTGCTCTTGTGAAGAGCAATTTGGTCTC 60
Qy      61 AGAGCAAGATGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db      61 AGAGCAAGATGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy      121 AGCAAGTGGGCACTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy      181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db      181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Qy      241 GGGCGTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300

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Db 241 GCGCGCTTGTGAGACCAACGACACTGTGCTATGAAACACTCAGAAACAAGATGGGCAAG 300
Qy 301 TGGTGCTGCACTGCTTCCCTGTCGACAGGGGAGGCGAAGAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGCTGCACTGCTTCCCTGTCGACAGGGGAGGCGAAGAGCAAGTGGGCGCTTGG 360
Qy 361 GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAAGTCTG 420
Db 361 GGAAGCTACGATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAAGTCTG 420
Qy 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
Qy 481 CTCAGGGACACTGACGTGAAACAAGAGCAAGCAAAAAGAGACTGCTCTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAAACAAGAGCAAGCAAAAAGAGACTGCTCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGACAGACGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGACAGACGATGTCACTTAAT 600
Qy 601 GTCTTGGACACAAAAAGAGACAGCTGTGATAAAGGCCGTACAAATGCCAGAAAGTGA 660
Db 601 GTCTTGGACACAAAAAGAGACAGCTGTGATAAAGGCCGTACAAATGCCAGAAAGTGA 660
Qy 661 TGTGGGTAAATGTTGTGGAACATGCGCACTGATCCAAATATTCGAGATGATGGAAT 720
Db 661 TGTGGGTAAATGTTGTGGAACATGCGCACTGATCCAAATATTCGAGATGATGGAAT 720
Qy 721 ACCACTGTGCACTACGCTATCTATATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTATATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
Qy 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGCTCACAACCACTGTTACTTGTGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAAGCATGCTCACAACCACTGTTACTTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGCAATGCGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAATGCGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
Qy 901 CTGSAATAGATATGGAAGAGCTGCTCATACTTGTGTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGSAATAGATATGGAAGAGCTGCTCATACTTGTGTGATGTTGTGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
Qy 1021 GCGAGAGATATGCTGTTCTAGTCAATCATCATGTAATTTGCAAGTACTTTCTGACTAC 1080
Db 1021 GCGAGAGATATGCTGTTCTAGTCAATCATCATGTAATTTGCAAGTACTTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATCTCTCTGAAAAACAGCAATCCAGAAACAAGCTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAATCTCTCTGAAAAACAGCAATCCAGAAACAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAAAGGAGTGAATTAAGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAGAGTTCAAAAGGAGTGAATTAAGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTTGGAATTAATAGAAAACTGACTAATGTTGCTGCTGAC 1320
Db 1261 AAGCATGAAGATTAATATGTTGGAATTAATAGAAAACTGACTAATGTTGCTGCTGAC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAAGCAATTT 1380
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Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACACTGAAATCAGCAATTT 1380
Qy 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAAATTAATGTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCGCAAAATTAATCTCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Db 1441 AAAAGATGCGCAAAATTAATCTCTCTGAAAAACAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGTCACAAGAGCTTGAAGGCAAGTAAATGCGCAGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGTCACAAGAGCTTGAAGGCAAGTAAATGCGCAGCCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCAAGAAATTAATAGATGATATGAGAGCTAGAAATTTTAATGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATAGATGATATGAGAGCTAGAAATTTTAATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGCAGCAAGTACTCATGTGGAATTCAGAAAACTGACTAATGAGTGC 1680
Db 1621 GAAATGAAGAGCAGCAAGTACTCATGTGGAATTCAGAAAACTGACTAATGAGTGC 1680
Qy 1681 ACTGCTGCAATGTGATGATGATTAATTCCTCAAGAGAGAGCAACACTGAAAGC 1740
Db 1681 ACTGCTGCAATGTGATGATGATTAATTCCTCAAGAGAGAGCAACACTGAAAGC 1740
Qy 1741 CAGCAATTTCTGCACTGAGATGAAGATGATCAAGTGAAGCAAAATGATCTGAG 1800
Db 1741 CAGCAATTTCTGCACTGAGATGAAGATGATCAAGTGAAGCAAAATGATCTGAG 1800
Qy 1801 AAGCAATTTTGTGAAGACAGAACACTGGAATATTACAGATGATCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACACTGGAATATTACAGATGATCTGATTCATGAA 1860
Qy 1861 GAAAGCAGATGAGAGTGGTGAAGAAATGAATTTGAGCTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAGAGTGGTGAAGAAATGAATTTGAGCTTCTTATGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTGCATGAAATATGTAATGTTGCGGGAAGAAATTCGATGCTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGCATGAAATATGTAATGTTGCGGGAAGAAATTCGATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTTAATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTTAATTAATTAATTAATTAATTAATTAAT 2040

RESULT 9
AAS9859
ID AAS9859 standard; cDNA; 2040 BP.
XX
AC AAS9859;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11a1 splice variant B11C-9,16.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN W0200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590383.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX
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PA (CORI-) CORIXA CORP.
XX
XX Fundakie TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skeiky YAM, Harlocker SL, Day CH;
XX
XX WPI; 2002-089919/12.
DR P-PSDB; AAU74379.
XX
PT New breast tumor proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response.
XX
XX
XX Claim 1; Page 224-225; 245bp; English.
XX
XX The invention relates to novel breast tumor polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response,
XX particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation, in the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumor polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS9570-AAS9888
XX represent novel human breast cancer protein coding sequences and PCR
XX primers of the invention
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGTGTGATTCATGCGCGCTCTTCTGTGAAGAACATTGGTCTC 60
DB 1 ATGTGTTGAGTGTGATTCATGCGCGCTCTTCTGTGAAGAACATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTCCCTGCTGCAAGGAGACGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTCCCTGCTGCAAGGAGACGGCAAG 120
QY 121 AGCAAGTGGGCACTTTGTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTTGTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
QY 241 GGGCTTTGGGAGACCAAGGAGCTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGCTTTGGGAGACCAAGGAGCTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGTACGATGACAGTGGCTTCATGAGACCCAGGTACCAAGTGGGCAAGTGG 420
DB 361 GGAAGTACGATGACAGTGGCTTCATGAGACCCAGGTACCAAGTGGGCAAGTGG 420
QY 421 GAAAGCTCCAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATCTGCTAG 480
DB 421 GAAAGCTCCAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATCTGCTAG 480
QY 481 CTCAGGAGACACTGACGTGAACAAGAGGACAAAGAAAGAGACTGCTCTACATCTGGCC 540
DB 481 CTCAGGAGACACTGACGTGAACAAGAGGACAAAGAAAGAGACTGCTCTACATCTGGCC 540
QY 541 TCTGCGAATGGGAATTCAGAAATGATGAAAATCTCTGCTGAGACAGATGTCATTTAAT 600
DB 541 TCTGCGAATGGGAATTCAGAAATGATGAAAATCTCTGCTGAGACAGATGTCATTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGAA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACAAATGCCAGAAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACAGTGCACGTATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTAAATGTTGCTGGAACAGTGCACGTATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGACATACCTCTATCTAATGAAGATTAATGAGCAAGACAGCTCTTGA 780
DB 721 ACCACTCTGACATACCTCTATCTAATGAAGATTAATGAGCAAGACAGCTCTTGA 780
QY 781 TATGTCGTGATATGCAATCAAAAAAAGCATGGGCTCACACACTGTTACTGGTGA 840
DB 781 TATGTCGTGATATGCAATCAAAAAAAGCATGGGCTCACACACTGTTACTGGTGA 840
QY 841 CATGACCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
DB 841 CATGACCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCTCATCTTCTGCTGATGTTGTGATCAGCAATGA 960
DB 901 CTGGATAGATATGGAAGAGCTGCTCTCATCTTCTGCTGATGTTGTGATCAGCAATGA 960
QY 961 GTGAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTGAGCTTCTACTTGAAGAAAAATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCGAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGTGTCTAAATCTTTCTGAAAAACAGCAATCTCAGACAAAGCTTAAAG 1140
DB 1081 AAAAGAAAAACAGTGTCTAAATCTTTCTGAAAAACAGCAATCTCAGACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATTTGCCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTCACAAAAGTTCAAAAGCAGTGAATTTGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAAACCAAGAAATAAATAGATGTGATAGAGAGTTGAGAAAGATGAAAG 1260
DB 1201 ATGTCTCAAGAAACCAAGAAATAAATAGATGTGATAGAGAGTTGAGAAAGATGAAAG 1260
QY 1261 AAGCATGAAGATTAATATGATGGGATTACTGAAAACTGATCTATGATGTCACCTGGCG 1320
DB 1261 AAGCATGAAGATTAATATGATGGGATTACTGAAAACTGATCTATGATGTCACCTGGCG 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGAGAAACCTGAAATTCAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAAAGAGAGAAACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCACAGAAATTTTGGCAATTTAGTTCTGACTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCACAGAAATTTTGGCAATTTAGTTCTGACTCAAGAA 1440
QY 1441 AAAAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACCAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAAACCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATGCCAAAGGCTTGAAGGAGCAAGTGAATTTGGCCAGCAAGAAATATCT 1560
DB 1501 TCAGAGGAAGATGCCAAAGGCTTGAAGGAGCAAGTGAATTTGGCCAGCAAGAAATATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGACTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGACACGAAAGTACTCATGTGGAATTCAGAAAACTTGAATTAATGCTGCC 1680
DB 1621 GAAATGAAGACACGAAAGTACTCATGTGGAATTCAGAAAACTTGAATTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGGTATGATGATTAATTTCCCAAGAAAGAGCAAGCACTGAAAG 1740

Db 1681 ACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAGAGACGAAACACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACTGAGAGAACTAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACTGAGAGAACTAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACTGTGAATATTAACAGATGAGATTTCTGATTCAGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACTGTGAATATTAACAGATGAGATTTCTGATTCAGAA 1860
Qy 1861 GAAAGCAATGAAGTGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
Db 1861 GAAAGCAATGAAGTGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGCATCTTGACATGAAAAATAGTACGTTGCGGAGAGAAATTCGCTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGACATGAAAAATAGTACGTTGCGGAGAGAAATTCGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 10

ACC95344
ID ACC95344 standard; cDNA; 2040 BP.

ACC95344;

28-AUG-2003 (first entry)

Prostate tumour specific cDNA sequence SEQ ID 375.

Cytostatic; gene therapy; prostate-specific protein; PSP; human; immune response; prostate cancer; ss.

Homo sapiens.

W0200289747-A2.

14-NOV-2002.

09-MAY-2002; 2002MO-US014753.

09-MAY-2001; 2001US-00852911.

29-JUN-2001; 2001US-00895814.

10-DEC-2001; 2001US-00012896.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA, Kales MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Hural J, McNeill PD, Houghton RL, Vinals Y De Bassolis, Foy TM, Matanabe Y, Deng T;

MPI; 2003-167130/16.

New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer in a patient.

Example 11; Page 416; 691pp; English.

The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2040; Conservative 0;

Qy 1 ATGTGTTGATGATGATTCATGCGGCTGCTCTTGTGAGAAAGCCATTTGGTCTC 60
Db 1 ATGTGTTGATGATGATTCATGCGGCTGCTCTTGTGAGAAAGCCATTTGGTCTC 60
Qy 61 AAGAGCAAGTGGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAG 120
Db 61 AAGAGCAAGTGGCAAGTGTGCTGCTGCTTCCCTGCTGAGAGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 181 ATGGGCAAGTGGGCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGGGCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 GAGCGCTTGTGAG 300
Db 241 GAGCGCTTGTGAG 300
Qy 301 TGGTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGGTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 GAGAGCTAGATGACAGTGCCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GAGAGCTAGATGACAGTGCCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 GACAGAGCTTCCAG 480
Db 421 GACAGAGCTTCCAG 480
Qy 481 CTGAG 540
Db 481 CTGAG 540
Qy 541 TCTGCAATGGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TCTGCAATGGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 GTCTTGTGACAG 660
Db 601 GTCTTGTGACAG 660
Qy 661 TGTGCTTAAATGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 TGTGCTTAAATGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ACCACTGTGACAG 780
Db 721 ACCACTGTGACAG 780
Qy 781 TATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 TATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 841 CATGAGCAAG 900
Db 841 CATGAGCAAG 900
Qy 901 CTGATAGATAG 960
Db 901 CTGATAGATAG 960
Qy 961 GTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
Db 961 GTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020

```
QY 1021 GCCAGAGATGCTGTTCTTAGCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
    |||||
Db 1021 GCCAGAGATGCTGTTCTTAGCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACAGACTTAAAG 1140
    |||||
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAAAGCGAGTAAATAGCCAGAGAAA 1200
    |||||
Db 1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAAAGCGAGTAAATAGCCAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
    |||||
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAAGTAAATATGTTGGGATTACTAGAAAACTGACTATGTTGCTGCTGCG 1320
    |||||
Db 1261 AAGCATGAAAAGTAAATATGTTGGGATTACTAGAAAACTGACTATGTTGCTGCTGCG 1320
QY 1321 AATGTTGATATGATTAATTTCTCTCAAGAGAGAGCAAAACCTGAAAATCAGCAATTT 1380
    |||||
Db 1321 AATGTTGATATGATTAATTTCTCTCAAGAGAGAGCAAAACCTGAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGAGTATCAAGAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
    |||||
Db 1381 CCTGACAAAGAGAGAGTATCAAGAAATTTGGGAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||||
Db 1441 AAAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCACAAAAGGCTTGAAGGAGAGTGAATTAATGAGCAAGAAAGATCT 1560
    |||||
Db 1501 TCAGAGAGAGAGTCACAAAAGGCTTGAAGGAGAGTGAATTAATGAGCAAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATTAATTAAGAGTGTGATGAGAGTGAATTAATTTATGCTATCGAA 1620
    |||||
Db 1561 CAAGAACCCAGAAATTAATTAAGAGTGTGATGAGAGTGAATTAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTTCCAGAAAAACCTGACTAATGTTGCC 1680
    |||||
Db 1621 GAAATGAAAGAGCAGGAAGTACTCATGTGCAATTTCCAGAAAAACCTGACTAATGTTGCC 1680
QY 1681 ACTGCTGGCAATGTTGATGATGATTAATTTCTCTCAAGAGAGAGCAAAACCTGAAAGC 1740
    |||||
Db 1681 ACTGCTGGCAATGTTGATGATGATTAATTTCTCTCAAGAGAGAGCAAAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGCACTGAGAAATGAAAGTATCAAGTGAAGCAAAATGATTAATCTCAG 1800
    |||||
Db 1741 CAGCAATTTCTGCACTGAGAAATGAAAGTATCAAGTGAAGCAAAATGATTAATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTCTGATTCATGAA 1860
    |||||
Db 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTCTGATTCATGAA 1860
QY 1861 GAAAGACAGATAGAACTGTTGAAAAATGAAATTTCTGAGTTTCTTATGTTGAAGAA 1920
    |||||
Db 1861 GAAAGACAGATAGAACTGTTGAAAAATGAAATTTCTGAGTTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCCGGGAGAAATTTGCCATGCTAAAGCTG 1980
    |||||
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCCGGGAGAAATTTGCCATGCTAAAGCTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCAGCTAAAAATGAAAAATGAAAAATGAAAAA 2040
    |||||
Db 1981 GAGCTAGACACATGAAACATCAGAGCAGCTAAAAATGAAAAATGAAAAATGAAAAA 2040
XX ADAL1382 standard; cDNA; 2040 BP.
```

```
AC ADAL1382:
XX
XX
DT 06-NOV-2003 (first entry)
XX
DE Human breast cancer specific cDNA B11C-9.16.
XX
KW se; gene; human; breast cancer; cytosolic; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002165371-A1.
XX
PD 07-NOV-2002.
XX
PF 07-AUG-2001; 2001US-00924400.
XX
PR 11-JAN-1996; 96US-00585392.
PR 10-JAN-1997; 97MO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00991789.
PR 17-APR-1998; 98US-00062451.
PR 09-APR-1999; 99US-00289198.
PR 28-OCT-1999; 99US-00429755.
PR 23-MAR-2000; 2000US-00534825.
PR 24-MAY-2000; 2000US-00577505.
PR 08-JUN-2000; 2000US-00590583.
PR 26-OCT-2000; 2000US-00699295.
PR 16-MAR-2001; 2001US-00810936.
XX
XX (PRUD/) PRUDAKIS T N.
XX (REED/) REED S G.
XX (SMIT/) SMITH J M.
XX (MISH/) MISHNER J E.
XX (DILL/) DILLON D C.
XX (RETT/) RETTER M W.
XX (WANG/) WANG A.
XX (SKEL/) SKELKY Y A W.
XX (HARL/) HARLOCKER S L.
XX (DAYC/) DAY C H.
XX (LISX/) LI S X.
XX (DENG/) DENG T.
XX
XX Prudakis TM, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
XX Wang A, Skelky YAW, Harlocker SL, Day CH, Li SX, Deng T,
XX P-PSDB; ADAL1385.
XX
XX WPI; 2003-247262/24.
XX
XX New breast tumor proteins nucleic acids encoding such proteins, useful in
XX diagnosing, preventing and/or treating diseases such as cancer,
XX particularly breast cancer, and as markers for detecting the presence of
XX a cancer.
XX
XX Claim 1; Page 141; 190pp; English.
XX
XX The invention relates to a breast tumour polynucleotide selected from one
XX of the 275 fully defined nucleotide sequences (a) given in the
XX specification, including their complements, sequences consisting of at
XX least 20 contiguous residues of a sequence in (a), sequences that
XX hybridise to a sequence in (a) under moderately stringent conditions,
XX sequences having at least 75% or 90% identity to a sequence in (a), or
XX degenerate variants of a sequence in (a). Also included are an isolated
XX polypeptide (ii) (comprising an amino acid sequence selected from
XX sequences encoded by (a)), sequences having at least 70% or 90% identity
XX to a sequence encoded by (a), sequences of 30 fully defined amino acid
XX sequences (c), and sequences having at least 70% or 90% identity to a
XX sequence in (c), expression vectors comprising (a), a host cell
XX transformed or transfected with the expression vector, an isolated
XX antibody or its antigen-binding fragment that specifically binds to (ii),
XX a method for detecting the presence of a cancer in a patient, a fusion
XX protein comprising at least one polypeptide (ii), an oligonucleotide that
XX hybridises to (a), under moderately stringent conditions, a method for
XX stimulating and/or expanding T cells specific for a tumour protein (by
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CC contacting T cells with at least one component selected from (a), (ii)
CC and antigen-presenting cells that express (ii), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (ii), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour of the tumour
CC is useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a breast cancer specific cDNA of the
CC invention.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTTGAAGTTATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
DB 1 ATGTGCTTGAAGTTATTCATGCGGCTGCTCTTCTGTGAAGACCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 ATGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 ATGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 241 ATGTGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
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DB 301 TGTGCTGTCACCTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 GGAAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 GGAAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 GACAAGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAAGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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DB 601 GTCCTTGAACAACAAAGAGGAGCAGCTGATGATGATGATGATGATGATGATGATG 660
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DB 661 TGTGCTTATGTTGCTGCAAGTGGCACTGATCCAAATATTCAGATGATGATGATG 720
QY 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCT 780
DB 721 ACCACTCTGCACTACGCTATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCT 780

QY 781 TATGTGCTGATATGGAATCAAAAACAAGCATGGCTTCACACCACTGTTAGTGGTGA 840
DB 781 TATGTGCTGATATGGAATCAAAAACAAGCATGGCTTCACACCACTGTTAGTGGTGA 840
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DB 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGATATTTGCAAGTATCTTCTGATC 1080
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DB 1141 CTGATATGAGAGAGAGTCAAAAAGTTCAAAAGCAAGAAATTAAGCAGCAGAGAA 1200
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DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
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DB 1681 ACTGCTGAGAGAGAGAGAGTGAATTTTCTTCAAGAGAGAGAGAGAGAGAGAG 1740
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DB 1741 CAGCAATTTCTGAGAGAGAGAGAGTGAATTTTCAAGAGAGAGAGAGAGAGAGAG 1800
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DB 1801 AAGCAATTTTGAAG 1860

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 DB 1981 GAGCTAGACACATGAAACATGACAGCCGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
 RESULT 12
 ADCL5355
 ID ADCL5355 standard; DNA; 2040 BP.
 AC ADCL5355;
 DT 18-DEC-2003 (first entry)
 DE Human breast tumour protein DNA, SEQ ID 303.
 KW Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
 OS de.
 XX Homo sapiens.
 OS WO2003013431-A2.
 PN 20-FEB-2003.
 PD 05-AUG-2002; 2002WO-US024917.
 PF 07-AUG-2001; 2001US-00924400.
 PR 20-FEB-2002; 2002US-00079137.
 PR 02-AUG-2002; 2002US-00212679.
 XX (CORI-) CORIXA CORP.
 PA Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH,
 PI Kalos MD;
 XX MPI; 2003-342398/32.
 DR New polynucleotide, useful for preparing a composition for diagnosing,
 PT treating or preventing cancer.
 PS Example 1; SEQ ID NO 303; 308bp; English.
 XX The present invention relates to compositions and methods for the therapy
 CC and diagnosis of cancer, particularly breast cancer. The method for
 CC detecting the presence of a cancer in a patient comprises: obtaining a
 CC biological sample from the patient; contacting the biological sample with
 CC a binding agent that binds to the polypeptide; detecting in the sample an
 CC amount of the polypeptide that binds to the binding agent; and comparing
 CC the amount of the polypeptide to a predetermined cut-off value. Treating
 CC breast cancer comprises administering a composition comprising breast
 CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
 CC specific for the tumour protein. The present sequence was used to
 CC illustrate the invention.
 SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2040; DB 10; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
 DB 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
 QY 61 AGAGAGCAATGAGGCAAGTGTGCTGCGTTCCTGCTGCTGAGGAGCGGCAAG 120

DB 61 AGAGAGCAATGAGGCAAGTGTGCTGCGTTCCTGCTGCTGAGGAGCGGCAAG 120
 QY 121 AGCAACGTGGGCACTTTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180
 DB 121 AGCAACGTGGGCACTTTCTGGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAG 180
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 DB 181 ATGGCAATGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
 QY 241 GCGCTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
 DB 241 GCGCTTCTGAGACCAAGCACTCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
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 DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGGCGCTTGG 360
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 DB 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCAGGTACACGTCCGTGGAAGATCTG 420
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 DB 421 GACAAAGCTCCAGAGCTGCGCTGTGGGGTAAGTCCCAAGAAAGATCTCATGCTG 480
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 DB 601 GTCTTGAACAACAAAAGAGGACAGCTGATTAAGCCGTCAATGCGAGGAAGTGA 660
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 DB 721 ACCACTCTGCACTACGCTATCTATATGAAGTAATTAATGCGCAAGCACTGCTTGA 780
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 DB 841 CATGACAAAACAAAGCATGCGTGAATTTTAAATCAAGAAAACGATTTAAATGA 900
 QY 901 CTGATATATATGAAAGCATGCTCTCAATCTTCTGATGTGTGATGACCAAGTATA 960
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Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAACACCTGAAATATGACAAATTT 1380
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Qy 1441 AAACAGATGCCAAATATCTTTCTGAAAAACAGAACCCAGAACCAAGACTTAAAGCTGACA 1500
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Qy 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGACCACTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGACCACTGAAAGC 1740
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Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTGATTCATGAA 1860
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Db 1861 GAAAAACCAATGAAAGTGTGAAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTGATGAAAAATGATGTTGCGGAGAGAAATTTGCCATGTAGACTG 1980
Db 1921 GAAAAAGACATCTGATGAAAAATGATGTTGCGGAGAGAAATTTGCCATGTAGACTG 1980
Qy 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GAGCTAGACACATGAAATCATGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 13
ADBI3825
ID ADBI3825 standard; cDNA; 2040 BP.
XX
XX ADBI3825;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human prostate specific cDNA B305 splice variant #10.
DB
XX
XX Human; ss; prostate specific cDNA; cytosolic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.

XX Homo sapiens.
OS
XX
XX US2003185830-A1.
XX
XX
PD 02-OCT-2003.
PF 12-NOV-2002; 2002US-00294025.
XX
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
PI
XX
XX MPI: 2003-756193/71.
DR
XX
XX P-PsDB; ADBI3830.
DR
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 11; Page; 101pp; English.
PS
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC of value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20030185830.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 10; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGTGGGCAAGTGTCTGCGCTTCCCTGCTGCAAGGAGACGGCAAG 120
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DB 661 TGTGCGTAAATGTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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DB 721 ACCACTCTGCACTACCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTCTTA 780
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Db      1921  GAAAAAGACATCTTGGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGTAAGCTG 1980
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RESULT 15
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AC AAA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cytostatic; vaccine; ss.
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XX
PN WO200004149-A2.
XX
PD 27-JUN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
XX
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XX
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XX
PR 15-JAN-1999; 99US-00232149.
XX
PR 15-JAN-1999; 99US-00232880.
XX
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 223-224; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PRP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express the
CC polypeptides, antibodies against the polypeptides and vaccines comprising
CC them can be used for inhibiting the development of prostate cancer in a
CC patient. The polypeptides can be used to generate antibodies or anti-
CC idiotypic antibodies for passive immuno therapy. A portion of the
CC polynucleotides encoding the polypeptides can be used as a probe or to
CC modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
CC the present invention
XX
SO Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 U; 0 Other;
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Query Match 97.5%; Score 1989; DB 3; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2040	100.0	2040	3	US-09-352-616A-375
3	2040	100.0	2040	3	US-09-289-198-303
4	2040	100.0	2040	3	US-09-636-215-375
5	2040	100.0	2040	3	US-09-685-166A-375
6	2040	100.0	2040	3	US-09-429-755-303
7	2040	100.0	2040	3	US-09-679-426-375
8	2040	100.0	2040	3	US-09-759-143-375
9	2040	100.0	2040	3	US-09-651-236-375
10	2040	100.0	2040	3	US-09-699-295-303
11	2040	100.0	2040	3	US-09-534-825A-303
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ALIGNMENTS

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US-09-439-313-375
; Sequence 375, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaios, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
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Qy 961 GTGAGCTTCTATGAGCAAAAATATGATGTAATCTTCAAGATCTATGAGCAGAG 1020
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Db 1021 GCCAGAGATATGCTGTTTCTAGTCACTCATGTAATTTGCCAGTTACTTCTGACTAC 1080
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Db 1081 AAAAGAAAAACAGATGCTAAATCTCTTGTAAAAACAGCAATTCAGAACTTAAAG 1140
Qy 1141 CTGACATCAGAGAAAGTCAAAAGTTCAAAGGAGGAAATGAGCAAGGAGAA 1200
Db 1141 CTGACATCAGAGAAAGTCAAAAGTTCAAAGGAGGAAATGAGCAAGGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATATATGTGGATTACTGAAAACTGACTAATGTGTCACTGCTGAC 1320
Db 1261 AAGCATGAAGATATATGTGGATTACTGAAAACTGACTAATGTGTCACTGCTGAC 1320

Qy 1321 AATGGTGAATATGATTAATTCCTCAAGGAAGACAGAACCTGAAATGAGCAATTT 1380
Db 1321 AATGGTGAATATGATTAATTCCTCAAGGAAGACAGAACCTGAAATGAGCAATTT 1380
Qy 1381 CCTGACCAAGAAAGTGAAGATATCAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACCAAGAAAGTGAAGATATCAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
Qy 1441 AAGCATATCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAAGCTGACA 1500
Db 1441 AAGCATATCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAAAGTCAAAAGGCTTGAAGGCGGTGAAAAATGGCAGCCAGAGAAAAAGATCT 1560
Db 1501 TCAGAGAAAGTCAAAAGGCTTGAAGGCGGTGAAAAATGGCAGCCAGAGAAAAAGATCT 1560
Qy 1561 CAGAACCAAGAAATTAATAGATGATGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAGAACCAAGAAATTAATAGATGATGATAGAGACTAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAACACGAAAGTACTCATGTCCGATTCGAGAAACCTGACTAATGTGCTC 1680
Db 1621 GAAATGAAGAACACGAAAGTACTCATGTCCGATTCGAGAAACCTGACTAATGTGCTC 1680
Qy 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGGAAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGGAAGAGCAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGATGAGATGATCAAGTGAAGCAAAATGATATCTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATCAAGTGAAGCAAAATGATATCTGAG 1800
Qy 1801 AAGCAATTTGTGAAGAACAGAACCTGGAATATTAACGAGAGATTTCTGATGATA 1860
Db 1801 AAGCAATTTGTGAAGAACAGAACCTGGAATATTAACGAGAGATTTCTGATGATA 1860
Qy 1861 GAAAGCAGATGAGATGATGAAAAATGAAATTTGAGCTTCTCTTAGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAGATGATGAAAAATGAAATTTGAGCTTCTCTTAGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 2
US-09-352-616A-375
; Sequence 375, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Liang, Yuxui
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGGTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGGTGATTCATGCGGCTGCTCTTGTGTGAAGAAGCCATTGGTCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGTCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGTCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGGAGACAGAGACTCTGTATGAAGACATCAGAGACAG 180
DB 121 AGCAAGTGGGCACTTCTGGAGACAGAGACTCTGTATGAAGACATCAGAGACAG 180

QY 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGT 240

QY 241 GGGGCTTCTGGAGACAGAGACTCTGTATGAAGACATCAGAGCAAGATGGGCAAG 300
DB 241 GGGGCTTCTGGAGACAGAGACTCTGTATGAAGACATCAGAGCAAGATGGGCAAG 300

QY 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360

QY 361 GGAGATCAGATGACAGTGTGCTTCAATGAGCCAGGATACAGTCCGTGGAGAGATCTG 420
DB 361 GGAGATCAGATGACAGTGTGCTTCAATGAGCCAGGATACAGTCCGTGGAGAGATCTG 420

QY 421 GACAACTTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAACTTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480

QY 481 CTCAGGAGACATGACCTGAAACAAGAGGCAAGCAAAAGAGGCTCTCATCTGATG 540
DB 481 CTCAGGAGACATGACCTGAAACAAGAGGCAAGCAAAAGAGGCTCTCATCTGATG 540

QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGAGCAGAGATGCACTTAAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGAGCAGAGATGCACTTAAAT 600

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DB 601 GTCTTGAACAACAAAAGAGGACAGCTGTATGAAGCGGTACATGCGAGAAATGAA 660

QY 661 TGTGCGTTAATGTTGTGGAACATGGCACTGATCCAAATATTCGAATGATGTGAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGGCACTGATCCAAATATTCGAATGATGTGAAT 720

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DB 721 ACCACTGTGCACTACGCTATCTATATGAAGATTAATTAAGSCAAAGCACTGCTTAA 780

QY 781 TATGTGTGATATTCGAATCAAAAAACAGCATGGCTCACACATGTTACTTGTGTGA 840
DB 781 TATGTGTGATATTCGAATCAAAAAACAGCATGGCTCACACATGTTACTTGTGTGA 840

QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGGAATTTAAATGCA 900

QY 901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTGTATGTTGTGTGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGAGCTGCTCATCTGCTGTATGTTGTGTGATCAGCAAGTATA 960

QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020

QY 1021 GCCAGAGATATGCTGTTTCTATCATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080

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DB 1081 AAAAGAAAAACAGATGCTAAATAATCTTCTGTAAAAACAGCAATTCAGAACAGACTTAAAG 1140

QY 1141 CTGACATCAGAGGAAAGTCACAAAAGTTCAAAAGGATGAAATATGCCAGCCAGGAAA 1200
DB 1141 CTGACATCAGAGGAAAGTCACAAAAGTTCAAAAGGATGAAATATGCCAGCCAGGAAA 1200

QY 1201 ATGTCTCAAGAACCAAGAAATTAATAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATATGTTGGATTAATCTAGAAAACCTGACTAATGTTGTCACTGTGCG 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTAATCTAGAAAACCTGACTAATGTTGTCACTGTGCG 1320

QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACCTGAAAAATCAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGAGCAACCTGAAAAATCAGCAATTT 1380

QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTAGTTCTGACTTCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTTAGTTCTGACTTCAAAAGAA 1440

QY 1441 AAACGATGCCAAATATCTTCTGTAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
DB 1441 AAACGATGCCAAATATCTTCTGTAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500

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DB 1501 TCAAGGAAAGATCACAAAGCTTGAAGGCACTGAAAAATGGCCAGCAGAGAAAGATCT 1560

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DB 1561 CAAGAACCAAGAAATTAATAAGATGTGTAGAGAGCTGAAATTTTATGCTATCGAA 1620

QY 1621 GAAATGAAGAACCAAGAGATCTCATATGCGAATTTCCAGAAAACTGTAAATGTTGCTGAC 1680
DB 1621 GAAATGAAGAACCAAGAGATCTCATATGCGAATTTCCAGAAAACTGTAAATGTTGCTGAC 1680

QY 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAAGC 1740
DB 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAAGC 1740

QY 1741 CAGCAATTTCCGACACCTGAGAAATGAAGATATCAAGTGAAGAACTAAATGATCTACG 1800
DB 1741 CAGCAATTTCCGACACCTGAGAAATGAAGATATCAAGTGAAGAACTAAATGATCTACG 1800

QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCAGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCAGAA 1860

QY 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGTAAAGAA 1920
DB 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGTAAAGAA 1920

QY 1921 GAAAAAGCATCTGATGATGAAAAATGATGCTTGGGGAAGAAATTCAGATCTGAACATG 1980
DB 1921 GAAAAAGCATCTGATGATGAAAAATGATGCTTGGGGAAGAAATTCAGATCTGAACATG 1980

QY 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 3
US-09-289-198-303
; Sequence 303, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US 09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: PaeSeo for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGTGTGAGTGGATTCATGCGCGCTCTTCTGTGAAGAGCCATTGGTCTC 60
1 ATGGTGTGAGTGGATTCATGCGCGCTCTTCTGTGAAGAGCCATTGGTCTC 60
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181 ATGGGCAAGTGTGCGGCACTGCTCCCTGCTGAGAGGAGAGTGGCAAGCACTG 240
181 ATGGGCAAGTGTGCGGCACTGCTCCCTGCTGAGAGGAGAGTGGCAAGCACTG 240
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361 GGAAGATTAAGTGAAGTGTGCTGAGAGCCAGTACCGTCCGTGGAAGATCTG 420
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1201 ATGTCTCAAGAACAGAAATTAATGAAGTGTATGAGAGGTTGAAGAAATGAAAG 1260
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1261 AAGCATGAAGTAAATATGTTGGAATTAATGAAGAACTGAACTAAATGCTGTC 1320
1321 AATGTTGAATATGATTAATCTCTCAAGAGAGAGACAGAACCTGAAATCAGCAATT 1380
1321 AATGTTGAATATGATTAATCTCTCAAGAGAGAGACAGAACCTGAAATCAGCAATT 1380
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1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAAGTGGCAGCAGAGAAAGATCT 1560
1501 TCAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAAGTGGCAGCAGAGAAAGATCT 1560
1561 CAAGAACAGAAATTAAGATGATGATAGAGCTTGAAGAAATTTATGGCTATCGAA 1620
1561 CAAGAACAGAAATTAAGATGATGATAGAGCTTGAAGAAATTTATGGCTATCGAA 1620
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1621 GAAATGAAGAGAGAGAGTACTATGTCGATTTCCAGAAAACCTGACTAATGCTGTC 1680
1681 ACTGCTGGCAATGATGATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAAGC 1740

Db	1681	ACTGTGCGAATGGTATGATGATTAATTTCTCCAGAGAAACACAGAACCTGGAAGC	1740
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Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAGAACGATAGAAAGTGGTGAAGAAAAATGAATTCGTGACTTTCTCTAGTTGTGAAGAA	1920
Db	1861	GAAGAACGATAGAAAGTGGTGAAGAAAAATGAATTCGTGACTTTCTCTAGTTGTGAAGAA	1920
Qy	1921	GAAGAAAGCATCTTGCATGAATAATAGTACGTTGCGGAGAAAGAAATTCGCATCTAAGCTG	1980
Db	1921	GAAGAAAGCATCTTGCATGAATAATAGTACGTTGCGGAGAAAGAAATTCGCATCTAAGCTG	1980
Qy	1981	GAGCTAGACAAATGAACAATCAGAGCGCACTTAAAAAATAAAAAATAAAAAATAAAAA	2040
Db	1981	GAGCTAGACAAATGAACAATCAGAGCGCACTTAAAAAATAAAAAATAAAAAATAAAAA	2040

RESULT 4

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US-09-636-215-375
? Sequence 375, Application US/09636215
? Patent No. 6620922
? GENERAL INFORMATION:
? APPLICANT: Xu, Jiangchun
? APPLICANT: Dillon, Davin C.
? APPLICANT: Mitcham, Jennifer L.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Jiang, Yugu
? APPLICANT: Henderson, Robert A.
? APPLICANT: Kalos, Michael D.
? APPLICANT: Fanger, Gary R.
? APPLICANT: Retter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darrick
? APPLICANT: Li, Samuel
? APPLICANT: Wang, Aijun
? APPLICANT: Skeiky, Yasir A. W.
? APPLICANT: Hepler, William
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? FILE REFERENCE: 210121.42717C17
? CURRENT APPLICATION NUMBER: US/09/636,215
? CURRENT FILING DATE: 2000-08-10
? NUMBER OF SEQ ID NOS: 852
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 375
? LENGTH: 2040
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-636-215-375

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Query Match	Similarity	Score 2040;	DB 3;	Length 2040;
Best Local	Similarity	100.0%;	Pred. No. 0;	Mismatches 0;
Matched 2040;	Conservative	0;	Indels 0;	Gaps 0;
Qy	1	ATGGTGGTTGAGTTGATTCATGCGCGCTCCTCTTCTGTGAAGAACCATTTGCTCTC	60	
Db	1	ATGGTGGTTGAGTTGATTCATGCGCGCTCCTCTTCTGTGAAGAACCATTTGCTCTC	60	
Qy	61	AGGAGCAAGATGGGCGAAGTGTGTCGCCGCTTCCCTCCTCAGGAGAAAGGGCGAAG	120	
Db	61	AGGAGCAAGATGGGCGAAGTGTGTCGCCGCTTCCCTCCTCAGGAGAAAGGGCGAAG	120	
Qy	121	AGCAACGTGGCACTTCTGAGAACCAAGCAACTCTGTATGAAGACACTCAGAGCGAAG	180	

Db	121	AGCAACGTGGCACTTCTTGAGACCAAGACACTCTGCTATGAAGACACTCAGAGCAAG	180
OY	181	ATGGGCAAGTGGTCCCGCACTGCTTCCCTCTGTGCAAGGGGAGTGGCAAGCAACGTG	240
Db	181	ATGGGCAAGTGGTCCCGCACTGCTTCCCTGTGCAAGGGGAGTGGCAAGCAACGTG	240
OY	241	GGCGCTTGGAGACCAAGACGACTCTGTCTATGAAGACACTCAGGAACAGATGGGCAAG	300
Db	241	GGCGCTTGGAGACCAAGACGACTCTGTCTATGAAGACACTCAGGAACAGATGGGCAAG	300
OY	301	TGGGTGGCCACTGCTTCCCTGTGCAAGGGGGAGCGGCAAGACAGTGGGGCGTTGG	360
Db	301	TGGGTGGCCACTGCTTCCCTGTGCAAGGGGGAGCGGCAAGACAGTGGGGCGTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGCCAGGTATCAAGTCCGTGGAGAAATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGGAGCGCCAGGTATCAAGTCCGTGGAGAAATCTG	420
OY	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAAGATCTCATGCTCATG	480
Db	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAAGATCTCATGCTCATG	480
OY	481	CTCAGGGACACTGACCTGTGACAAAGAGACAAAGAAAGAGACTGCTCTACATCTGCGC	540
Db	481	CTCAGGGACACTGACCTGTGACAAAGAGACAAAGAAAGAGACTGCTCTACATCTGCGC	540
OY	541	TCTGCGCAATGGGAATTCAGAGTGTGTAATACTCTGCTGACAGACGATGCACCTTAT	600
Db	541	TCTGCGCAATGGGAATTCAGAGTGTGTAATACTCTGCTGACAGACGATGCACCTTAT	600
OY	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGCAGAAAGATGA	660
Db	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGCAGAAAGATGA	660
OY	661	TGTGCGTAAATGTTGCTGTGAACAATGSGACTGTATCCAAATATCCAGATGAGATGAAAT	720
Db	661	TGTGCGTAAATGTTGCTGTGAACAATGSGACTGTATCCAAATATCCAGATGAGATGAAAT	720
OY	721	ACCACTGTGACCTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
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OY	781	TATGGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGTGA	840
Db	781	TATGGTGTGATATCGAATCAAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGTGA	840
OY	841	CATGACCAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATGACCAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGGACTGCTCTCAATCTTGTATGTTGTGATGTCGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCAATCTTGTATGTTGTGATGTCGCAAGTATA	960
OY	961	GTCAGCCCTTCACTTGGAGCAAAATATGATATCTTCTCAAGATCTATCTGGACAGAGCG	1020
Db	961	GTCAGCCCTTCACTTGGAGCAAAATATGATATCTTCTCAAGATCTATCTGGACAGAGCG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAATCATCATCTAATTTGGCCAGTTACTTTCTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAATCATCATCTAATTTGGCCAGTTACTTTCTGACATAC	1080
OY	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAAAGACTTAAG	1140
OY	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAGGCACTGAAAATAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCACAAAAGTTCAAGGCACTGAAAATAGCCAGAGAA	1200
OY	1201	ATGTTCTCAGAACCAAGAAATTAATAGATGTGTATAGAGGTTGAAGAAATGAG	1260
Db	1201	ATGTTCTCAGAACCAAGAAATTAATAGATGTGTATAGAGGTTGAAGAAATGAG	1260

QY 1261 AAGCATGAAAGTATATGTTGGGATTACTAGAAAACTGACTAATGGTGTCACTGCTGCG 1320
DB 1261 AAGCATGAAAGTATATGTTGGGATTACTAGAAAACTGACTAATGGTGTCACTGCTGCG 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACCTGAAATATGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAACACCTGAAATATGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGTATCAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGTATCAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAAAGAGCAACCCAGAACCAAGCTTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTCTGAAAAAGAGCAACCCAGAACCAAGCTTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGAGTCACAAAAGGCTTGAAGGCAAGTGAATATGGCCAGAGAAAGATCT 1560
DB 1501 TCAGAGAAAGAGTCACAAAAGGCTTGAAGGCAAGTGAATATGGCCAGAGAAAGATCT 1560
QY 1561 CAAGAAACCAAGAAATTAATAGATGGTATAGAGAGTCAAGAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAAACCAAGAAATTAATAGATGGTATAGAGAGTCAAGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAGAGTACTCATGTCCGATTCCTGAGAAAACTGACTAATGGTGC 1680
DB 1621 GAAATGAAGAGCAGGAGAGTACTCATGTCCGATTCCTGAGAAAACTGACTAATGGTGC 1680
QY 1681 ACTGTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTCTGACCTGAGAGATGAAAGTATCAAGAGAGAGAGCAACCAATGATCTCAG 1800
DB 1741 CAGCAATTTCTCTGACCTGAGAGATGAAAGTATCAAGAGAGAGAGCAACCAATGATCTCAG 1800
QY 1801 AAGCAATTTTCTGAGAGAGAGAGCACTGGAATTTACAGATGAGATTTGATTTCTGAA 1860
DB 1801 AAGCAATTTTCTGAGAGAGAGAGCACTGGAATTTACAGATGAGATTTGATTTCTGAA 1860
QY 1861 GAAAGCAGATGAGAGTGTGTAATAATGAAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
DB 1861 GAAAGCAGATGAGAGTGTGTAATAATGAAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
QY 1921 GAAAGAGATCTTGTGATGAAATTAATGATGCTTGGGAGAGAAATTCCTGCTAAGATCTG 1980
DB 1921 GAAAGAGATCTTGTGATGAAATTAATGATGCTTGGGAGAGAAATTCCTGCTAAGATCTG 1980
QY 1981 GAGCTAGACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 2040
DB 1981 GAGCTAGACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 2040

RESULT 5
US-09-685-166A-375
Sequence 375, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Herlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685.166A
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-685-166A-375
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGTGTTGAGGTTGATTCATGCGGCTGCTTCTGAGAAAGCATTTGGTCTC 60
DB 1 AATGTGTTGAGGTTGATTCATGCGGCTGCTTCTGAGAAAGCATTTGGTCTC 60
QY 61 AGAGCAAGATGGCAAGTGTGCTGCGTTGCTTCCCTGCTGCAAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGCAAGTGTGCTGCGTTGCTTCCCTGCTGCAAGAGCGGCAAG 120
QY 121 AGCAACGTGGCACTTTGTGAGACCAAGAGCACTGCTATGAGAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGCACTTTGTGAGACCAAGAGCACTGCTATGAGAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAG 240
QY 241 GGGCTTCTGAGACCAAGAGCACTGCTATGAGAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GGGCTTCTGAGACCAAGAGCACTGCTATGAGAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGCTAGAGAGAGAGCTTCAATGAGAGCCAGATACAGCTGCTGAGAGATCTG 420
DB 361 GGAAGCTAGAGAGAGAGCTTCAATGAGAGCCAGATACAGCTGCTGAGAGATCTG 420
QY 421 GACAAGCTTCAAGAGAGCTGCTGAGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
DB 421 GACAAGCTTCAAGAGAGCTGCTGAGAGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGAGACTGAGCTGAAAGAGAGCAAGAGCAAGAGAGAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGAGACTGAGCTGAAAGAGAGCAAGAGCAAGAGAGAGCTGCTTACATCTGGCC 540
QY 541 TTTGCAATGAGAAATTCAGAAATTAATGATGCTTGGAGAGAGAGTCAATCTAT 600
DB 541 TTTGCAATGAGAAATTCAGAAATTAATGATGCTTGGAGAGAGAGTCAATCTAT 600
QY 601 GTCTTGAACAAG 660
DB 601 GTCTTGAACAAG 660
QY 661 TGTGCTTAATGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TGTGCTTAATGTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 ACCACTGCACTAGAGCTATCTATATGAGAGTAAATTAATGAGAGAGAGAGAGAG 780
DB 721 ACCACTGCACTAGAGCTATCTATATGAGAGTAAATTAATGAGAGAGAGAGAGAG 780
QY 781 TATGCTGATGATGAAATCAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

Db 781 TATGCTGATATGCAATCAAAAACAGCATGGCTCAACCACTGTTACTTGGTGA 840
Qy 841 CATGACAAAAACAGCAAGTCTGAAAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACAAAAACAGCAAGTCTGAAAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATGATATGAGAGAGCTGCTCATCTTGTCTGATGTTGTGTGATCAGCAATATTA 960
Db 901 CTGATGATATGAGAGAGCTGCTCATCTTGTCTGATGTTGTGTGATCAGCAATATTA 960
Qy 961 GTGAGCTTCTAATTGAGCAAAATATTTGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTAATTGAGCAAAATATTTGATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATGCTGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATGCTGCTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACCTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACCTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAATAGCCAGAGAGAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTTGATTAATCAAGAACTTAATGCTGCTGCTGCTG 1320
Db 1261 AAGCATGAAGATTAATATGTTGATTAATCAAGAACTTAATGCTGCTGCTGCTGCTG 1320
Qy 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACTTAATGCTGCTGCTG 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACTTAATGCTGCTGCTGCTG 1380
Qy 1381 CCTGACAAAGAGTGAAGATTAATCAAGAACTTAATGCTGCTGCTGCTGCTGCTG 1440
Db 1381 CCTGACAAAGAGTGAAGATTAATCAAGAACTTAATGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1441 AAAACAGATCCCAAAATCTCTTCTGAAAACAGCAATCCAGAACCTTAATGCTGCTG 1500
Db 1441 AAAACAGATCCCAAAATCTCTTCTGAAAACAGCAATCCAGAACCTTAATGCTGCTGCTG 1500
Qy 1501 TCAGAGAGAGAGTCACAAAGCTTGAAGGAGTGAAGAAATGGCCAGAGAGAGAGAGT 1560
Db 1501 TCAGAGAGAGAGTCACAAAGCTTGAAGGAGTGAAGAAATGGCCAGAGAGAGAGAGT 1560
Qy 1561 CAAGAACCAAGAAATTAAGATGCTGATAGAGCTGAGAAATTTATGCTGCTGCTG 1620
Db 1561 CAAGAACCAAGAAATTAAGATGCTGATAGAGCTGAGAAATTTATGCTGCTGCTGCTG 1620
Qy 1621 GAAATGAAGAGAGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 GAAATGAAGAGAGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1681 ACTGCTGAGAGAGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 ACTGCTGAGAGAGAGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1741 CAGCAATTTCTGCACTGAGATGAAGATTAATCAAGTGAAGAGAGAGAGAGAGTGA 1800
Db 1741 CAGCAATTTCTGCACTGAGATGAAGATTAATCAAGTGAAGAGAGAGAGAGTGAAGTGA 1800
Qy 1801 AAGCAATTTTGTGAAGAGAGAGAGTGAAGATTAATCAAGTGAAGAGAGAGAGTGAAG 1860
Db 1801 AAGCAATTTTGTGAAGAGAGAGAGTGAAGATTAATCAAGTGAAGAGAGAGAGTGAAG 1860
Qy 1861 GAAAGAGAGATGAAG 1920
Db 1861 GAAAGAGAGATGAAG 1920

Db 1861 GAAAGAGAGATGAAG 1920
Qy 1921 GAAAGAGAGATGAAG 1980
Db 1921 GAAAGAGAGATGAAG 1980
Qy 1981 GAGCTGAG 2040
Db 1981 GAGCTGAG 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John W.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGAGTGAATTCATGCGCGCTGCTCTTCTGTAAGAGAGAGAGAGAGAG 60
Db 1 ATGCTGTTGAGAGTGAATTCATGCGCGCTGCTCTTCTGTAAGAGAGAGAGAGAGAG 60
Qy 61 AG 120
Db 61 AG 120
Qy 121 AG 180
Db 121 AG 180
Qy 181 ATGAG 240
Db 181 ATGAG 240
Qy 241 GCGGCTTCTGAG 300
Db 241 GCGGCTTCTGAG 300
Qy 301 TGGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TGGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 361 GAG 420
Db 361 GAG 420
Qy 421 GAG 480
Db 421 GAG 480
Qy 481 CTCAG 540
Db 481 CTCAG 540

Db	481	CTCAGGAGACCTGAGGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTCAGAGTGAATAAATCTCTGCTGACACAGATGCACTTAAAT	600
Db	541	TCTGCCAATGGGAATTCAGAGTGAATAAATCTCTGCTGACACAGATGCACTTAAAT	600
OY	601	GTCCCTTGACAAACAAAAGAGGAGCAGTCTGATPAAAGGCGGTCAATGCCAGGAAGATGA	660
OY	601	GTCCCTTGACAAACAAAAGAGGAGCAGTCTGATPAAAGGCGGTCAATGCCAGGAAGATGA	660
Db	661	TGTGCGTTAATGTTGCTGAGACATGACCTGATCCAAATATTTCCAGATGAGTATGAAAT	720
Db	661	TGTGCGTTAATGTTGCTGAGACATGACCTGATCCAAATATTTCCAGATGAGTATGAAAT	720
OY	721	ACCACTCTGCACCTAGGCTTCTATATGAAGTAAATTAATGCCCAGAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACCTAGGCTTCTATATGAAGTAAATTAATGCCCAGAGCACTGCTCTTA	780
OY	781	TATGTCGTGATATGGAATCAAAAAACAAGATGGCTCACACACTGTTACTTGCTGTA	840
Db	781	TATGTCGTGATATGGAATCAAAAAACAAGATGGCTCACACACTGTTACTTGCTGTA	840
OY	841	CATGAGCAAAAAACAGCAATCGTGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGA	900
Db	841	CATGAGCAAAAAACAGCAATCGTGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGA	900
OY	901	CTGGATAGATATGAAAGACTGCTCTCATACTTCTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGAAAGACTGCTCTCATACTTCTGTATGTTGTGATCAGCAAGTATA	960
OY	961	GTACACCTTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTTAATCGACAGAG	1020
Db	961	GTACACCTTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTTAATCGACAGAG	1020
OY	1021	GCCAGAGAGTATGCTGTTTCTAGTATCATATGTAATTTGCGAGTTACITTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAGTATCATATGTAATTTGCGAGTTACITTTCTGACTAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
OY	1141	CTGAATATCAGAGGAAGTCACAAAAGTTCAAAAGCATGGAATAATGCCACAGAGAAA	1200
Db	1141	CTGAATATCAGAGGAAGTCACAAAAGTTCAAAAGCATGGAATAATGCCACAGAGAAA	1200
OY	1201	ATGTCCTCAAGAACCAAAATTAATTAAGATGATGATAGAGAGTTGAAGAAGAAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCAAAATTAATTAAGATGATGATAGAGAGTTGAAGAAGAAATGAAG	1260
OY	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAATGTGTCTCACTGTGAC	1320
Db	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAATGTGTCTCACTGTGAC	1320
OY	1321	AATGTTGATTAATGATTAATTTCTCTCAAAAGGAAGAGACAACCTGAATAATCAGCAATTT	1380
Db	1321	AATGTTGATTAATGATTAATTTCTCTCAAAAGGAAGAGACAACCTGAATAATCAGCAATTT	1380
OY	1381	CCTGACAACGAAGGAAGATATCACAGAAATTTGGGAAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAACGAAGGAAGATATCACAGAAATTTGGGAAATTAAGTTTCTGACTACAAAGAA	1440
OY	1441	AAACGATGCCCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
OY	1501	TCAGAGGAAGTCACAAAAGCTTGAGGCGACTGAATAATGGCCAGCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAGTCACAAAAGCTTGAGGCGACTGAATAATGGCCAGCAGAGAAAAAGATCT	1560
OY	1561	CAAGAACCAAGAAATTAATTAAGATGCTGATAGAGCTAGAAAATTTTATGTGCTATCGAA	1620
Db	1561	CAAGAACCAAGAAATTAATTAAGATGCTGATAGAGCTAGAAAATTTTATGTGCTATCGAA	1620

[illegible]

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RESULT 7
US-09-679-426-375
; Sequence 375, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Hatlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yassir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-375

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	Query Match	Score 2040;	DB 3;	Length 2040;
	Best Local Similarity	100.0%;	Pred. No. 0;	
	Matches 2040;	Conservative 0;	Mismatches 0;	Gaps 0;
Oy	1	ATGATGTTGAGGTGATTCATCCGCGCTCTTCTGTGAAGAAGCATTTGCTC	60	
Db	1	ATGATGTTGAGGTGATTCATCCGCGCTCTTCTGTGAAGAAGCATTTGCTC	60	


```
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGGAAGCAAGCACTCTGTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240
QY 241 GGGCTTTCTGAGACCAAGCACTCTGTATGAAACACTCAGAAACAAGATGGGCAAG 300
DB 241 GGGCTTTCTGAGACCAAGCACTCTGTATGAAACACTCAGAAACAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGTGG 360
QY 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACCAAGTCCGTGGAGAGT 420
DB 361 GGAAGCTACGATGACAGTGCCTTCAATGAGCCCAAGTACCAAGTCCGTGGAGAGT 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGCACTGACGTGAAACAAGAGACCAAGCAAAAGAGAGCTGCTTCAATCTG 540
DB 481 CTCAGGAGCACTGACGTGAAACAAGAGACCAAGCAAAAGAGAGCTGCTTCAATCTG 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTGGACAGAGATGTCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAATCTCTGTGGACAGAGATGTCAACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGAGCAGCTGTGATTAAGCCGTACAAATTCAGAGATGAA 660
DB 601 GTCTTTGACAAACAAAAGAGAGCAGCTGTGATTAAGCCGTACAAATTCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGGAAT 720
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QY 721 ACCACTGCACTACGCTATCTATATGAAAGTAAATTAATGCCAAGCACTGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAAAGTAAATTAATGCCAAGCACTGCTCTTA 780
QY 781 TATGTGCTGATATGAAATCAAAAACAAAGCTGCGCTCACACCTGTTACTTGGTGT 840
DB 781 TATGTGCTGATATGAAATCAAAAACAAAGCTGCGCTCACACCTGTTACTTGGTGT 840
QY 841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAATGCA 900
DB 841 CATGACAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAATGCA 900
QY 901 CTGATATGATATGAAAGAGCTGCTCATCTACTGCTGATGTGGATGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAAGAGCTGCTCATCTACTGCTGATGTGGATGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTTCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGTTCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATAGCTGTTTCTAGCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATAGCTGTTTCTAGCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
QY 1141 CTGACATCAGAGGAAGATCACAAGGTTCAAAAGGATGAAATATGCCACAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGATCACAAGGTTCAAAAGGATGAAATATGCCACAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGGATGGTGAATGAGAGTTGAAAGAAATGAA 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGGATGGTGAATGAGAGTTGAAAGAAATGAA 1260
QY 1261 AAGCATGAAAGTAATATGTGGAAATTAATAGAAAACTGTACTTAATGTGTCTGCTG 1320
DB 1261 AAGCATGAAAGTAATATGTGGAAATTAATAGAAAACTGTACTTAATGTGTCTGCTG 1320
QY 1321 AATGTGATATGATTAATTTCTTCAAGAAAGAGAGAGCACTGTAATATGACAAATTT 1380
DB 1321 AATGTGATATGATTAATTTCTTCAAGAAAGAGAGAGCACTGTAATATGACAAATTT 1380
QY 1381 CCTGACCAAGGAAGGAGAGATATCAAGAAATTTGCGAATTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACCAAGGAAGGAGAGATATCAAGAAATTTGCGAATTTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGACTTAATAGCTGACA 1500
DB 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGACTTAATAGCTGACA 1500
QY 1501 TCAAGAGAAAGTCACAAAAGCTTGAAGGCACTGAAATATGCGCAGAGAGAAAGATTT 1560
DB 1501 TCAAGAGAAAGTCACAAAAGCTTGAAGGCACTGAAATATGCGCAGAGAGAAAGATTT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGATGATAGAGCTAGAAATTTTAATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGATGATAGAGCTAGAAATTTTAATGCTATCGAA 1620
QY 1621 GAAATGAAAGACAGAAAGTACTCATGTGCGATTTCCAGAAAACTGCTAATGATGTC 1680
DB 1621 GAAATGAAAGACAGAAAGTACTCATGTGCGATTTCCAGAAAACTGCTAATGATGTC 1680
QY 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGAGAACACTGTAAGC 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATTTCTTCAAGAGAGAGAGAACACTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAAGTGAAGCAAAATGATACTCG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAAGTGAAGCAAAATGATACTCG 1800
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QY 1801 AAGCAATTTTGTGAAGACAGACACTGGAATATTAACAAGATTCATGATTCATGAA 1860
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Db 1801 AAGCAATTTTGTGAAGACAGACACTGGAATATTAACAAGATTCATGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGTTGAAAAAATGAAATTCCTGAGCTTTCTTTAGTTGTAAGAA 1920
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Db 1861 GAAAGCAGATAGAGTGTGTTGAAAAAATGAAATTCCTGAGCTTTCTTTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATAGTACCTTGGGGGAAAGAAATTCGCTTAAGACTG 1980
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Db 1921 GAAAAAGACATCTTGATGAAAAATAGTACCTTGGGGGAAAGAAATTCGCTTAAGACTG 1980
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Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

RESULT 9
US-09-651-236-375
/ Sequence 375, Application US/09651236
/ Patent No. 6818751
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqun
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.42718C18
/ CURRENT APPLICATION NUMBER: US/09/651,236
/ CURRENT FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 865
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-651-236-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCAATTTGTCTC 60
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Db 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGACCAATTTGTCTC 60
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Db 61 AGAGAGAAATGGGCAAGTGTGCTGCTGCTTCCCTGCGGAGGAGAGCGGCAAG 120
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Db 121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGCTATGAAACACTCAGAGCAAG 180
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Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
QY 241 GCGGCTTTGAGACCAAGCACTGCTATGAAACACTCAGAGCAAGAGTGGGCAAG 300
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Db 421 GACAAAGCTCCAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATCTGCTAG 480
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Db 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCAAAATTTCCAGATGAGTGAAT 720
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Db 721 ACCACTCTGCACTAGGCTATCTAATATGAAGTAATTAATGSCCAAGCACTGCTTA 780
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Db 1261 AAGCATGAAAGTAATATGTTGGGATTTCTAGAAAACTGACTAATGTTCTCACTGTGGC 1320
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Db 1321 AATGGATTAATGATTAATTTCTCAAGGAAGAGCAAGCACTGAAATCAGCAATTT 1380
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Db	1321	AAATGGTATTAATGGATTAAATTCCTCAAGAAAGACAGACAACTGAAATATCAGCAATTT	1380
Oy	1381	CCTGACAAACGAAAGTGAAGAGTATCAACGAATTTGCGAATTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAAGTGAAGAGTATCAACGAATTTGCGAATTAGTTTCTGACTACAAAGAA	1440
Oy	1441	AAACGATATGCACAAATATCTTCTTGAAACAGCAACCCAGAACAAAGACTTAAGGTGACA	1500
Db	1441	AAACGATATGCACAAATATCTTCTTGAAACAGCAACCCAGAACAAAGACTTAAGGTGACA	1500
Oy	1501	TCAGAGAAAGTCAACAAAGCTTGAGGGCAGTGAATAATGCGCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGAAAGTCAACAAAGCTTGAGGGCAGTGAATAATGCGCAGCCAGAGAAAAGATCT	1560
Oy	1561	CAAGAACACAGAAATTAATTAAGGATGAGATAGAGGCTAAGAAATTTTATGAGCTATCGAA	1620
Db	1561	CAAGAACACAGAAATTAATTAAGGATGAGATAGAGGCTAAGAAATTTTATGAGCTATCGAA	1620
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Db	1621	GAAATGAAAGAACACGGAAGTACTCATGTGCGAATTCGCCAGAAAACCTGACTAATAGTGCC	1680
Oy	1681	ACTGCTGGCAATGCTGATGATGGAATTAATTCCTCCAGGAAGAGCAGAACACTGAAAGC	1740
Db	1681	ACTGCTGGCAATGCTGATGATGGAATTAATTCCTCCAGGAAGAGCAGAACACTGAAAGC	1740
Oy	1741	CAGCAATTTTCCGACACTGAGAAATGAAGATATCACTGTGACGAACAAAATGATACTCGAG	1800
Db	1741	CAGCAATTTTCCGACACTGAGAAATGAAGATATCACTGTGACGAACAAAATGATACTCGAG	1800
Oy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGATTTCTGATTCATGAA	1860
Oy	1861	GAAAAAGCAGATAGAAAGTGTTGAAAAAATGAAATCTGAGCTTTCTCTTAGTTGTAAGAA	1920
Db	1861	GAAAAAGCAGATAGAAAGTGTTGAAAAAATGAAATCTGAGCTTTCTCTTAGTTGTAAGAA	1920
Oy	1921	GA AAAAGACATCTTGACATGA AAATAGTACGTTGCGGAAAGAAATTTGCCATGCTAAGCTG	1980
Db	1921	GA AAAAGACATCTTGACATGA AAATAGTACGTTGCGGAAAGAAATTTGCCATGCTAAGCTG	1980
Oy	1981	GAGCTAGACAAATGAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACAAATGAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040

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RESULT 10
US-09-699-295-303
Sequence 303: Application US/0969295
Patent No. 6828431
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Devin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 21021.419C10
CURRENT APPLICATION NUMBER: US/09/699,295
CURRENT FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 336
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-699-295-303

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Query Match	100.0%	Score 2040;	DB 3;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	1	ATGTGTGGTGAAGTGAATTCATCCGGCTGCCTCTTGTGGAAAGAACCATTTGGTCTC	60
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Db	61	AGAGCAAGATGGGCAGAGTGTGCTGCCGTGTCTTCCCCTGCTGACGGAGAGCGGCAG	120
OY	121	AGCAACGTGGGCATTCTGTGGAGACCAAGAGACTCTGTATGAAGACACTGAGAGCAAG	180
Db	121	AGCAACGTGGGCATTCTGTGGAGACCAAGAGACTCTGTATGAAGACACTGAGAGCAAG	180
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Db	181	ATGGGCAAGTGGTCCCGCACTGCTTCCCCTGCTGACGGGGAGGTGGCAAGCAACGTG	240
OY	241	GGCGCTTCTGGAGACACAGACGACTCTGTATGAAGACACTGAGAACCAAGATGGCAAG	300
Db	241	GGCGCTTCTGGAGACACAGACGACTCTGTATGAAGACACTGAGAACCAAGATGGCAAG	300
OY	301	TGGTGCTGCACCTGCTTCCCCTGCTGACGGGGAGCGGCAGACAGTGGGGCTTGG	360
Db	301	TGGTGCTGCACCTGCTTCCCCTGCTGACGGGGAGCGGCAGACAGTGGGGCTTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGATACCAAGTCCGTGAGAAAGTCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGATACCAAGTCCGTGAGAAAGTCTG	420
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Db	421	GACAACTCCACAGAGCTGCTGGTGGGGTAAATCCCGAGAAAGAGATCTATGTCATG	480
OY	481	CTCAGGGGACACTGACGTGAACAAAGAGGACAAAGGAGAGAGACTGCTCATCTGACC	540
Db	481	CTCAGGGGACACTGACGTGAACAAAGAGGAGCAAGCAAGAAAGAGAGCTGCTCATCTGACC	540
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Db	541	TCTGCCAATGGGAATTCAGAAAGTAAAACTCCTGCTGACAGACGATGTCAACTTAAT	600
OY	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTATAAAGCCGTACATGTCAGAGAGATGAA	660
Db	601	GTCCTTGACAACAAAAAGAGACAGCTCTGTATAAAGCCGTACATGTCAGAGAGATGAA	660
OY	661	TGTGCGTTAATGTTGCTGGAACTATGGCACTATCCAAATATTCAGATGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACTATGGCACTATCCAAATATTCAGATGATGGAAT	720
OY	721	ACCACTGTGACCTACGCTATCTATATGAGATAAATTAATGGCCAAAGCACTGCTTAA	780
Db	721	ACCACTGTGACCTACGCTATCTATATGAGATAAATTAATGGCCAAAGCACTGCTTAA	780
OY	781	TATGTGTGTATATTCGAATCAAAAAACAAGATGGCTCAACCACTGTATCTTGGTGT	840
Db	781	TATGTGTGTATATTCGAATCAAAAAACAAGATGGCTGTACCACTGTATCTTGGTGT	840
OY	841	CATAGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
Db	841	CATAGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA	900
OY	901	CTGATAGATATGGAAGACTGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA	960
Db	901	CTGATAGATATGGAAGACTGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA	960
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Db	961	GTCAGCCTTCTACTTGGACAAAATATGATATCTTCTCAAGATCTATCTGGACAGCG	1020

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1261 AAGCATGAAAGTAAATATGTTGGGATTACTAGAAAACCTGACTAATGTTCTGCTGGC 1320
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1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAAAACCTGAAATACGCAATTT 1380
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1621 GAAATGAGAGAGCAAGAGATCTCATGTCGATTCGCAAAAACTGACTAATGTTGCTG 1680
1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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1861 GAAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
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1921 GAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1981 GAGCTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
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RESULT 11
US-09-534-825A-303
; Sequence 303, Application us/09534825A
; Patent No. 6861506

GENERAL INFORMATION:
APPLICANT: Fruedakis, Tony N.
APPLICANT: Smith, John W.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534,825A
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-534-825A-303
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCAATTTGCTTC 60
61 AGGACAGAGATGAGGAGAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
61 AGGACAGAGATGAGGAGAGTGTGCTGCGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
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121 ACCTGCTGAGGCACTTCTGAGAGCAAGCAAGCACTGCTGATGAGCACTGAGAGCAAG 180
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Db 781 TATGCTGCGATATATGAATCAAAAACAGCATGCGCTACACCACTGTATCTTGATGTA 840
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Db 1021 GCCAGAGATATGCTGTTCTATGATCATCATATGTAATTTGCGAGTTACTTTCTGACTAC 1080
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Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTTAAG 1140
Qy 1141 CTGACATCGAGAGAGAGTCACAAAAGTTCAAAGGACAGTAAATAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCGAGAGAGAGTCACAAAAGTTCAAAGGACAGTAAATAGCCAGCAGAGAAA 1200
Qy 1201 ATGCTCAAGAAACAGAAATATAAGATGATGATGAGAGAGTGAAGAAATGAG 1260
Db 1201 ATGCTCAAGAAACAGAAATATAAGATGATGATGAGAGAGTGAAGAAATGAG 1260
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Qy 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAGTTATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGCAACAGAAAGTGAAGATATCAAGAAATTTGCGAGTTATGTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGAACTTAAAGCTGACA 1500
Db 1441 AAACGATGCAAAATATCTTCTGAAAAACAGCAACCCAGAACAGAACTTAAAGCTGACA 1500
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Db 1501 TCAGAGGAAAGATGATCAAAAGGCTTGAAGGCACTGAAAAATGCGCAGCAAGAAAGATCT 1560
Qy 1561 CAAGAACCCAGAAATATAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 CAAGAACCCAGAAATATAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 GAAATGAAGAGACGGAAGTACTATGTCGATTCGAGAAACCTGACTAATGATGTC 1680
Db 1621 GAAATGAAGAGACGGAAGTACTATGTCGATTCGAGAAACCTGACTAATGATGTC 1680
Qy 1681 ACTGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 1681 ACTGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
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Db 1741 CAGCAATTTCTGACACTGAGAAATGAGAGTATCAAGTGAAGAACTTAATGATGATGATGATG 1800
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RESULT 12
US-09-657-279-375
/ Sequence 375, Application US/09657279
/ Patent No. 6894146
GENERAL INFORMATION:
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqun
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedrick, Thomas S.
/ APPLICANT: Carter, Darick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C19
/ CURRENT APPLICATION NUMBER: US/09/657.279
/ CURRENT FILING DATE: 2000-09-06
/ NUMBER OF SEQ ID NOS: 877
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO: 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-657-279-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGATCTC 60
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Db 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTGTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240
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Qy 241 GCGGCTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGAAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACAGACGACTCTGCTATGAAAGCACTCAGAGAAAGATGGGCAAG 300

QY 301 TGGGCTGACCACTGCTTCCCTGCTGCAAGGGGGAGGGCAAGAGAGGTGGGGCTTGG 360
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Db 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGGGGAGGGCAAGAGAGGTGGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTTCATGAGCCCGAGTACCACTGCTGGAGAGATCTG 420
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Db 361 GGAGACTACGATGACAGTGGCTTTCATGAGCCCGAGTACCACTGCTGGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATCTCATG 480
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Db 481 CTGAGGGGACATGACGCGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db 841 CATGAG 900
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Db 901 CTGAGATGATATGAT 960
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Db 1081 AAAG 1140
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Db 1141 CTGACATCAG 1200
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Db 1501 TCAGAGAGAGATCAAG 1560
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QY 1921 GAAAG 1980
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QY 1981 GAGCTGAG 2040
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RESULT 13
US-10-012-896-375
; Sequence 375, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchell, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kaios, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hedler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassole, Carlota
; APPLICANT: Roy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro

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APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61 AGGAGCAATATGGGCAAGTGTGTCTGCTTCCCTGCTGTGAGAGGCGGCAAG 120
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QY      241 GGGCGCTTCTGAGAGCAACCAAGCACTCTGTATGAAACATCTGAGAGCAAGTGTG
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QY      301 TGGTGTGCGCACTGCTTCCCTGTGTGAGGAGGAGGAGCAAGGAGTGTGCGCTTGG
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DB      361 GGAAGACTAGATGACAGTGTCTTCTGTGAGGAGGAGGAGGAGTACAGTGTGAGAGAGTCTG
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DB      421 GACAACTCCACAGAGCTGTGTGTGTGAGTAAAGTCTCCAGAAAGAGTCTCATGTCTATG
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DB      481 CTGAGGAGCACTGACGTGAAACAAGAGCAAGCAAAAGAGAGCTGTCTACATCTGGGC
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RESULT 15
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; Sequence 374, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuxi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-374

Query Match      76.0%; Score 1551; DB 3; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTGTGCGGCTGCTCTTCTGTGAAGAGCCAGGCAAG 120
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 21:07:27 : Search time 1660.28 Seconds
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Title: US-09-924-400-303

Perfect score: 2040
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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 9793542 seqs, 413469305 residues

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10: /cgn2_6/prodata/1/pubpna/US10G_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2040	100.0	2040	3	US-09-825-301-7 Sequence 7, App11
2	2040	100.0	2040	3	US-09-759-143-375 Sequence 375, App
3	2040	100.0	2040	3	US-09-780-669-375 Sequence 375, App
4	2040	100.0	2040	3	US-09-810-936-303 Sequence 303, App
5	2040	100.0	2040	3	US-09-822-827-375 Sequence 375, App
6	2040	100.0	2040	3	US-09-429-755-303 Sequence 303, App
7	2040	100.0	2040	3	US-09-924-400-303 Sequence 303, App
8	2040	100.0	2040	3	US-09-895-793-375 Sequence 375, App
9	2040	100.0	2040	3	US-09-895-814-375 Sequence 375, App
10	2040	100.0	2040	5	US-10-012-896-375 Sequence 375, App
11	2040	100.0	2040	5	US-10-010-940-375 Sequence 375, App
12	2040	100.0	2040	6	US-10-212-679-303 Sequence 303, App
13	2040	100.0	2040	6	US-10-144-678A-375 Sequence 375, App
14	2040	100.0	2040	6	US-10-033-527-7 Sequence 7, App11
15	2040	100.0	2040	7	US-10-294-025-375 Sequence 375, App
16	2040	100.0	2040	6	US-10-079-137B-303 Sequence 303, App
17	1551	76.0	2000	3	US-09-825-301-6 Sequence 6, App11
18	1551	76.0	2000	3	US-09-759-143-374 Sequence 374, App
19	1551	76.0	2000	3	US-09-780-669-374 Sequence 374, App
20	1551	76.0	2000	3	US-09-810-936-302 Sequence 302, App
21	1551	76.0	2000	3	US-09-822-827-374 Sequence 374, App
22	1551	76.0	2000	3	US-09-429-755-302 Sequence 302, App
23	1551	76.0	2000	3	US-09-924-400-302 Sequence 302, App

24	1551	76.0	2000	3	US-09-895-793-374 Sequence 374, App
25	1551	76.0	2000	3	US-09-895-814-374 Sequence 374, App
26	1551	76.0	2000	5	US-10-012-896-374 Sequence 374, App
27	1551	76.0	2000	5	US-10-010-940-374 Sequence 374, App
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29	1551	76.0	2000	6	US-10-144-678A-374 Sequence 374, App
30	1551	76.0	2000	6	US-10-033-527-6 Sequence 6, App11
31	1551	76.0	2000	6	US-10-294-025-374 Sequence 374, App
32	1551	76.0	2000	7	US-10-079-137B-302 Sequence 302, App
33	1128	55.3	1155	3	US-09-825-301-5 Sequence 5, App11
34	1128	55.3	1155	3	US-09-759-143-373 Sequence 373, App
35	1128	55.3	1155	3	US-09-780-669-373 Sequence 373, App
36	1128	55.3	1155	3	US-09-810-936-301 Sequence 301, App
37	1128	55.3	1155	3	US-09-822-827-373 Sequence 373, App
38	1128	55.3	1155	3	US-09-429-755-301 Sequence 301, App
39	1128	55.3	1155	3	US-09-924-400-301 Sequence 301, App
40	1128	55.3	1155	3	US-09-895-793-373 Sequence 373, App
41	1128	55.3	1155	3	US-09-895-814-373 Sequence 373, App
42	1128	55.3	1155	5	US-10-012-896-373 Sequence 373, App
43	1128	55.3	1155	5	US-10-010-940-373 Sequence 373, App
44	1128	55.3	1155	6	US-10-212-679-301 Sequence 301, App
45	1128	55.3	1155	6	US-10-144-678A-373 Sequence 373, App

ALIGNMENTS

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RESULT 1
US-09-825-301-7
: Sequence 7, Application US/09825301
: Patent No. US20020809738A1
: GENERAL INFORMATION:
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Dillon, David C.
: APPLICANT: Molese, David A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Zehentner, Barbara
: APPLICANT: Pershing, David H.
: TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
: FILE REFERENCE: 210121.513
: CURRENT APPLICATION NUMBER: US/09/825,301
: CURRENT FILING DATE: 2001-04-02
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-825-301-7

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best local similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTTCATTCATCGCGGCTCTTCTGTGAAGACATTGGTCTC 60
    |||
DB 1 ATGGTGGTGAAGTTCATTCATCGCGGCTCTTCTGTGAAGACATTGGTCTC 60
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QY 61 AGAGCAATATGGGCAAGTGTGCTCCCTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
    |||
DB 61 AGAGCAATATGGGCAAGTGTGCTCCCTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
    |||

QY 121 ACCAAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGACACTGAGAGCAAG 180
    |||
DB 121 ACCAAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGACACTGAGAGCAAG 180
    |||

QY 181 ATGGGCAATGTGTCCGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGACGTC 240
    |||
DB 181 ATGGGCAATGTGTCCGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGACGTC 240
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QY 241 GGGGCTTGGAGACGACGACGACTCTGTATGAAGACACTGAGAAAGTGGCAAG 300
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DB 241 GGGGCTTGGAGACGACGACGACTCTGTATGAAGACACTGAGAAAGTGGCAAG 300
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Db 241 GCGGCTTTGGAGACCAAGCACTCTGTATGAGACA CTCAGAACAAATGGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGGTGGGCGCTTG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGGTGGGCGCTTG 360
Qy 361 GAGACTACGATGACAGTGTCTTCATGAGAGCCAGGTACCACTGCTGAGAGAGATCTG 420
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Qy 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGACAG 480
Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGACAG 480
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Db 661 TGTGCTTAATGTTGCTGGAACAATGGAATTCATCAATATTCAGATGATGAGAAAT 720
Qy 721 ACCACTCTGCACTACCTATCTAATTAAGAAATTAATGAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTACCTATCTAATTAAGAAATTAATGAGCACTGCTCTTA 780
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Db 841 CATGACCAAAAACAGCAAGCTGTGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
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Db 901 CTGATAGATATGGAAGAGCTGCTCATATCTGCTGATGTTGTTGAGATCAGCAATATA 960
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Db 1261 AAGCATGAAGATTAATATGAGATTACTAGAAAACCTGACTAATGCTGCTGAGC 1320
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Db 1321 AATGATGAATATGATTAATTTCTCAAGAGAGAGAGAACCTGATAAATCAGCAATTT 1380

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Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCCAAAATACCTTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
Db 1441 AAAAGATGCCAAAATACCTTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
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Db 1501 TCAGAGAAAGATGCAAAAAGCTTGAAGGCAATGAAAATGGCCAGCAGAGAAAGATCT 1560
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Db 1561 CAAGAACCAAGAAATTAAGATGATGATAGAGCTAGAAATTTTAATGCTATCGAA 1620
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Db 1621 GAATGAAGAGACAGAAAGTACTATGTCGAGATTCAGAAAACCTGACTAATGATGTC 1680
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Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCCAGAGAGAGAGCAAAATGATCTCAG 1740
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Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATCAAGTACAGAACCAAAATGATCTCAG 1800
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Db 1981 GAGCTAGACACATGAGAACATGAGAGCAGCTTAAATTTTAAATTTTAAATTTTAAAT 2040

RESULT 2
US-09-759-143-375
Sequence 375, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaeli A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 21021.427C3
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1981  GAGCTAGACACAAATGAAACATCAGAGCCAGCTGTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2041

RESULT 3
US-09-780-669-375
; Sequence 375, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguí
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepier, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780, 669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGTGTGTTGAGTGGATTTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGTGTC 60
DB      1  ATGTGTGTTGAGTGGATTTCATGCGGCTGCTCTTCTGTGAAGAAGCCATTGTGTC 60

QY      61  AGAGCAAGATGGGAGCAAGTGTGTCGCGTTCCTCCCTGTGCAAGGAGAGCGGCAAG 120
DB      61  AGAGCAAGATGGGAGCAAGTGTGTCGCGTTCCTCCCTGTGCAAGGAGAGCGGCAAG 120

QY      121  AGCAACGTGGGCACTTTCTGAGACACGACGACTCTGTGTTATGAAGACCTCAGAGCAAG 180
DB      121  AGCAACGTGGGCACTTTCTGAGACACGACGACTCTGTGTTATGAAGACCTCAGAGCAAG 180

QY      181  ATGGGCAAGTGGTGGCGGCACTGCTCCCTCTGTGCAAGGGGAGTGGCAAGCAAGTGG 240
DB      181  ATGGGCAAGTGGTGGCGGCACTGCTCCCTCTGTGCAAGGGGAGTGGCAAGCAAGTGG 240

QY      241  GGGCGTTCTGAGAGACGACGACCTCTGTATGAAGACCTCAGAGCAAGTGGGCAAG 300
DB      241  GGGCGTTCTGAGAGACGACGACCTCTGTATGAAGACCTCAGAGCAAGTGGGCAAG 300

QY      301  TGTGTCTGCCACTGCTTCCCTCTGTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360
DB      301  TGTGTCTGCCACTGCTTCCCTCTGTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG 360

QY      361  GGAGACTACATGATGACATGTCCTTCAATGAGAGCCAGAGTACACAGTCCGTGAGAGAGATTGG 420
DB      361  GGAGACTACATGATGACATGTCCTTCAATGAGAGCCAGAGTACACAGTCCGTGAGAGAGATTGG 420

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QY	481	CTCAGAGGACACTGACAGTGAACAAAGAGGACAAAGAAAGAGACTGCTCTACATCTGGCC	540
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QY	541	TCTGCCAATGGGAATTCAAGAGTAGTAAACTCTGCTGGACAGACGATGTCACTTAAT	600
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QY	661	TGTGCGTAAATGTTGCTGGAACTATGSCACTGATCCAAATATTCACAGTAGTAGTGAAT	720
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QY	841	CATGAGCAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGATAGATATGGAAGACTGCTCTCATCTTGTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGATAGATATGGAAGACTGCTCTCATCTTGTGTATGTTGTGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATTTGATGTAATCTTCAAGATCTATCTGACAGAG	1020
QY	1021	GCCAGAGAGTAGTCTGTTCTAGTCATCATCTGTAATTTGCGAGTTACTTCTGCACTAC	1080
Db	1021	GCCAGAGAGTAGTCTGTTCTAGTCATCATCTGTAATTTGCGAGTTACTTCTGCACTAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACCAAGCTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACCAAGCTTAAAG	1140
QY	1141	CTGACATCAGAGAAAGACTCACAAAGGTTCAAAAGCAGTGAATAATGCCACCAAGAA	1200
Db	1141	CTGACATCAGAGAAAGACTCACAAAGGTTCAAAAGCAGTGAATAATGCCACCAAGAA	1200
QY	1201	ATGTTCTCAAGAACCGAATTAATTAAGATGTTGATAGAGAGTTGAAAGAAATGAAG	1260
Db	1201	ATGTTCTCAAGAACCGAATTAATTAAGATGTTGATAGAGAGTTGAAAGAAATGAAG	1260
QY	1261	AAGCATGAAGTAATATGTTGGATTACTAGAAAACTGACTAATGTTGTCACTGCTGGC	1320
Db	1261	AAGCATGAAGTAATATGTTGGATTACTAGAAAACTGACTAATGTTGTCACTGCTGGC	1320
QY	1321	AATGTTGATTAATGATTATTTCTTCAAGAGGACAGAACACCTGAAATATCAGCAATTT	1380
Db	1321	AATGTTGATTAATGATTATTTCTTCAAGAGGACAGAACACCTGAAATATCAGCAATTT	1380
QY	1381	CCTGACACAGAAAGTAGAGAGATACACGAATTTGCGAATTAATGTTCTGATCAAAAGAA	1440
Db	1381	CCTGACACAGAAAGTAGAGAGATACACGAATTTGCGAATTAATGTTCTGATCAAAAGAA	1440
QY	1441	AAACAGATGCAAAATATCTTTCTGAAAAACAGCAACCAAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCAAAATATCTTTCTGAAAAACAGCAACCAAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAGAGTCACAAAAGCTTGAAGGCGAGTGAATAATGGCCAGCCAGAAAAAGATCT	1560

Db 1501 TCAGAGAGAGATGCAAAAGGCTTGAGGGAGATGAAATATGGCCAGGAGAAAGATCT 1560
Qy 1561 CAGAAACAGAAATAAATAAGATGATAGAGAGCTAGAAAATTTATAGGCTATCGAA 1620
Db 1561 CAGAAACAGAAATAAATAAGATGATAGAGAGCTAGAAAATTTATAGGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACGGAATACTCATGTGGATTTCCAGAAAACCTGACTAATGGTGCC 1680
Db 1621 GAAATGAAGAGACGGAATACTCATGTGGATTTCCAGAAAACCTGACTAATGGTGCC 1680
Qy 1681 ACTGTGGCAATGGTATGATGATTAATTCCTCCAGAGAGAGAGAACCTGAAAGC 1740
Db 1681 ACTGTGGCAATGGTATGATGATTAATTCCTCCAGAGAGAGAGAACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCACAGTACGAAACAAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCACAGTACGAAACAAAATGATCTCAG 1800
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Db 1801 AAGCAATTTGTGAAGAGAGAACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
Qy 1861 GAAAGAGAGATAGAGGTGTGAAAAATGAATTTGAGCTTCTCTAGTTGTAAGAA 1920
Db 1861 GAAAGAGAGATAGAGGTGTGAAAAATGAATTTGAGCTTCTCTAGTTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTGATGAAAAATAGTACCTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGAAAAATAGTACCTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Qy 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTGACACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 4
US-09-810-936-303
; Sequence 303, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Ajjun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AGAGCAAGATGGGCAAGTGTCTGCTTCCCTGCTGAGGAGAGCGGAG 120

Db 61 AGAGCAAGATGGGCAAGTGTGTCTGCTTCCCTGCTGAGGAGAGCGGAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGAGACAGACACTCTGTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGACAGACACTCTGTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGACAGT 240
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Db 241 GGGCTTCTGAGAGACAGACACTGCTGTATGAAAGCACTCAGAAACAAGTGGCAAG 300
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Qy 361 GGAAGCTACGATGACAGTGCCTTATGAGAGCCAGGTACCACTCCGTGAGAGATCTG 420
Db 361 GGAAGCTACGATGACAGTGCCTTATGAGAGCCAGGTACCACTCCGTGAGAGATCTG 420
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Db 781 TATGTGCTGATATGCAATCAAAAAAAGAGCATGCTGACCACTGTTACTTGGTGA 840
Qy 841 CATGACAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAACGAATTTAATGCA 900
Db 841 CATGACAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAACGAATTTAATGCA 900
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Db 901 CTGGATAGATATGGAAGAGCTGCTCATTACTTGTGTAATGTTGTGATCAGCAATGA 960
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Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
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Db 1021 GCCAGAGATATGCTTTCTAGTCAATCAATGATTTGSCAGTTACTTCTGACTAC 1080
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Db 1081 AAGAAAAACAGATGCTAAATCTCTTGAAGACAGCAATCAGCAAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGGAAGTCAAAAGTTCAAAGGAGTGAATGACCAAGCCAGAGAA 1200

Db 1141 CTGACATCAGAGGAGAGTCAACAAGTTCAAAAGCATGAAATATGCCACGACAGAGAA 1200
QY 1201 ATGTCTCAAGAACCCAGAAATTAATAGATGTGATAGAGGTTGAGAGAAATGAG 1260
Db 1201 ATGTCTCAAGAACCCAGAAATTAATAGATGTGATAGAGGTTGAGAGAAATGAG 1260
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Db 1261 AAGCATGAAAGTAAATATGTGGATTATAGAAAACCTGACTTAATGTGTCACTGTGC 1320
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QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db 1621 GAAATGAGAGAGACGGAAGTACTCATGTCCGAAATTCAGAAACCTGACTAATGTGTC 1680
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Db 1921 GAAAAAGACATCTGATGATAAATAGTACGTTGCGGAGAAATGGCAATGCTAAGACTG 1980
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Db 1981 GAGCTAGACACATGAATCATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAAATG 2040

RESULT 5
US-09-822-827-375

/ Sequence 375, Application US/09822827

/ Patent No. US20020816801

/ GENERAL INFORMATION:

/ APPLICANT: Xu, Jiangchun

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

/ FILE REFERENCE: 210121.534C1

/ CURRENT APPLICATION NUMBER: US/09/822, 827

/ NUMBER OF SEQ ID NOS: 982

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 375

/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-822-827-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTTGATTTCCATGCCGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
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QY 721 ACCACTCTGCACTAGCTATCTAATGAAGTAAATTAATGAGCCAAAGCACTGCTTTA 780
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Db 781 TATGTGCTGATATGAAATCAAAAACAGAGTGTGCTGCAAGCACTGTTACTTGGTGA 840
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Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAATCAAGAAAAAGCAATTTAATGCA 900
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Db 901 CTGATATGATGAGAGAGTGTCTCATCTTGTGCTGATGTGTGATCAGCAAGTATA 960

QY 961 GTGAGCTTCTACTGAGCAAAATATGTATCTTCTCAAGATCTATCGACAGACG 1020
DB 961 GTGAGCTTCTACTTACTGAGCAAAATATGTATCTTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGATATGCTCTTCTTCTAGTCTATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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DB 1081 AAAAGAAAACAGATGCTAAATAATCTCTCTGAAAACAGCAATCAGAACAGACTTAAG 1140
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DB 1141 CTGACATCAGAGAGAGATCACAAGGTTCAAGAGAGTAAATATGCCAGCAGAGAAA 1200
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DB 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGTTGAAGAGATGAAG 1260
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DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAACCTGAAATCAGCAATT 1380
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DB 1501 TCAGAGAGAGATCACAAGGCTTGAGGAGAGTAAATGAGCAGAGAGAGAGAGATCT 1560
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DB 1741 CAGCAATTTCTGACATGAGATGAAGATATCAAGTGAAGAGAGAGAGAGAGAGAGAG 1800
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DB 1861 GAAAGAGATGAAGATGATGATGATTAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
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RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGTGTTGATGAGTGAATTCATGCGGCTGCTCTTGTGAAGAGCAATTTGGTCTC 60
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DB 241 GGGCGTTTGTGAGAGACCAAGCACTCTGCTATGAAGACATCAGAGCAAGATGGCAAG 300
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DB 601 GTCTTGAACAATAAG 660
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Db      721  ACCACTCTGCACTAGGCTATCTTAATGAAATTAATTAATGCGCAAGCACTGCTCTTA 780
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Qy      841  CATGAGCAAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
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Db      1561  CAAGAACCAGAAATTAATAGATGCTGATAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy      1621  GAAATGAAGAGACGGAAGTACTCATGTGCGAATTTCCAGAAAACTGATGATGCTGC 1680
Db      1621  GAAATGAAGAGACGGAAGTACTCATGTGCGAATTTCCAGAAAACTGATGATGCTGC 1680
Qy      1681  ACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGCAACCTGAAAC 1740
Db      1681  ACTGCTGGCAATGCTGATGATTAATTTCTCCAGAGAAAGCAACCTGAAAC 1740
Qy      1741  CAGCAATTTCTGACATGAGATGAAAGTATCAAGTACGAACAAATGATACTGAG 1800

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Db      1741  CAGCAATTTCTGCACTGAGATGAGATATCAAGTACAGAACAAATGATACTGAG 1800
Qy      1801  AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGATTTCTGATTAAG 1860
Db      1801  AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGATTTCTGATTAAG 1860
Qy      1861  GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTAAGAA 1920
Db      1861  GAAAAAGCATATGAAAGTGTGAAAAATGAAATTTGAGCTTTCTTTAGTTGTAAGAA 1920
Qy      1921  GAAAAAGCATTTGTCATGAAATATGATGTCGGGAGAAATTTGCAATGCTAAGACTG 1980
Db      1921  GAAAAAGCATTTGTCATGAAATATGATGTCGGGAGAAATTTGCAATGCTAAGACTG 1980
Qy      1981  GAGCTTAGACACAAATGAAATCATGAGCCAGCTTAAAAATTTTAAAAATTTTAAAA 2040
Db      1981  GAGCTTAGACACAAATGAAATCATGAGCCAGCTTAAAAATTTTAAAAATTTTAAAA 2040

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RESULT 7
US-09-924-400-303
; Sequence 303, Application US/09924400
; Patent No. US20020165371A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Lynda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-303

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Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGTGTGATGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGCTTC 60
Db      1  ATGGTGTGATGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGCTTC 60
Qy      61  AGAGCAAGATGGGCAAGTGTGCTGCGGTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db      61  AGAGCAAGATGGGCAAGTGTGCTGCGGTTCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy      121  AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGCTATAGAAACCTCAGAGCAAG 180
Db      121  AGCAACGTGGGCACTTCTGAGACCAAGCAAGCTGCTATAGAAACCTCAGAGCAAG 180
Qy      181  ATGGCAAGATGGTGGCCGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTA 240
Db      181  ATGGCAAGATGGTGGCCGCTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGTA 240
Qy      241  GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAAGCACTCAGAAACAAGATGGCAAG 300
Db      241  GCGGCTTCTGAGACCAAGCAAGCTCTGCTATGAAAGCACTCAGAAACAAGATGGCAAG 300

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OY	301	TGAGCTGCACATGCTTCCCTCCGCTGCAGAGGGGAGACGGACAGACAAAGTGGGCGCTTG	360
Db	301	TGATGCTCACTGCTGCTCCCTGCTGCAGGGGGAGCGGAGAGCAAGTGGGCGCTTG	360
OY	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGAGTACCACTGCTCGTGGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGAGTACCACTGCTCGTGGAGAAAGATCTG	420
OY	421	GACAAAGTCCACACAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG	480
Db	421	GACAAAGTCCACACAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGTCATG	480
OY	481	CTCAGGGGACATGAGGTGAACAAGAAAGACAAGCAAAAGAGACGTGCTCATCTGTCATG	540
Db	481	CTCAGGGGACATGAGGTGAACAAGAAAGACAAGCAAAAGAGACGTGCTCATCTGTCATG	540
OY	541	TCTGCGCAATGGGAATTCAGAAAGTAAATACTCCGCTGCGACAGACGATGCACTTAAAT	600
Db	541	TCTGCGCAATGGGAATTCAGAAAGTAAATACTCCGCTGCGACAGACGATGCACTTAAAT	600
OY	601	GTCCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCGCGTACAAATGCGAGGAAGATGA	660
Db	601	GTCCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCGCGTACAAATGCGAGGAAGATGA	660
OY	661	TGTGGCTTAATGTTGCTGGAACAATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
Db	661	TGTGGCTTAATGTTGCTGGAACAATGGCACTGATCCAAATATTCAGATGAGTATGGAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGTAAATTAATGCGCAAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGTAAATTAATGCGCAAAAGCACTGCTCTTA	780
OY	781	TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGT	840
Db	781	TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGT	840
OY	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATATGCA	900
OY	901	CTGATATATATGGAAGAGACTGCTCTCAATCTGCTGATATGTTGGATTCAGCAAGTATA	960
Db	901	CTGATATATATGGAAGAGACTGCTCTCAATCTGCTGATATGTTGGATTCAGCAAGTATA	960
OY	961	GTCAGCCTTCTACTTGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
OY	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTCTTGAAAAACACCAATCCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTTGAAAAACACCAATCCAGAACCAAGACTTAAAG	1140
OY	1141	CTGACATCAGAGAGAGTCACAAAGTTCAAAGGCACTGAAAAATAGCAGCGCAGAGAA	1200
Db	1141	CTGACATCAGAGAGAGTCACAAAGTTCAAAGGCACTGAAAAATAGCAGCGCAGAGAA	1200
OY	1201	ATGTCCTCAAGAACCGAATTAATTAAGATGGTGTATAGAGGTTGAAGAAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCGAATTAATTAAGATGGTGTATAGAGGTTGAAGAAATGAAG	1260
OY	1261	AAGCATGAAGTAAATATGTTGGGATTAATCAAAAACTGACTAATGTTGCTCACTGCTGGC	1320
Db	1261	AAGCATGAAGTAAATATGTTGGGATTAATCAAAAACTGACTAATGTTGCTCACTGCTGGC	1320
OY	1321	AATGCTGATTAATGATTAATTCCTCAAAAGAGACAGACAACCTGAAATATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTAATTCCTCAAAAGAGAGCAGACAACCTGAAATATCAGCAATTT	1380
OY	1381	CCTGACAAAGAAATGAAGATATCACAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440

[illegible]

FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGTAAGAAGCATTTGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGTCGCGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGTCGCGTTCCTCCCTGCTGCAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAAGACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCCGCACTGCTCCCTGCTGAGGGGAGAGTGGCAAGCAACTG 240
DB 181 ATGGGCAATGGTGGCCGCACTGCTCCCTGCTGAGGGGAGAGTGGCAAGCAACTG 240
QY 241 GCGCTTCTGAGAGCAGCAGCACTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GCGCTTCTGAGAGCAGCAGCACTCTGTATGAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGGTGGCGCTTG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGGTGGCGCTTG 360
QY 361 GGAAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACAGTCCGTGGAAGAACTG 420
DB 361 GGAAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACAGTCCGTGGAAGAACTG 420
QY 421 GACAAGCTTCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTG 480
DB 421 GACAAGCTTCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGCTGCTCATATCTGCG 540
DB 481 CTCAGGAGCACTGACGTGAACAAGAAAGCAAGCAAAAGAGCTGCTCATATCTGCG 540
QY 541 TCTGCCAATGGGAATTCAAGATGTAATACTCTGCTGACAGACAGATGTAATTAAT 600
DB 541 TCTGCCAATGGGAATTCAAGATGTAATACTCTGCTGACAGACAGATGTAATTAAT 600
QY 601 GTCTCTGACAAACAAAAGAGACAGCTGTATGAAGCCGTACAATGCGAGAAAGTGA 660
DB 601 GTCTCTGACAAACAAAAGAGACAGCTGTATGAAGCCGTACAATGCGAGAAAGTGA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACCTGCACTACGCTATCTATATGAAGTAAATTAATGCGCAACATGCTCTTA 780
DB 721 ACCACCTGCACTACGCTATCTATATGAAGTAAATTAATGCGCAACATGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAACAAGCATGGCTCAGACACTGTGTAATTGGTGA 840
DB 781 TATGCTGCTGATATCGAATCAAAAACAAGCATGGCTCAGACACTGTGTAATTGGTGA 840
QY 841 CATGACAAAACAGCAAGTCTGGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTCTGGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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DB 841 CATGACAAAACAGCAAGTCTGGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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DB 901 CTGATATATATGGAAGACGTCTCTCATCTTGTGTATGTTGGATACAGCAATTA 960
QY 961 GTCACTCTTCTTATGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGAGACG 1020
DB 961 GTCACTCTTCTTATGAGCAAAAATATGATGATCTTCTCAAGATCTATCTGAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTATGTCATCATCATGTAATTTGCCAGTACTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTATGTCATCATCATGTAATTTGCCAGTACTTCTGATAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTGTGAAAACAGAAATCCGAACAAACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTGTGAAAACAGAAATCCGAACAAACTTAAG 1140
QY 1141 CTGATCATGAGGAAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAA 1200
DB 1141 CTGATCATGAGGAAGAGTCACAAAAGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGCTTGAAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATAGAGCTTGAAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATTAATGTTGGAATTACTGAAAACCTGACCTAATGTTGTCCTGTCG 1320
DB 1261 AAGCATGAAGTAATTAATGTTGGAATTACTGAAAACCTGACCTAATGTTGTCCTGTCG 1320
QY 1321 AATGTTGATTAATGATTAATTCCTCAAGAAAGAGACAGAACACTGAAATACGCAATTT 1380
DB 1321 AATGTTGATTAATGATTAATTCCTCAAGAAAGAGACAGAACACTGAAATACGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGATTTGATTTGATCTTCAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGATTTGATTTGATCTTCAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCAAGAACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCAAGAACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCAAGTGAATAATGGCAGACAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTCACAAAAGCTTGAAGGCAAGTGAATAATGGCAGACAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGTGTGATAGAGCTTGAAGAAATTTTATGCTTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATGAAGTGTGATAGAGCTTGAAGAAATTTTATGCTTATCGAA 1620
QY 1621 GAAATGAAGGAAGCAAGAAATCTCATGTCGGAATCCAGAAACCTGACTTAATGCTGCC 1680
DB 1621 GAAATGAAGGAAGCAAGAAATCTCATGTCGGAATCCAGAAACCTGACTTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGTGATGATGATTAATTCCTCCAGAGGAAGAGACACTGTAAGC 1740
DB 1681 ACTGCTGCAATGTGATGATGATTAATTCCTCCAGAGGAAGAGACACTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATGATCAAGTGAAGAACAAATATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATGATCAAGTGAAGAACAAATATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTAATTAACAGATGAATCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTAATTAACAGATGAATCTGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAGTGGTGAATAATGAATCTGAGCTTCTCTTATGTTGAAGAA 1920
DB 1861 GAAAAGCAGATGAAGTGGTGAATAATGAATCTGAGCTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTTAAGACTG 1980
DB 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTTAAGACTG 1980
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QY 1981 GAGCTAGACACATGAAGACATCAGAGCCAGCTAAAAA 2040
DB 1981 GAGCTAGACACATGAAGACATCAGAGCCAGCTAAAAA 2040

RESULT 9
US-09-895-814-375
Sequence 375, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedavick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carloca
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895.814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-814-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GGAGACTAAGATGACAGTGCCTTCAATGAGCCAGTACCAGTCCGTGGAGAAATCTG 420
DB 361 GGAGACTAAGATGACAGTGCCTTCAATGAGCCAGTACCAGTCCGTGGAGAAATCTG 420

QY 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCATG 480

QY 481 CTCAGGGACATGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGGACATGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540

QY 541 TCTGCCAAATGGAAATTCAGAAATGTAATAATCTCTGTGACAGAGATCACTTAAT 600
DB 541 TCTGCCAAATGGAAATTCAGAAATGTAATAATCTCTGTGACAGAGATCACTTAAT 600

QY 601 GTCCCTGACAAACAAAAGAGAGAGCTGTATTAAGCCGTACAAATGCCAGAAAGATGAA 660
DB 601 GTCCCTGACAAACAAAAGAGAGAGCTGTATTAAGCCGTACAAATGCCAGAAAGATGAA 660

QY 661 TGTGCGTTAATGTTGTGGAACATGACACTGATCCAAATATTCAGATGATATGAAAT 720
DB 661 TGTGCGTTAATGTTGTGGAACATGACACTGATCCAAATATTCAGATGATATGAAAT 720

QY 721 ACCACTCTGACATGACCTATCTAATATGAAGATTAATATGCGCAAGCACTGCTTTA 780
DB 721 ACCACTCTGACATGACCTATCTAATATGAAGATTAATATGCGCAAGCACTGCTTTA 780

QY 781 TATGTCGTATATGCAATCAAAAACAGCATGGCTCACACCTGATCTTGTGATGTA 840
DB 781 TATGTCGTATATGCAATCAAAAACAGCATGGCTCACACCTGATCTTGTGATGTA 840

QY 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGAATTTAAATGCA 900

QY 901 CTGATATGATATGGAAGAGCTGCTCATATCTGCTATATGTTGTGATCAGCAATATA 960
DB 901 CTGATATGATATGGAAGAGCTGCTCATATCTGCTATATGTTGTGATCAGCAATATA 960

QY 961 GTGAGCTTCTAATTGAGCAAAATATGATATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATATCTTCAAGATCTATCTGAGCAGAG 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGATATTTGCGATTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGATATTTGCGATTACTTCTGACTAC 1080

QY 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGCAAGTAAATGCGCAGCAAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGCAAGTAAATGCGCAGCAAGAAA 1200

QY 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATAGAGAGGTTAAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAAGATGATAGAGAGGTTAAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATATGATGAGATTAAGAAAACCTGATATGATGCTGCTGCG 1320
DB 1261 AAGCATGAAAGTAAATATGATGAGATTAAGAAAACCTGATATGATGCTGCTGCG 1320

QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGAACCTGAAATATGCAATTT 1380
DB 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGAACCTGAAATATGCAATTT 1380

QY 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGGAATTTGATTTCTGATCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGGAATTTGATTTCTGATCAAAAGAA 1440

QY 1441 AACAGATGCCAAAATACTCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
DB 1441 AACAGATGCCAAAATACTCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATGACAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAAGAAAAGATCT 1560
DB 1501 TCAGAGAAAGATGACAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAAGAAAAGATCT 1560
QY 1561 CAGAAACAGAAATTAATAAGATGATGATAGAGACTGAAAATTTTATGCTATCGAA 1620
DB 1561 CAGAAACAGAAATTAATAAGATGATGATAGAGACTGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAGAAAGCAAGCAAGTACTCATGTCGATTCGAAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAGAAAGCAAGCAAGTACTCATGTCGATTCGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAAAGAGCAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAAAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACCTGAGAAAGTATCAAGAGTACGAACAAATGATCTCG 1800
DB 1741 CAGCAATTTCTGACACCTGAGAAAGTATCAAGAGTACGAACAAATGATCTCG 1800
QY 1801 AAGCAATTTTGTGAAGAAAGCACTGGAATATTCAGAGTATGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAAAGCACTGGAATATTCAGAGTATGATTCATGAA 1860
QY 1861 GAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCTGATGTTAGAAA 1920
DB 1861 GAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCTGATGTTAGAAA 1920
QY 1921 GAAAAAGATCTGTGATGATAAATAGTACGTCGCGGAGAAATTCGCTGATGTTAGAAA 1980
DB 1921 GAAAAAGATCTGTGATGATAAATAGTACGTCGCGGAGAAATTCGCTGATGTTAGAAA 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 10
US-10-012-896-375
Sequence 375, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basels, Carlot
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27

QY 1441 AACAGATGCCAAAATACTCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
DB 1441 AACAGATGCCAAAATACTCTTCTGAAAAAGCAACCCAGAAACAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATGACAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAAGAAAAGATCT 1560
DB 1501 TCAGAGAAAGATGACAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAAGAAAAGATCT 1560
QY 1561 CAGAAACAGAAATTAATAAGATGATGATAGAGACTGAAAATTTTATGCTATCGAA 1620
DB 1561 CAGAAACAGAAATTAATAAGATGATGATAGAGACTGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAGAAAGCAAGCAAGTACTCATGTCGATTCGAAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAGAAAGCAAGCAAGTACTCATGTCGATTCGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAAAGAGCAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAAAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACCTGAGAAAGTATCAAGAGTACGAACAAATGATCTCG 1800
DB 1741 CAGCAATTTCTGACACCTGAGAAAGTATCAAGAGTACGAACAAATGATCTCG 1800
QY 1801 AAGCAATTTTGTGAAGAAAGCACTGGAATATTCAGAGTATGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAAAGCACTGGAATATTCAGAGTATGATTCATGAA 1860
QY 1861 GAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCTGATGTTAGAAA 1920
DB 1861 GAAAGCAGATGAAAGTGTGAAAAATGAATTCGAGCTTTCTGATGTTAGAAA 1920
QY 1921 GAAAAAGATCTGTGATGATAAATAGTACGTCGCGGAGAAATTCGCTGATGTTAGAAA 1980
DB 1921 GAAAAAGATCTGTGATGATAAATAGTACGTCGCGGAGAAATTCGCTGATGTTAGAAA 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAA 2040

Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
DB 1 ATGCTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGTGGCAAGCAAGCTG 240
QY 241 GCGGCTTCTGAGACCAAGAGCTCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGAGCTCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGCTGCTCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGTGCTGCTCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GAGAGCTAGATGACAGTGTCTTCAATGAGCCAGGTAACAGTCCGTTGAGAGATCTG 420
DB 361 GAGAGCTAGATGACAGTGTCTTCAATGAGCCAGGTAACAGTCCGTTGAGAGATCTG 420
QY 421 GACAGCTTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATG 480
DB 421 GACAGCTTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATG 480
QY 481 CTCAGAGCACTGAGTGAACAAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 540
DB 481 CTCAGAGCACTGAGTGAACAAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGCTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGAGATGCTTAAT 600
QY 601 GTCTTGAACAAAG 660
DB 601 GTCTTGAACAAAG 660
QY 661 TGTGCTTAAATGTTGCTGGAACATGAGCTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCTTAAATGTTGCTGGAACATGAGCTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGCACTAGCTATCTATATGAAAGTAAATTAATGAGCAAGTCTCTTA 780
DB 721 ACCACTGCACTAGCTATCTATATGAAAGTAAATTAATGAGCAAGTCTCTTA 780
QY 781 TATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTTAAATGCA 900
DB 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAGAGCAATTTTAAATGCA 900

QY 901 CTGGATAGATATGGAAGGAGCTGCTCATATCTTCTGTATGTTGATGATCAGCAATATTA 960
 DB 901 CTGGATAGATATGGAAGGAGCTGCTCATATCTTCTGTATGTTGATGATCAGCAATATTA 960
 QY 961 GTTCAGCCTTCTACTTGTAGGCAAAATATTTGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
 DB 961 GTTCAGCCTTCTACTTGTAGGCAAAATATTTGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
 QY 1021 GCCAGAGATGCTGCTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACATAC 1080
 DB 1021 GCCAGAGATGCTGCTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACATAC 1080
 QY 1081 AAGAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB 1081 AAGAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTAAATAGCCAGCAGAGAAA 1200
 DB 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTAAATAGCCAGCAGAGAAA 1200
 QY 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGGTTGAGAGAGAAATGAAG 1260
 DB 1201 ATGCTCTCAAGAACCAAGAAATTAATAGATGCTGATAGAGAGGTTGAGAGAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAATTAATGCGGATTAATGAAAACCTGACTTAATGCTGCTGCTG 1320
 DB 1261 AAGCATGAAAGTAATTAATGCGGATTAATGAAAACCTGACTTAATGCTGCTGCTG 1320
 QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACCTGAAATTCAGCAATTT 1380
 DB 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAACCTGAAATTCAGCAATTT 1380
 QY 1381 CCTGACACGAAAGTGAAGAGATATCAAGAAATTTGGAAATTAATTTCTGACTTCAAAAGAA 1440
 DB 1381 CCTGACACGAAAGTGAAGAGATATCAAGAAATTTGGAAATTAATTTCTGACTTCAAAAGAA 1440
 QY 1441 AAAACGATGCCAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCACTTAAAGCTGAGCA 1500
 DB 1441 AAAACGATGCCAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCACTTAAAGCTGAGCA 1500
 QY 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGAGAAAGATCT 1560
 DB 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGAGAAAGATCT 1560
 QY 1561 CAAGAACCGAAGATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTATGCTATCGAA 1620
 DB 1561 CAAGAACCGAAGATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTATGCTATCGAA 1620
 QY 1621 GAAATGAGAGAGACGGAAGTACTCATGTCGATTCCTCAGAAAACCTGACTAATGCTGCC 1680
 DB 1621 GAAATGAGAGAGACGGAAGTACTCATGTCGATTCCTCAGAAAACCTGACTAATGCTGCC 1680
 QY 1681 ACTGCTGGCAATGCTGATGATGATTAATCTCTCAAGAGAGAGAGAACCACTGGAAGC 1740
 DB 1681 ACTGCTGGCAATGCTGATGATGATTAATCTCTCAAGAGAGAGAGAACCACTGGAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
 DB 1741 CAGCAATTTCTGACACTGAGATGAAGAGATATCAAGTGAAGCAAAATGATATCTGAG 1800
 QY 1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
 DB 1801 AAGCAATTTTGTGAGAGACAGAACACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
 QY 1861 GAAAGACAGATGAGATGCTGAAAAATGAATTCAGCTTTCTGATGTTGATGAGAA 1920
 DB 1861 GAAAGACAGATGAGATGCTGAAAAATGAATTCAGCTTTCTGATGTTGATGAGAA 1920
 QY 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAGAAATTCGATGCTTAAGACTG 1980
 DB 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAGAAATTCGATGCTTAAGACTG 1980

QY 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATAAAAAATAAAAAATAAAAA 2040
 DB 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATAAAAAATAAAAAATAAAAA 2040
 RESULT 11
 US-10-010-940-375
 ; Sequence 375, Application US/10010940
 ; Publication No. US2003008062A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yugu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kaloer, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427D3
 ; CURRENT APPLICATION NUMBER: US/10/010,940
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-010-940-375

Query Match 100.0%; Score 2040; DB 5; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGCTC 60
 DB 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGCTC 60
 QY 61 AGGAGCAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
 DB 61 AGGAGCAAGTGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGAGAGACAGACGACTGCTATGAAGCACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGAGAGACAGACGACTGCTATGAAGCACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
 DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
 QY 241 GCGGCTTCTGAGAGACAGACGACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
 DB 241 GCGGCTTCTGAGAGACAGACGACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
 QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGGCAAGGCGCTTGG 360
 DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGGCAAGGCGCTTGG 360
 QY 361 GGAGACTAGATGAGAGTGCCTTCAATGAGAGCCAGATACCACTCGTGGAGAAATCTG 420
 DB 361 GGAGACTAGATGAGAGTGCCTTCAATGAGAGCCAGATACCACTCGTGGAGAAATCTG 420
 QY 421 GACAAAGCTTCAAGAGCTGCTGCTGGGGTAAAGTCCCGAAGAAAGATCTTACCTG 480
 DB 421 GACAAAGCTTCAAGAGCTGCTGCTGGGGTAAAGTCCCGAAGAAAGATCTTACCTG 480
 QY 481 CTCAGAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
 DB 481 CTCAGAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540


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QY 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGAGACAGATGCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGAGACAGATGCAACTTAAT 600
QY 601 GTCTCTGACACAAAGGAGAGACAGCTGTGATTAAGCCGCTCAATGCCAGGAAGATGA 660
DB 601 GTCTCTGACACAAAGGAGAGACAGCTGTGATTAAGCCGCTCAATGCCAGGAAGATGA 660
QY 661 TGTGGCTTATGTGTGGAACATGGCACTGATCCAAATATCCAGATAGATGGAAT 720
DB 661 TGTGGCTTATGTGTGGAACATGGCACTGATCCAAATATCCAGATAGATGGAAT 720
QY 721 ACCACTCTGACACTACGCTATCTAATAATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTCTGACACTACGCTATCTAATAATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTGTGATATGCAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGTGA 840
DB 781 TATGTGTGATATGCAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGTGA 840
QY 841 CATGAGCAAAAAACAGCAATCGTGAAATTTTATATCAAGAAAAACGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAATCGTGAAATTTTATATCAAGAAAAACGCAATTTAAATGCA 900
QY 901 CTGAGATAGATGGAAGAGACTGCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA 960
DB 901 CTGAGATAGATGGAAGAGACTGCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTAATTGAGCAAAAAATATGATATCTTCTCAAGATCTATCTGAGACAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAAAATATGATATCTTCTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCCAGAGATATGCTCTTCTAGTATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTCTTCTAGTATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
DB 1081 AAGAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTGAATATGACCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGGCAAGTGAATATGACCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCGAAATTAATAGATGTGTGAATGAGAGAGTTGAATAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCGAAATTAATAGATGTGTGAATGAGAGAGTTGAATAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTGGGATTTACTAGAAAACTGACTTAATGTGTCACTGCTGAC 1320
DB 1261 AAGCATGAAGATTAATATGTGGGATTTACTAGAAAACTGACTTAATGTGTGTCACTGCTGAC 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGAGAACACTTGAATAATGACAAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGAGAACACTTGAATAATGACAAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAATTAAGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGGAATTAAGTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
DB 1441 AAAACAGATGCAAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAAAGATCACAAGAGCTTGAAGGCAAGTGAATATGAGCAAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAAAGATCACAAGAGCTTGAAGGCAAGTGAATATGAGCAAGAGAAAGATCT 1560
QY 1561 CAAAGAACCAAGAAATTAATAGATGTGTATAGAGACTGAAAAATTTTATGTGCTATCGAA 1620
DB 1561 CAAAGAACCAAGAAATTAATAGATGTGTATAGAGACTGAAAAATTTTATGTGCTATCGAA 1620

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QY 1621 GAATGAAGAGACAGGAAGTACTCATGTCCGATTTCCAGAAAACTGACTAATGTGTGC 1680
DB 1621 GAATGAAGAGACAGGAAGTACTCATGTCCGATTTCCAGAAAACTGACTAATGTGTGC 1680
QY 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGAGAACACTTGAAGC 1740
DB 1681 ACTGCTGGCAATGTGTATGATGATTAATTTCTCCAGAGAGAGAGAACACTTGAAGC 1740
QY 1741 CAGCAATTTCCGACATCGAGAAATGAAGATATCAAGTGAAGAGAACAAATGATCTCGAG 1800
DB 1741 CAGCAATTTCCGACATCGAGAAATGAAGATATCAAGTGAAGAGAACAAATGATCTCGAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGATTTCTGATTAAGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGATTTCTGATTAAGAA 1860
QY 1861 GAAAAGCAGATGGAAGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTTGAAGAA 1920
DB 1861 GAAAAGCAGATGGAAGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTTGAAGAA 1920
QY 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGAGAAATGGCCATGCTTAAGACTG 1980
DB 1921 GAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGAGAAATGGCCATGCTTAAGACTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 12
US-10-212-679-303
; Sequence 303, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Roy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Peking, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-303

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 GGCGCTTGTGAGACCAAGCACTGCTGATGAAAGCACTGAGAAACAAGTGGCAAG 300
 Db 241 GGCGCTTGTGAGACCAAGCACTGCTGATGAAAGCACTGAGAAACAAGTGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGTGGCGCTGG 360
 Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGAGGCGCAAGAGCAAGTGGCGCTGG 360
 QY 361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCAGGTAACAAGTGGTGAAGATCTG 420
 Db 361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCAGGTAACAAGTGGTGAAGATCTG 420
 QY 421 GACAAGCTCAAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCAATGCAAG 480
 Db 421 GACAAGCTCAAGAGCTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCAATGCAAG 480
 QY 481 CTCAGAGGACATGACCTGAGCAAGAAAGCAAGCAAAAGAGAGTCTCTCAATCTGGCC 540
 Db 481 CTCAGAGGACATGACCTGAGCAAGAAAGCAAGCAAAAGAGAGTCTCTCAATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAGTATGTAATCTCTGCTGAGCAAGAGTGTCAATCTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAGTATGTAATCTCTGCTGAGCAAGAGTGTCAATCTTAAT 600
 QY 601 GTCCCTTGAACAACAAAAGAGAGCAAGCTGATTAAGCCGTAACAAATGCAAGAGATGAA 660
 Db 601 GTCCCTTGAACAACAAAAGAGAGCAAGCTGATTAAGCCGTAACAAATGCAAGAGATGAA 660
 QY 661 TGTGCTTATGTTGTGTGCAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
 Db 661 TGTGCTTATGTTGTGTGCAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTGTGCACTAGCCTATCTAATAAGAGATTAATGAGCAAGCACTGCTCTTA 780
 Db 721 ACCACTGTGCACTAGCCTATCTAATAAGAGATTAATGAGCAAGCACTGCTCTTA 780
 QY 781 TATGTGCTGATATGCAATCAAAACAAAGCATGGCTCAACCACTGTTACTTGGTGA 840
 Db 781 TATGTGCTGATATGCAATCAAAACAAAGCATGGCTCAACCACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
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 Db 901 CTGAGTATGATGAGAGAGCTGCTCTCAATCTTGTGATGTTGTGATCAAGCAATATA 960
 QY 961 GTACGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTTATCTGACAGC 1020
 Db 961 GTACGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTTATCTGACAGC 1020
 QY 1021 GCGAGAGATATGCTGTTCTGATCATCATGTAATTTGCAAGTCTTCTGCTGCTAC 1080
 Db 1021 GCGAGAGATATGCTGTTCTGATCATCATGTAATTTGCAAGTCTTCTGCTGCTAC 1080
 QY 1081 AAAAGAAAAACAGATGCTAAATTTCTTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
 Db 1081 AAAAGAAAAACAGATGCTAAATTTCTTCTGAAAACAGCAATCCAGAACAGCTTAAAG 1140
 QY 1141 CTGACATTCAGAGAGAGTCAACAAAGGTTCAAAAGGCAAGTAAATGCGCAGAGAAA 1200
 Db 1141 CTGACATTCAGAGAGAGTCAACAAAGGTTCAAAAGGCAAGTAAATGCGCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAGAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGAGAGGTTGAGAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATATGATGATGATTAAGAAACCTGACTAATGTGTCACTGTGCG 1320
 Db 1261 AAGCATGAAAGTAAATATGATGATGATTAAGAAACCTGACTAATGTGTCACTGTGCG 1320

QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGCAAAATTT 1380
 Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAATGCAAAATTT 1380
 QY 1381 CCTGACAGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTCAAGAA 1440
 Db 1381 CCTGACAGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGACTCAAGAA 1440
 QY 1441 AAAACAGATCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGTGA 1500
 Db 1441 AAAACAGATCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGTGA 1500
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 Db 1501 TCAGAGAGAGTCAAAAGGCTTGAAGGAGGAGTAAAGGCGAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACAGAAATTAATAGATGATGATAGAGAGCTAGAAATTTATGCTATCGAA 1620
 Db 1561 CAAGAACAGAAATTAATAGATGATGATAGAGAGCTAGAAATTTATGCTATCGAA 1620
 QY 1621 GAAATGAGAGAGCAGAGAGTACTCATGTGGAATTCAGAAAACCTGACTAATGCTGCC 1680
 Db 1621 GAAATGAGAGAGCAGAGAGTACTCATGTGGAATTCAGAAAACCTGACTAATGCTGCC 1680
 QY 1681 ACTGCTGCGAATGATGATGATGATTAATTCCTCAAGAGAGAGCAACCTGAAAGC 1740
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 Db 1801 AAGCAATTTTGAAGAGACAGAACTGGAATATTAACAGATGATGATGATGATGAA 1860
 QY 1861 GAAAAGCAGATGAGAGTGTGTAAGAAATGAAATTTGAGACTTCTTGTGTTAGAAA 1920
 Db 1861 GAAAAGCAGATGAGAGTGTGTAAGAAATGAAATTTGAGACTTCTTGTGTTAGAAA 1920
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 Db 1981 GAGCTAGACACATGAGAAATGATGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2040

RESULT 13
 US-10-144-678A-375
 ; Sequence 375, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darriek
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yashir A. W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.

```
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals Y de Baesols, Carlota
/ APPLICANT: Foy, Teresa M.
/ APPLICANT: Matanabe, Yoshihiro
/ APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144,678A
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FaSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-144-678A-375

Query Match      100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGTGTTGAGGTGATTCATGCCGCTCTTCTGTGAAGACCATTTGCTTC      60
DB      1 ATGGTGTTGAGGTGATTCATGCCGCTCTTCTGTGAAGACCATTTGCTTC      60
QY      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG      120
DB      61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG      120
QY      121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAG      180
DB      121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAG      180
QY      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG      240
DB      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG      240
QY      241 GGGGCTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAGATGGGCAAG      300
DB      241 GGGGCTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAGATGGGCAAG      300
QY      301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGGCGCTTGG      360
DB      301 TGGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGAGTGGGCGCTTGG      360
QY      361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGAGAGATCTG      420
DB      361 GGAAGCTACGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTCCGTGAGAGATCTG      420
QY      421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG      480
DB      421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG      480
QY      481 CTCAGGAGACATGACGCTGACCAAGAGACCAAGCAAAAGAGAGCTCTCTACATCTGGCC      540
DB      481 CTCAGGAGACATGACGCTGACCAAGAGACCAAGCAAAAGAGAGCTCTCTACATCTGGCC      540
QY      541 TCTGCCAATGGGAATTCAGAGATGTAATACTCTGCTGAGACAGAGATGTAATACTTAAT      600
DB      541 TCTGCCAATGGGAATTCAGAGATGTAATACTCTGCTGAGACAGAGATGTAATACTTAAT      600
QY      601 GTCCTTGAACAACAAAGAGAGAGCTGATTAAGCGGTAACTGAGCAAGAGATGTAAG      660
DB      601 GTCCTTGAACAACAAAGAGAGAGCTGATTAAGCGGTAACTGAGCAAGAGATGTAAG      660
QY      661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGGAAT      720
DB      661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGGAAT      720
QY      721 ACCACTCTGCACTACGCTATCTAATAAGATTAATAATGAGCAAGCACTGCTTAA      780
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DB      841 CATGACAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAAATGCA      900
QY      901 CTGATTAATATGGAAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA      960
DB      901 CTGATTAATATGGAAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA      960
QY      961 GTGACCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG      1020
DB      961 GTGACCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG      1020
QY      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC      1080
DB      1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC      1080
QY      1081 AAAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCCAGAACTTAAG      1140
DB      1081 AAAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCCAGAACTTAAG      1140
QY      1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAAAGGAGTAAATAGCCAGCAGAGAAA      1200
DB      1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAAAGGAGTAAATAGCCAGCAGAGAAA      1200
QY      1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAAAG      1260
DB      1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAAAG      1260
QY      1261 AAGCATGAAAGTAAATATGATGATTTACTAGAAAACTGCACTAATGATGCTCTGGC      1320
DB      1261 AAGCATGAAAGTAAATATGATGATTTACTAGAAAACTGCACTAATGATGCTCTGGC      1320
QY      1321 AATGGTAAATATGATTAATCTCAAAAGAAAGACAGAACCTGAAATCAGCAATTT      1380
DB      1321 AATGGTAAATATGATTAATCTCAAAAGAAAGACAGAACCTGAAATCAGCAATTT      1380
QY      1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA      1440
DB      1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA      1440
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DB      1441 AAACGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACTTAAGCTGACA      1500
QY      1501 TCAGAGAAAGATGCAAAAGCTTGAAGGCAATGAAAAATGGCCAGCAGAGAAAAAGATCT      1560
DB      1501 TCAGAGAAAGATGCAAAAGCTTGAAGGCAATGAAAAATGGCCAGCAGAGAAAAAGATCT      1560
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DB      1561 CAAGAACAGAAATTAATAGATGATGATAGAGAGCTAGAAATTTTAATGCTATCGAA      1620
QY      1621 GAAATGAAAGACAGGAAGTCTCATGTCGAAATTTCCAGAAAACTGACTAATGATGTC      1680
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QY      1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCCAAAGGAAGAGCAACCTGAAAGC      1740
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Dd	1921	GAAAAAGCATCTTGCATGAAAAATTGATCGTTGCCGGGAAAGAAATTGCCATCCTAAGACTG	1980
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Dd	1981	GAGCTGACACAATGATAAACATCAAGAGCCAGCTTAAAAAAAAAAAAAAAAAAAAAAAAA	2040

RESULT 14

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US-10-033-527-7
; Sequence 7, Application US/10033527
; Publication No. US20030170631A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; TITLE OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513C1
; CURRENT APPLICATION NUMBER: US/10/033,527
; CURRENT FILING DATE: 2001-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-033-527-7

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				Gaps 0;

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Db	1	ATGTGTGTTGAGTTGATTCATGCGGCTCCCTTCTGTGAAGAAGCCATTTGGTTC	60
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Db	61	AGAGCAAGATGGCGAAGTGTGCTGCTGCTTCCCTCTGCAAGGAGCGGCAAG	120
OY	121	AGCAACGGGGCATTCTGTGAGACCAAGACGACTCTGTATGAAGACACTGAGAGCAAG	180
Db	121	AGCAACGGGGCATTCTGTGAGACCAAGACGACTCTGTATGAAGACACTGAGAGCAAG	180
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OY	241	GGCGCTTCTGGAGACACGACGACTTGTCTATGAAGACACTCAGGAACAAGTGGCAAG	300
Db	241	GGCGCTTCTGGAGACACGACGACTTGTCTATGAAGACACTCAGGAACAAGTGGCAAG	300
OY	301	TGTTGCTGCACTGCTTCCCGTGCAGGGGGAGCGGCAGAGCAAGTGTGGGCGCTTGG	360
Db	301	TGTTGCTGCACTGCTTCCCGTGCAGGGGGAGCGGCAGAGCAAGTGTGGGCGCTTGG	360
OY	361	GGAGCTTACGATGACAGTGCCTTCAATGAGGCCAAGTACCACTGTCCTGTGAGGAAGATCTG	420
Db	361	GGAGCTTACGATGACAGTGCCTTCAATGAGGCCAAGTACCACTGTCCTGTGAGGAAGATCTG	420
OY	421	GACCAAGTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCAAAAGAAGATCTATGTCATG	480
Db	421	GACCAAGTCCACAGAGCTGCTGTGTGGGGTAAAGTCCCAAAAGAAGATCTATGTCATG	480

OY	481	CTCAGGGACA	CTGACGGGAA	CAAGAGGACA	GACGAAAGAGGAC	CTGCTCAATCTGGCC	540
Db	481	CTCAGGGACA	CTGACGGGAA	CAAGAGGACA	GACGAAAGAGGAC	TGCTCTACATCTGGCC	540
OY	541	TCTGSCAATGGGA	ATTTCAGAAAGTATGTA	AAATCTCCCTGTCAGACAGATGTCAACTTAAT			600
Db	541	TCTGCCAATGGGA	ATTTCAGAAAGTATGTA	AAATCTCCCTGTCAGACAGATGTCAACTTAAT			600
OY	601	GTCCTTGACAA	CAAAAAAGAGACAGCTCTGATVAAAGCCGTACATGCCAGGAAGATGAA				660
Db	601	GTCCTTGACAA	CAAAAAAGAGACAGCTCTGATVAAAGCCGTACATGCCAGGAAGATGAA				660
OY	661	TGTGCGTAAATGTTGTCGGAA	CAATGGGACGTATCCAAATATTCACAGATGATGTGAAT				720
Db	661	TGTGCGTAAATGTTGTCGGAA	CAATGGGACGTATCCAAATATTCACAGATGATGTGAAT				720
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OY	841	CATAGACAAAA	CAGCAAGTCGTGAAATTTTATATCAAGAAAAAGCGAATTTAATATGA				900
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OY	901	CTGATATGATATGGA	AGAGCGTCTCATATCTTGATGTTGTGGAATGAGAAATAT				960
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Db	1201	ATGCTCTAAGA	ACCAAAATTAATTAAGATGTTGATAGAGGTTGAAGAAATGTAAG				1260
OY	1261	AAGCATGAAATTA	TATGCGGATTTCTTGAAAACTGACTAATGTTGTCTGCTGGC				1320
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OY	1321	AATGATGATATG	ATTAATTTCCCAAAAGGAGGAGCAACCTGTAATATTCAGCAATTT				1380
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OY	1381	CCTGACACAGA	AAAGTGAAGATATCA	CAGAAATTTGGAAATTAAGTTTCTGA	CTACAAAGAA		1440
Db	1381	CCTGACACAGA	AAAGTGAAGATATCA	CAGAAATTTGGAAATTAAGTTTCTGA	CTACAAAGAA		1440
OY	1441	AAACAGATGCC	CAAAATCTCTTCTGAAAAACGCAACCCAGAACAAAGCTTAAGCTTACA				1500
Db	1441	AAACAGATGCC	CAAAATCTCTTCTGAAAAACGCAACCCAGAACAAAGCTTAAGCTTACA				1500
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Db	1501	TCAGAGGAAG	ATGTCACAAAGGCTTTGAGGCGAGTGAATATGGCCAGCCAGAGAAAGATCT				1560
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RESULT 15
US-10-294-025-375

/ Sequence 375, Application US/10294025
/ Publication No. US20030185830A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Kalos, Michael D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C29
/ CURRENT APPLICATION NUMBER: US/10/294,025
/ CURRENT FILING DATE: 2002-11-12
/ NUMBER OF SEQ ID NOS: 1038
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-294-025-375

Query Match 100.0%; Score 2040; DB 6; Length 2040;
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Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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9: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq3:*
10: /cgn2_6/prodata/1/pubpna/us60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	1.6	201	6	US-10-995-561-30293
2	32	1.6	201	6	US-10-995-561-30293
3	32	1.6	201	6	US-10-995-561-30411
4	32	1.6	201	6	US-10-995-561-30414
5	32	1.6	148220	7	US-11-121-086-90
6	32	1.6	187986	6	US-10-995-561-13252
7	31	1.5	201	6	US-10-995-561-82843
8	31	1.5	66131	6	US-10-995-561-13501
9	31	1.5	167891	7	US-11-121-086-14
10	31	1.5	179892	7	US-11-112-908-39
11	30	1.5	201	6	US-10-995-561-26191
12	30	1.5	201	6	US-10-995-561-46434
13	30	1.5	201	6	US-10-995-561-50343
14	30	1.5	201	6	US-10-995-561-50425
15	30	1.5	201	6	US-10-995-561-51237
16	30	1.5	201	6	US-10-995-561-68585
17	30	1.5	201	6	US-10-995-561-68607
18	30	1.5	201	6	US-10-995-561-68609
19	30	1.5	356	6	US-10-508-424-8
20	30	1.5	600	7	US-11-123-896-256
21	30	1.5	722	6	US-10-689-742-79
22	30	1.5	779	7	US-11-051-568-22
23	30	1.5	1279	7	US-11-179-411-31

24	30	1.5	1279	7	US-11-175-766-31	Sequence 31, Appl
25	30	1.5	1478	6	US-10-909-125-1744	Sequence 1744, Ap
26	30	1.5	1968	6	US-10-131-826A-163	Sequence 163, App
27	30	1.5	2036	6	US-10-996-217A-8	Sequence 8, Appl
28	30	1.5	2120	7	US-11-167-856-29	Sequence 29, Appl
29	30	1.5	2408	7	US-11-090-439-55	Sequence 55, Appl
30	30	1.5	3001	7	US-11-145-703-153	Sequence 153, Appl
31	30	1.5	3001	7	US-11-145-703-153	Sequence 153, Appl
32	30	1.5	14082	6	US-10-995-561-13445	Sequence 13445, A
33	30	1.5	48763	6	US-10-663-794-3	Sequence 3, Appl
34	30	1.5	56054	6	US-10-995-561-13402	Sequence 13402, A
35	30	1.5	86950	6	US-10-857-780-5	Sequence 5, Appl
36	30	1.5	87672	6	US-10-995-561-13237	Sequence 13237, A
37	30	1.5	119160	7	US-11-121-086-12	Sequence 12, Appl
38	30	1.5	120096	7	US-11-121-086-24	Sequence 24, Appl
39	30	1.5	127340	7	US-11-112-908-35	Sequence 35, Appl
40	30	1.5	146656	7	US-11-121-086-68	Sequence 68, Appl
41	30	1.5	146656	7	US-11-121-086-68	Sequence 68, Appl
42	30	1.5	149419	7	US-11-112-908-49	Sequence 49, Appl
43	30	1.5	153376	7	US-11-121-086-5	Sequence 5, Appl
44	30	1.5	155515	7	US-11-112-908-42	Sequence 42, Appl
45	30	1.5	159497	7	US-11-112-908-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-995-561-30293/c
; Sequence 30293, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30293
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-30293

Query Match 1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 145 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 114

RESULT 2
US-10-995-561-30411/c
; Sequence 30411, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30411
; LENGTH: 201
; TYPE: DNA

ORGANISM: Homo sapiens
US-10-995-561-30411

Query Match 1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAA 2040
DB 148 AGCTAAAAAAAAAAAAAAAAAAAAA 117

RESULT 3
US-10-995-561-30414/C
Sequence 30414, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30414

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-995-561-30414

Query Match 1.6%; Score 32; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAA 2040
DB 98 AGCTAAAAAAAAAAAAAAAAAAAAA 67

RESULT 4
US-11-121-086-90
Sequence 90, Application US/11121086
Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POUlsen, TIM S.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 90

LENGTH: 148220

TYPE: DNA

ORGANISM: Homo sapiens

US-11-121-086-90

Query Match 1.6%; Score 32; DB 7; Length 148220;
Best Local Similarity 100.0%; Pred. No. 0.00047;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAA 2040
DB 144334 AGCTAAAAAAAAAAAAAAAAAAAAA 144365

RESULT 5
US-10-995-561-13252/C

Sequence 13252, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13252

LENGTH: 187986

TYPE: DNA

ORGANISM: Homo sapiens

US-10-995-561-13252

Query Match 1.6%; Score 32; DB 6; Length 187986;
Best Local Similarity 100.0%; Pred. No. 0.00046;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAA 2040
DB 139832 AGCTAAAAAAAAAAAAAAAAAAAAA 139801

RESULT 6
US-10-995-561-82843/C
Sequence 82843, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82843

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-995-561-82843

Query Match 1.5%; Score 31; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2010 GCTAAAAAAAAAAAAAAAAAAAAA 2040
DB 152 GCTAAAAAAAAAAAAAAAAAAAAA 122

RESULT 7
US-10-995-561-13501/C
Sequence 13501, Application US/10995561
Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

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TYPE: DNA
ORGANISM: Homo sapiens
US-11-112-908-39

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2010 GCTTAAAAA... 2040
|||||
Db 103513 GCTTAAAAA... 103543

RESULT 10
US-10-995-561-26191/c
Sequence 26191, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26191
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-26191

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTGAAAAAA... 2040
|||||
Db 152 CTGAAAAAA... 123

RESULT 11
US-10-995-561-46434
Sequence 46434, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46434
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-46434

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTGAAAAAA... 2040
|||||
Db 107 CTGAAAAAA... 136

RESULT 12
US-10-995-561-50343/c
```

```

; Sequence 50343, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50343
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-50343

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 132 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 103

RESULT 13
US-10-995-561-50425/c
; Sequence 50425, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50425
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-50425

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 94 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 65

RESULT 14
US-10-995-561-51237/c
; Sequence 51237, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51237
; LENGTH: 201
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
US-10-995-561-51237

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 131 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 102

RESULT 15
US-10-995-561-68585
; Sequence 68585, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68585
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68585

Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
DB 141 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 170

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Search completed: December 19, 2005, 09:12:38
Job time : 251.436 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 08:08:19 ; Search time 8222.61 Seconds
(without alignments)
11607.702 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040
Sequence: 1 atgctgtgtcgtgagctgattc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82154912

Minimum DB seq length: 10

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gsa1: *
10: gb_gsa2: *
11: gb_gsa3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	24.1	729	5	BU930826
2	184	9.0	521	9	AQ0204617 HS_3229_B
3	141	6.9	865	2	BF676987 602084215
4	140	6.9	451	1	AI804733 t42d03.x
5	137	6.7	289	1	AAS33501
6	129	6.3	531	9	AQ615477 HS_5144_B
7	117	5.7	621	3	BM763942 K-EST0045
8	117	5.7	633	3	BM763453 K-EST0044
9	117	5.7	817	5	BQ441373
10	90	4.4	263	10	AG192933
11	89	4.4	400	9	AQ124119 HS_3122_A
12	87	4.3	339	9	AQ030111 RPI11-39
13	87	4.3	544	1	AL703938 DKF2P868
14	79	3.9	279	3	BI461255 603206584
15	76	3.7	6098	4	BSM809270
16	74	3.6	505	5	EX492731
17	73	3.6	385	5	EX492731 DKF2P781C
18	65	3.2	322	5	AQ063365
19	64	3.1	381	2	BU584009 2275475H1
20	59	2.9	707	10	CR747857 CR747857
21	57	2.8	607	9	AG045796 Pan trogl
22	52	2.5	380	2	B48260 RPI11-6K4
					BF329652 RCG-BN027

23	50	2.5	592	9	AQ372700
24	49	2.4	493	10	AG193231
25	49	2.4	495	9	AQ469831
26	49	2.4	495	9	AQ469831
27	49	2.4	557	9	AQ469663
28	49	2.4	667	10	AG156382
29	47	2.3	697	9	AQ030113
30	47	2.3	187	2	BE069869
31	46	2.3	476	9	AQ392059
32	46	2.3	351	7	CV383025
33	46	2.3	400	9	AQ057106
34	45	2.2	218	5	BU584404
35	45	2.2	259	5	BU584020
36	45	2.2	338	5	BU584405
37	45	2.2	423	5	BU584403
38	45	2.2	874	6	CD358418
39	45	2.2	894	6	BF675049
40	44	2.2	5483	4	BC063888
41	44	2.2	460	9	AQ360298
42	41	2.0	710	10	AG165908
43	40	2.0	503	9	B55862
44	40	2.0	632	7	CV341500
45	39	1.9	1011	9	AQ090910
					AQ247090

ALIGNMENTS

RESULT 1	BU930826	729 bp	RNA	linear	EST 18-OCT-2002
LOCUS	BU930826				
DEFINITION	AGENCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956				
ACCESSION	BU930826				
VERSION	BU930826.1	GI:24119645			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 729)				
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L10M2943 row: 0 column: 04 High quality sequence stop: 555. Location/Qualifiers 1. 729 /organism="Homo sapiens" /mol_type="RNA" /db_xref="taxon:9606" /clone="IMAGE:6668956" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH MGC 83" /note="Organ: prostate; Vector: pMDR-LIB (Clontech); Site 1: SfiI (ggcgccggccgccc); Site 2: SfiI (ggccatcgccc); 5' and 3' adaptor were used in cloning as follows: 5' adaptor sequence: 5'-ATTCGAGCGCGCGCGCGCGCATGATG-3' and 3' adaptor sequence: 5'-CACGCCCATATGAGCC-3' 5'-ATTCGAGCGCGCGCGCGCGCATGATG-3' (30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones				

ORIGIN and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 24.1%; Score 492; DB 5; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.3e-230;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

635 AGGCCCTACAAATCCAGAAAGATGATGCGTTAATGTCGTAACATGGACATGATC 694
DB AGGCCCTACAAATCCAGAAAGATGATGCGTTAATGTCGTAACATGGACATGATC 148
695 CAAATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
DB CAAATATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 208
755 AATTATGCGCAAGACATGCTCTTATATGTCGATATGCAATCAAAAAACAGCATG 814
DB AATTATGCGCAAGACATGCTCTTATATGTCGATATGCAATCAAAAAACAGCATG 268
815 GCCTCACACCACTGTTACTTGTGTACATGACGCAAAAAACAGCAAGTCGTAATTTTAA 874
DB GCCTCACACCACTGTTACTTGTGTACATGACGCAAAAAACAGCAAGTCGTAATTTTAA 328
875 TCAGAAAAAAGCAATTTAATGACCTGATGATGATGATGATGATGATGATGATG 934
DB TCAGAAAAAAGCAATTTAATGACCTGATGATGATGATGATGATGATGATGATG 388
935 CTGTATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 994
DB CTGTATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 448
995 CTCTCAAGATCTATCTGACAGACGCGCAGAGAGATGCTGTTCTAGCATCATCANG 1054
DB CTCTCAAGATCTATCTGACAGACGCGCAGAGAGATGCTGTTCTAGCATCATCANG 508
1055 TAATTGGCAGTTACTTCTGACTACAAAGAAAAACAGATGCTAAATCTCTTGAAA 1114
DB TAATTGGCAGTTACTTCTGACTACAAAGAAAAACAGATGCTAAATCTCTTGAAA 568
1115 ACAGCATTCAG 1126
DB ACAGCATTCAG 580

RESULT 2
LOCUS AQ04617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3229_B1.G12.T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=23 Row=N, genomic survey sequence.

ACCESSION AQ04617
VERSION AQ04617.1 GI:3615187
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas G., Wallace J.C., Hood L.
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

FEATURES
source
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 Row: N Column: 23
Class: BAC ends
High quality sequence stop: 521.
Location/Qualifiers
1..521
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3229 Col=23 Row=N"
/sex="male"
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 9.0%; Score 184; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 8.6e-79;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1595 AGCTGAAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTGTCGAT 1654
DB 221 AGCTGAAAATTTTATGCTATCGAAGAAATGAAGACGGAAGTACTGTCGAT 290
1655 TCCGAAAAACCTGACTAATGATGTCGACCTGTCGCAATGATGATGATTAATTCCTC 1714
DB 221 TCCGAAAAACCTGACTAATGATGTCGACCTGTCGCAATGATGATGATTAATTCCTC 350
1715 CAAGGAAGACGAAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATC 1774
DB 351 CAAGGAAGACGAAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATC 410
1775 ACAG 1778
DB 411 ACAG 414

RESULT 3
LOCUS BF676987 865 bp mRNA linear EST 21-DEC-2000
DEFINITION 602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5', mRNA sequence.

ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers
1..865
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/lab_host="DH10B (TI phage-resistant)"

ORIGIN

/clone.lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccgcccgc); Site_2: SfiI
(ggccatcgcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCGCATTAAGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCCGCGCCGACATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

Query Match 6.9%; Score 141; DB 2; Length 865;
Best Local Similarity 100.0%; Pred.No. 1.4e-57;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 ACTGCTCTCATCTCTGATGTTGATGATGACGAAGTATGACCTTCTACTTGA 978
DB 353 ACTGCTCTCATCTCTGATGTTGATGATGACGAAGTATGACCTTCTACTTGA 412
QY 979 CAAATATATGATGATCTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGT 1038
DB 413 CAAATATATGATGATCTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGT 472
QY 1039 TCTAGTCATCATCATGTAAT 1059
DB 473 TCTAGTCATCATCATGTAAT 493

RESULT 4
AI804733 451 bp mRNA linear EST 07-MAR-2000
LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
DEFINITION mRNA sequence.
ACCESSION AI804733
VERSION AI804733.1 GI:5370205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 543 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES

source
1..451
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2253677"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="NCI CGAP Pr28"
/note="Organ: prostate; Vector: PT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the

ORIGIN

normalized library NCI CGAP Pr22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Patricia Bonaldo.

Query Match 6.9%; Score 140; DB 1; Length 451;
Best Local Similarity 100.0%; Pred.No. 4.2e-57;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 AGGACTGCTCTCATCTCTGATGTTGATGATGACGAAGTATGACCTTCTACTT 975
DB 47 AGGACTGCTCTCATCTCTGATGTTGATGATGACGAAGTATGACCTTCTACTT 106
QY 976 GAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGCGCCAGAGATGCT 1035
DB 107 GAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGCGCCAGAGATGCT 166
QY 1036 GTTCTAGTCATCATCATGT 1055
DB 167 GTTCTAGTCATCATCATGT 186

RESULT 5
AA533501 289 bp mRNA linear EST 21-AUG-1997
LOCUS nj96a04.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000302,
DEFINITION mRNA sequence.
ACCESSION AA533501
VERSION AA533501.1 GI:2277597
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuang, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 217 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham.

FEATURES

source
1..289
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1000302"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/clone.lib="NCI CGAP Pr11"
/clone.host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells. cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Library made by
D. Krizman, NIH."

ORIGIN

Query Match 6.7%; Score 137; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1788 AATGATCTCAGAACATTTTGTGAAGACGAACCTGGAATTTACAGATGAGT 1847
 DB 9 AATGATCTCAGAACATTTTGTGAAGACGAACCTGGAATTTACAGATGAGT 68
 QY 1848 TCTGATTCATGAAGAAAGACATAGAGTGTGTTGAAAAAATGAAATTCAGCTTCTCT 1907
 DB 69 TCTGATTCATGAAGAAAGACATAGAGTGTGTTGAAAAAATGAAATTCAGCTTCTCT 128
 QY 1908 TAGTGTGAAGAAAGAAA 1924
 DB 129 TAGTGTGAAGAAAGAAA 145

RESULT 6
 LOCUS A0615477 531 bp DNA linear GSS 15-JUN-1999
 DEFINITION HS 5144.B1.G01.T7A.RPCT-11 Human Male BAC library Homo sapiens
 ACCESSION A0615477
 VERSION A0615477.1 GI:5076753
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 531)
 Mahatra, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (1999) 9739-9744 (1999)
 10449764
 CONTACT: Mahatra GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.bufo.10.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.bufo.10.edu/ordering/bac.htm>)
 or from Research Genetics (<http://www.resgen.com>). BAC end Web Server:
<http://www.htsc.washington.edu>
 Plate: 720 row: N column: 1
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 531.
 Location/Qualifiers
 1..531
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=720 Col=1 Row=N"
 /sex="male"
 /clone_lib="RPCT-11 Human Male BAC library"
 /notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"

ORIGIN
 Query Match 6.3%; Score 129; DB 9; Length 531;
 Best Local Similarity 100.0%; Pred. No. 1.1e-51;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CATGGACGTGATCCAAATATTTCAGATGATGAAATPACCACTTGACCTAGCTATC 741
 DB 117 CATGGACGTGATCCAAATATTTCAGATGATGAAATPACCACTTGACCTAGCTATC 176
 QY 742 TATATGAAGATTAATTAATGAGCCAAAGACCTGCTTATATGATGCTGATATCAATCA 801
 DB 177 TATATGAAGATTAATTAATGAGCCAAAGACCTGCTTATATGATGCTGATATCAATCA 236
 QY 802 AAAACCAAG 810
 DB 237 AAAACCAAG 245

RESULT 7
 LOCUS BM763942 621 bp mRNA linear EST 04-MAR-2002
 DEFINITION K-EST0045367 S13KMS5 Homo sapiens CDNA clone S13KMS5-25-A11 5',
 mRNA sequence.
 ACCESSION BM763942
 VERSION BM763942.1 GI:19093557
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 621)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 25 row: A column: 11
 High quality sequence stop: 621.
 Location/Qualifiers
 1..621
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-25-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10P"
 /clone_lib="S13KMS5"
 /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then decapped with tobacco acid
 pyrophosphatase (TAP). The decapped intact mRNA was
 ligated with DNA-RNA linker including EcoRI site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dT-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoRI which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10P by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN
 Query Match 5.7%; Score 117; DB 3; Length 621;
 Best Local Similarity 99.1%; Pred. No. 9.3e-46;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 CAAGCAAAAGAGACGCTCTACATCTGGCTCTGCCAATGGGAAATTCAGAACTAGTAA 569
 Db 1 CAAGCAAAAGAGACGCTCTACATCTGGCTCTGCCAATGGGAAATTCAGAACTAGTAA 60
 QY 570 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGACAGCTCT 629
 Db 61 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGACAGCTCT 120
 QY 630 GATTAAGGCCGTACAATGCCAGGAAGATGATGTCCTTAATGTCTTGAACAATGGCAC 689
 Db 121 GACAAAGGCCGTACAATGCCAGGAAGATGATGTCCTTAATGTCTTGAACAATGGCAC 180
 QY 690 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 728
 Db 181 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 219

RESULT 8
 LOCUS BM763453 633 bp mRNA linear EST 04-MAR-2002
 DEFINITION K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
 mRNA sequence.
 ACCESSION BM763453
 VERSION BM763453.1 GI:19093068
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 633)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 high quality sequence stop: 633.
 Location/Qualifiers
 1..633
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10"
 /note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then deapped with tobacco acid
 pyrophosphatase (TAP). The deapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoR1 which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10" by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

TITLE
 JOURNAL
 COMMENT
 REFERENCE
 AUTHORS
 Kim,Y.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 16 row: A column: 11
 high quality sequence stop: 633.
 Location/Qualifiers
 1..633
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-16-A11"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10"
 /note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly
 (A) + RNA was dephosphorylated with bacterial alkaline
 phosphatase (BAP) and then deapped with tobacco acid
 pyrophosphatase (TAP). The deapped intact mRNA was
 ligated with DNA-RNA linker including EcoR I site by
 treatment of T4 RNA ligase and the first strand cDNA was
 synthesized from oligo dt-selected mRNA by priming with
 dt-tailed vector. The dt-tailed vector was adjusted to
 have about 60nt. The cDNA vector was circularized with E.
 coli DNA ligase after digestion of EcoR1 which site is
 also included in vector. An RNA strand converted to a DNA
 strand by Okayama-Berg method. The obtained cDNA vectors
 were used for transformation of competent cells E. coli
 Top10" by electroporation method. The cDNA libraries
 constructed by this method are full-length enriched cDNA
 library."

ORIGIN

Query Match 5.7%; Score 117; DB 3; Length 633;
 Best Local Similarity 99.1%; Pred. No. 9.3e-46;
 Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 CAAGCAAAAGAGACGCTCTACATCTGGCTCTGCCAATGGGAAATTCAGAACTAGTAA 569
 Db 1 CAAGCAAAAGAGACGCTCTACATCTGGCTCTGCCAATGGGAAATTCAGAACTAGTAA 60
 QY 570 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGACAGCTCT 629
 Db 61 ACTCTGCTGAGACAGACGATGTCACTTAATGTCTTGAACAACAAAAGAGACAGCTCT 120
 QY 630 GATTAAGGCCGTACAATGCCAGGAAGATGATGTCCTTAATGTCTTGAACAATGGCAC 689
 Db 121 GACAAAGGCCGTACAATGCCAGGAAGATGATGTCCTTAATGTCTTGAACAATGGCAC 180
 QY 690 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 728
 Db 181 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 219

RESULT 9
 LOCUS BQ441373 817 bp mRNA linear EST 24-MAY-2002
 DEFINITION AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
 5', mRNA sequence.
 ACCESSION BQ441373
 VERSION BQ441373.1 GI:21180449
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 817)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2340 row: m column: 08
 high quality sequence stop: 516.
 Location/Qualifiers
 1..817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6103855"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgccgtcgcc); Site 2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt (30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Query Match 5.7%; Score 117; DB 5; Length 817;
 Best Local Similarity 100.0%; Pred. No. 9.4e-46;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 AGAATTGGGAATTAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTCTGAA 1467
DB 319 AGAATTGGGAATTAGTTCTGACTACAAAGAAAACAGATGCCAAATTAATCTTCTGAA 378
QY 1468 AACAGACCCAGAACAGACTTAAAGTCATCATGAGAGAGTACAAAGGCTT 1524
DB 379 AACAGACCCAGAACAGACTTAAAGTCATCATGAGAGAGTACAAAGGCTT 435

RESULT 10
AG192933 263 bp DNA linear GSS 06-MAR-2004
LOCUS AG192933/c Pan troglodytes DNA, clone: RP43-069123.TU, genomic survey
DEFINITION sequence.
ACCESSION AG192933 GI:45225109
VERSION AG192933.1
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE BAC end sequences of library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 263)
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE Direct Substitution
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KIRIB), Genome Research Center (GRC), 52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kirib.re.kr, URL:http://phs.grc.kirib.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the RAD process and may have higher chance of clone tracking errors.
PRIMERS

ORIGIN
Sequencing: TU
LIBRARY Vector : PBACe3.6
R.Site 1 : EcorI
R.Site 2 : EcorI.
Location/Qualifiers
1. 263
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-069123.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 4.4%; Score 90; DB 10; Length 263;
Best Local Similarity 100.0%; Pred.No.1.8e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1784 AACCAATGATCTACGAGCAATTTTGGAGAGACAGACACTGAAATTATTCACAGATG 1843
DB 90 AACCAATGATCTACGAGCAATTTTGGAGAGACAGACACTGAAATTATTCACAGATG 31
QY 1844 AGATTCTGATTCATGAAGAAACAGATAG 1873
DB 30 AGATTCTGATTCATGAAGAAACAGATAG 1

RESULT 11
LOCUS AQ124119 400 bp DNA linear GSS 22-SEP-1998

DEFINITION HS_3122_A1_C07_MR_C17 Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122 Col=13 Row=E, genomic survey
sequence.
ACCESSION AQ124119
VERSION AQ124119.1 GI:3501285
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 400)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 Row: E Column: 13
Class: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3122 Col=13 Row=E"
/sex="male"
/clone_lib="C17 Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 4.4%; Score 89; DB 9; Length 400;
Best Local Similarity 100.0%; Pred.No.5.7e-32;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 AGCGGTACATGCCAGAGATGATGCGTTATGTTGCTGGAACATGCGACTGATC 694
DB 237 AGCGGTACATGCCAGAGATGATGCGTTATGTTGCTGGAACATGCGACTGATC 296
QY 695 CAAATTTTCAGATGATGGAATATC 723
DB 297 CAAATTTTCAGATGATGGAATATC 325

RESULT 12
AQ030111/c 399 bp DNA linear GSS 14-APR-1999
LOCUS AQ030111 RPCR11-39K18.TP RPCR11 Homo sapiens genomic clone RPCR11-39K18,
DEFINITION genomic survey sequence.
ACCESSION AQ030111
VERSION AQ030111.1 GI:3274075
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 399)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)

JOURNAL COMMENT

Unpublished (1998)
Other GSs: RPCI11-39K18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadm@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers

1..399
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7514849"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/sex="Male"
/cell_type="lymphocytes"
/clone_11b="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 5.5e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1777 AGTACGACAAATATGATCTCAGAACCAATTTTGTGAGAACAGAACCTGGAATATTA 1836
102 AGTACGACAAATATGATCTCAGAACCAATTTTGTGAGAACAGAACCTGGAATATTA 43
Db 1837 CACGATGAGATTCTGATTCATGAGAA 1863
42 CACGATGAGATTCTGATTCATGAGAA 16

RESULT 13
AL703938 544 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686E1728_r1.686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKFZp686E1728_5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 544)
Ostenwalder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
Wiemann, S.
EST (Ostenwalder, B., Obermaier, B., Mewes, H.W., Weil, B. and
Wiemann, S.)
Unpublished (2001)
Contact: MIPS

MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No 31 sequence
available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.

FEATURES

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

1..544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686E1728"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="686 (synonym: hlc3)"
/note="Vector: pTriblEx2; site_1: SfiI; site_2: SfiI;
cDNA-collection"

ORIGIN

Query Match 4.3%; Score 87; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 5.6e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1081 AAGAGAAAACAGATGCTAAATCTCTTGAAGACAGCAATCCAGAACAGCTTAAG 1140
432 AAGAGAAAACAGATGCTAAATCTCTTGAAGACAGCAATCCAGAACAGCTTAAG 491
Db 1141 CTGACATCAGAGAGAGTCACAAAG 1167
492 CTGACATCAGAGAGAGTCACAAAG 518

RESULT 14

BI461255/ 279 bp mRNA linear EST 21-AUG-2001

LOCUS BI461255
DEFINITION 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
mRNA sequence.

ACCESSION BI461255
VERSION BI461255.1 GI:15251911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 279)
NIH-MGC http://mgs.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1687 row: 9 column: 21
High quality sequence stop: 236.
Location/Qualifiers

FEATURES

source

1..279
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5272364"
/lab_host="DH10B"
/clone_11b="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptPR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcagc); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and a
constructed using the Cap-trapper method (Carninci), in
preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC library."

ORIGIN

Query Match 3.9%; Score 79; DB 3; Length 279;
Best Local Similarity 100.0%; Pred. No. 4.7e-27;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTCATTCATCCGCGCTCTTCTGTAAGAAGCATTTGATCTC 60
DB 84 ATGGTGGTTGAGTTCATTCATCCGCGCTCTTCTGTAAGAAGCATTTGATCTC 25
QY 61 AGGAGCAAGATGGCAAGT 79
DB 24 AGGAGCAAGATGGCAAGT 6

RESULT 15

LOCUS HSM809270 6098 bp mRNA linear HTC 20-JAN-2005

DEFINITION Homo sapiens mRNA, cDNA DKFZp686J0529 (from clone DKFZp686J0529).

ACCESSION BX649118

VERSION BX649118.1 GI:34368290

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 6098)

Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Oeanger, A.,

Fobo, G., Han, M., and Wiemann, S.

The German cDNA Consortium

Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764

Neuberberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

consortium of the German Genome Project.

This clone (DKFZp686J0529) is available at the RZPD Deutsches

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp686J0529

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers

1..6098

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="RZPD:DKFZp686J0529Q"

/db_xref="taxon:9606"

/clone="DKFZp686J0529"

/issue_type="testis"

/clone_lib="686 (synonym: hlc03). Vector pSport1_Sfi; host

DH10B; sites SfiIA + SfiIB"

/dev_stage="adult"

/note="putative transcript"

ORIGIN

Query Match 3.7%; Score 76; DB 4; Length 6098;

Best Local Similarity 100.0%; Pred. No. 1.8e-25;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 986 TTGATGATCTTCTCAAGATCTATCTGACAGACGCGCAGAGATGCTGTTCTAGTC 1045

DB 1426 TTGATGATCTTCTCAAGATCTATCTGACAGACGCGCAGAGATGCTGTTCTAGTC 1485

QY 1046 ATCATCATGTAATTG 1061

DB 1486 ATCATCATGTAATTG 1501

Search completed: December 19, 2005, 20:05:02
Job time : 8223.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:28:25 ; Search time 10314.6 Seconds
(without alignments)
11242.353 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atcggtgctgaggtgctgctc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_pro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hvg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	6	BD242273
2	2040	100.0	2040	6	AR278460
3	2040	100.0	2040	6	AR350944
4	2040	100.0	2040	6	AR367176
5	2040	100.0	2040	6	AR371072
6	2040	100.0	2040	6	AR400212
7	2040	100.0	2040	6	AR405479
8	2040	100.0	2040	6	AR433320
9	2040	100.0	2040	6	AR563859
10	2040	100.0	2040	6	AR568845
11	2040	100.0	2040	6	AR605665
12	2040	100.0	2040	6	AR642106
13	2040	100.0	2040	6	AR657004
14	2040	100.0	2040	6	AR657004
15	2040	100.0	2040	6	AX106594
16	2040	100.0	2040	6	AX140885
17	2040	100.0	2040	6	AX200745
18	2040	100.0	2040	6	AX267401

19	2040	100.0	2040	6	AX282958	AX282958	Sequence
20	2040	100.0	2040	6	AX316966	AX316966	Sequence
21	1999.8	98.0	2188	8	AY462871	AY462871	Homo sapi
22	1940	95.1	2000	6	BD242272	BD242272	Compounds
23	1940	95.1	2000	6	AR278479	AR278479	Sequence
24	1940	95.1	2000	6	AR350943	AR350943	Sequence
25	1940	95.1	2000	6	AR367175	AR367175	Sequence
26	1940	95.1	2000	6	AR371071	AR371071	Sequence
27	1940	95.1	2000	6	AR400211	AR400211	Sequence
28	1940	95.1	2000	6	AR405478	AR405478	Sequence
29	1940	95.1	2000	6	AR433319	AR433319	Sequence
30	1940	95.1	2000	6	AR563858	AR563858	Sequence
31	1940	95.1	2000	6	AR588844	AR588844	Sequence
32	1940	95.1	2000	6	AR605664	AR605664	Sequence
33	1940	95.1	2000	6	AR615063	AR615063	Sequence
34	1940	95.1	2000	6	AR642105	AR642105	Sequence
35	1940	95.1	2000	6	AR657003	AR657003	Sequence
36	1940	95.1	2000	6	AX106593	AX106593	Sequence
37	1940	95.1	2000	6	AX140884	AX140884	Sequence
38	1940	95.1	2000	6	AX200744	AX200744	Sequence
39	1940	95.1	2000	6	AX267400	AX267400	Sequence
40	1940	95.1	2000	6	AX282957	AX282957	Sequence
41	1940	95.1	2000	6	AX316965	AX316965	Sequence
42	1799	88.2	2146	8	AY462872	AY462872	Homo sapi
43	1759.4	86.2	2072	8	AY462873	AY462873	Homo sapi
44	1641.2	80.5	2027	8	AY462868	AY462868	Homo sapi
45	1298.6	63.7	1866	8	AY465172	AY465172	Homo sapi

ALIGNMENTS

RESULT 1
BD242273
LOCUS
DEFINITION
BD242273 2040 bp DNA linear PAT 17-JUL-2003
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.

ACCESSION
BD242273 GI:33052043
VERSION
JP 2002520054-A/360.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 2040)
Dillon,D.C., Harlocker,S.L., Yugu,J., Xu,J. and Mitcham,J.L.
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use
Patent: JP 2002520054-A 360 09-JUL-2002;
JOURNAL
CORIXA CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002520054-A/360
PD 09-JUL-2002
PF 14-JUL-1999 JP 2000560247
PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR
09-APR-1999 US 09/288946
PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YIQIU, PI
JIANGCHUN XU,
PI JENNIFER LYNN MITCHAM
PC C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,
PC C12N5/10,
PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
PC A61K37/02,
PC C12N5/00
CC Compounds for immunotherapy and diagnosis of prostate cancer
and methods
CC for their use
CC Key
FH Location/Qualifiers
FT 1. 2040
/organism='Homo sapiens (human)'.
FT source

FEATURES
source 1..2040
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGGTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGAGCAATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
DB 61 AGGAGCAATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAGACGACTCTGTATGAAGACCTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAGACGACTCTGTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCGAGAGAGTGGCAAGACGTG 240
DB 181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCGAGAGAGTGGCAAGACGTG 240
QY 241 GGGCGCTTCTGGAAGCAGACGACTCTGTATGAAGACCTCAGAGCAAGTGGGCAAG 300
DB 241 GGGCGCTTCTGGAAGCAGACGACTCTGTATGAAGACCTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCGAGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGCGAGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTAGTACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGGAAGAGTCTG 420
DB 361 GGAAGACTAGTACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGGAAGAGTCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAAAGATCTCATCTGCTAG 480
DB 421 GACAACTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGAAGAAAGATCTCATCTGCTAG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAAAGAGAGCTCTTCACTCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAAAGAGAGCTCTTCACTCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGGAACAGAGTGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGGAACAGAGTGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGACGCTGTATTAAGCCGTACAAATGCCAGGAAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGACGCTGTATTAAGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATTTTCCAATGATGTAAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATTTTCCAATGATGTAAGAAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATAATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTGCTGATATTCGAATCAAAAACAAAGATGCTTCAACCACTGTTACTTGTGTGA 840
DB 781 TATGTGCTGATATTCGAATCAAAAACAAAGATGCTTCAACCACTGTTACTTGTGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAATTAATTAATGGA 900
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QY 901 CTGGATAGATATGGAAGGACTGCTCTCATACTTGTGTGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGGACTGCTCTCATACTTGTGTGATCAGCAAGTATA 960
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DB 901 CTGGATAGATATGGAAGGACTGCTCTCATACTTGTGTGATCAGCAAGTATA 960
QY 961 GTCAAGCTTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATCTGGAACAGAG 1020
DB 961 GTCAAGCTTTCTACTTGAAGCAAAATTTGATGATCTTCTCAAGATCTATCTGGAACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTGGCAGTTACTTTCTGACATC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCTGTAATTTGGCAGTTACTTTCTGACATC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAAGCATGGAATATGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAAGCATGGAATATGCCAGCAGAGAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATGAAGATGATGAGAGGTTGAAGAAATAAG 1260
DB 1201 ATGCTCAAGAACAGAAATTAATGAAGATGATGAGAGGTTGAAGAAATAAG 1260
QY 1261 AAGCATGAAGATTAATGTGGATTACTAGAAAACTGACTAATGTGTCTACTGCTGGC 1320
DB 1261 AAGCATGAAGATTAATGTGGATTACTAGAAAACTGACTAATGTGTCTACTGCTGGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGACAGAACCTGAAATATGAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAAAGACAGAACCTGAAATATGAGCAATTT 1380
QY 1381 CCTGCAACGAAAGGAAAGATATCAGAAATTTGCAATTTGATTTGACTACAAAGAA 1440
DB 1381 CCTGCAACGAAAGGAAAGATATCAGAAATTTGCAATTTGATTTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
DB 1441 AAAAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
QY 1501 TCGAGGAAGAGTCAAAAGGCTTGAAGGCAATGAAAAATGGCAGCCAGAGAAAAAGATT 1560
DB 1501 TCGAGGAAGAGTCAAAAGGCTTGAAGGCAATGAAAAATGGCAGCCAGAGAAAAAGATT 1560
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RESULT 2
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LOCUS Sequence 375 from patent US 6512094.
DEFINITION AR278480
ACCESSION AR278480
VERSION AR278480.1 GI:29712726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
Unclassified.
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedvyck,T.S., Carter,D., Li,S.X., Wang,A., Skelly,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 375 28-JAN-2003;
Cortixa Corporation; Seattle, WA
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
AR350944
LOCUS AR350944 2040 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 303 from patent US 6586570.
ACCESSION AR350944
VERSION AR350944.1 GI:33752584
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Fridakis,T.N., Reed,S.G., Smith,J.M. and Misher,L.
TITLE Compositions and methods for the treatment and diagnosis of breast
cancer
JOURNAL Patent: US 6586570-A 303 01-JUN-2003;
Corixa Corporation; Seattle, WA
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RESULT 4
AR367176 2040 bp DNA linear PAT 12-SEP-2003
LOCUS AR367176
DEFINITION Sequence 375 from patent US 6329505.
ACCESSION AR367176
VERSION AR367176.1 GI:34600151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugi,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
TITLE Compositions and methods for therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6329505-A 375 11-DEC-2001;
FEATURES
Corixa Corporation; Seattle, WA
source 1..2040
Location/Qualifiers
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 DEFINITION AR371072
 ACCESSION AR371072
 VERSION AR371072.1 GI:34607965
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Ku,J., Dillon,P.C., Mitcham,J.L., Harlocker,S.L. and Yugiu,J.
 TITLE Prostate specific fusion protein compositions
 JOURNAL Patent: US 6395278-A 375 28-MAY-2002;
 Corixa Corporation; Seattle, WA

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RESULT 5
AR400212 2040 bp DNA linear PAT 18-DEC-2003
LOCUS AR400212 Sequence 375 from patent US 6620922.
DEFINITION AR400212
ACCESSION AR400212
VERSION AR400212.1 GI:40143377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kalos M.D., Panger G.R., Reiter M.W., Stolk J.A., Day C.H.,
Vedick T.S., Carter D., Li S.X., Wang A., Skelky Y.A.W.,
Hepler W.T. and Henderson R.A.
TITLES Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6620922-A 375 16-SEP-2003;
Corixa Corporation; Seattle, WA
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Location/Qualifiers
1..2040
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DEFINITION Sequence 375 from patent US 6630305.
ACCESSION AR405479
VERSION AR405479.1 GI:40154316
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kados,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate
cancer
PATENT: US 6630305-A 375 07-OCT-2003;
CORIXA CORPORATION; Seattle, WA;
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LOCUS	AR563859	2040 bp	DNA		linear
DEFINITION	Sequence 375 from patent US 6759515.				
ACCESSION	AR563859				
VERSION	AR563859.1	GI:53978910			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2040)				
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvik, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.				

Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6759515-A 375 06-JUN-2004;
Corixa Corporation; Seattle, WA

FEATURES
source
1. .2040
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGATGGGCAAGTGGTCTGCGCTTCCCTGCTGAGGAGAGCGGCAAG 120
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DB 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTCTGTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAACGTG 240
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Db	1441	AAACGATGCGAAATTA	1500
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AR615064	DEFINITION	Sequence 303 from patent US 6828431.											
AR615064	ACCESSION	AR615064											
AR615064.1	VERSION	GI:56671468											
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Unknown.	SOURCE												
Unknown.	ORGANISM												
Unclassified.	REFERENCE												
1 (bases 1 to 2040)	AUTHORS												
Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,													
Retter,M.W., Wang,A., Skelky,Y.A.W. and Harlocker,S.L.													
Compositions and methods for the therapy and diagnosis of breast	TITLE												
Cancer													
Patent: US 6828431-A 303 07-DEC-2004;	JOURNAL												
Corixa Corporation; Seattle, WA													
Location/Qualifiers	FEATURES												
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Query Match	100.0%	Score 2040;	DB 6;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2040; Conservative	0;	Mismatches	0;	Indels 0;
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RESULT 13
LOCUS AR642106 2040 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 303 from patent US 6861506.
ACCESSION AR642106
VERSION AR642106.1 GI:62778254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2040)
AUTHORS Frudekis,T.N., Smith,J.M., Reed,S.G., Misher,L.E., Retter,M.W. and Dillon,D.C.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6861506-A 303 01-MAR-2005;
FEATURES Corixa Corporation; Seattle, WA
LOCATION/Qualifiers
SOURCE 1. 2040
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
 Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
 Hepler,W.T. and Henderson,R.A.
 TITLES Compositions and methods for the therapy and diagnosis of prostate
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 Cortex Corporation; Seattle, WA
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 Homidae; Homo.

REFERENCE
 1 Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
 AUTHORS Compositions and methods for therapy and diagnosis of prostate
 TITLE cancer
 JOURNAL Patent: WO 0125272-A 375 12-APR-2001;
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GenCore version 5.1.6
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KW	breast cancer; B18Ag1; B11Ag1; B15Ag1; 88.
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PD	19-OCT-2000.
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XX	07-APR-2000; 2000WO-US009312.
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XX	09-APR-1999; 99US-00289198.
PR	28-OCT-1999; 99US-00429755.
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PR	23-MAR-2000; 2000US-00534825.
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DR	WPI; 2000-628403/60.
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PT	An isolated polypeptide comprising an immunogenic portion of a breast
XX	tumor protein used for inhibiting the development of cancer, especially
PT	breast cancer, and monitoring cancer progression in a patient.
XX	
PS	Claim 4; Page 178; 187p; English.
XX	
CC	The present sequence is given in a specification relating to compositions
CC	and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC	sequences that are preferentially expressed in breast tumour tissue, and
CC	the polypeptides encoded by such nucleotide sequences, are used in

CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points. CD4+
CC and/or CD8+ T-cells isolated from the cancer patient may be treated with
CC tumour-specific polypeptides, polynucleotides encoding the polypeptides
CC or antigen presenting cells expressing the polypeptides. The cells are
CC then administered to the patient to inhibit development of cancer
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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGATGAGATCTGATTAAGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACCTGGAATTAATACAGATGAGATCTGATTAAGAA 1860
QY 1861 GAAAAGCAGATGAGAGTGTGTAAGAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
DB 1861 GAAAAGCAGATGAGAGTGTGTAAGAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCATTTGATGATGAAAAATGATACGTTGCGGAGAAAGAAATGCTTAAG 1980
DB 1921 GAAAAAGCATTTGATGATGAAAAATGATACGTTGCGGAGAAAGAAATGCTTAAG 1980
```

QY 1981 GAGCTAGACATGAAACCTCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAA 2040
DB 1981 GAGCTAGACATGAAACCTCAGAGCCAGCTAAAAAAAAAAAAAAAAAAAA 2040

RESULT 2
AAH93716
ID AAH93716 standard; cDNA; 2040 BP.
XX AAH93716;
AC
XX
XX 04-OCT-2001 (first entry)
DT
XX
XX Human prostate-specific cDNA sequence B305D splice variant #10.
DE
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KM cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
XX MO200151633-A2.
XX
XX 19-JUL-2001.
PD
XX
XX 16-JUN-2001; 2001MO-US001574.
PF
XX
XX 14-JAN-2000; 2000US-00483672.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Ku J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YW,
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
DR
XX
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
PT
XX
XX
XX Claim 1; Page 348; 543pp; English.

CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAM0115 to AAM01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
CC
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
DB 1 ATGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120

QY 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTGCTATGAAGACATCAGAGCAAG 180

DB 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240

QY 241 GGGCTTCTGAGAGCAAGACGACTTGTCTATGAAGACCTCAGGAACAAGATGGCAAG 300
DB 241 GGGCTTCTGAGAGCAAGACGACTTGTCTATGAAGACCTCAGGAACAAGATGGCAAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGGCGCAAGAGTGGGCGCTTGG 360

QY 361 GGAGACTAGTAGACAGTGCCTTCATGAGAGCCAGGTACACGCTCCGTGGAAGATCTG 420
DB 361 GGAGACTAGTAGACAGTGCCTTCATGAGAGCCAGGTACACGCTCCGTGGAAGATCTG 420

QY 421 GACAGCTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480

QY 481 GACAGCTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 481 GACAGCTTCAAGAGCTGCTGTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480

QY 541 TCTGCCAATGGGAATCAGAAATGTAATACTCTCTGTCAGACAGATGTCATCTTAAT 600
DB 541 TCTGCCAATGGGAATCAGAAATGTAATACTCTCTGTCAGACAGATGTCATCTTAAT 600

QY 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCCGTACATGCCAGAAATGAA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCCGTACATGCCAGAAATGAA 660

QY 661 TGTGCGTTATGTGTGTAAGACATGCGACTGATCCAAATATTCAGATGATATGAAAT 720
DB 661 TGTGCGTTATGTGTGTAAGACATGCGACTGATCCAAATATTCAGATGATATGAAAT 720

QY 721 ACCACTGTCACACTACGCTATCTTAATGAAGTAATAATGAGCAAGCATGCTCTTA 780
DB 721 ACCACTGTCACACTACGCTATCTTAATGAAGTAATAATGAGCAAGCATGCTCTTA 780

QY 781 TATGTGCTGATATCGAATCAAAAAACAAGATGCGCTCACACACTGTTACTTGTGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAAACAAGATGCGCTCACACACTGTTACTTGTGTGA 840

QY 841 CATGAGCAAAAACAGAAATGCGTAATTTTAATCAAGAAAAACGTAATTAATGCA 900
DB 841 CATGAGCAAAAACAGAAATGCGTAATTTTAATCAAGAAAAACGTAATTAATGCA 900

QY 901 CTGATATGATATGAAGAGCTGCTCATATCTTGTGTGATGATGATGATGATGATGAT 960
DB 901 CTGATATGATATGAAGAGCTGCTCATATCTTGTGTGATGATGATGATGATGATGAT 960

QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGCAAGTACTTCTGATCTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGCAAGTACTTCTGATCTAC 1080

QY 1081 AAAAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCAGAAACAAGACTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCAGAAACAAGACTTAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAACAAGCTTCAAGGCAATGAAATGCAAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAGCTTCAAGGCAATGAAATGCAAGCCAGAGAA 1200

QY 1201 ATGTCTCAAGAACCAAGTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAAGAACCAAGTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1260

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Db      1201 ATGTCTCAAGAACCCAGAAATAAATGAAGATGTGATAGAGAGGTGAAGAAATGAAG 1260
Qy      1261 AAGCATGAAGTAATTAATGAGGATTAATCTAGAAAACCTGAATGATGCTGCTGGC 1320
Db      1261 AAGCATGAAGTAATTAATGAGGATTAATCTAGAAAACCTGAATGATGCTGCTGGC 1320
Qy      1321 AATGTGATTAATGATTAATCTCAAGAGAGAGAGACACTGTAATTCAGCAATTT 1380
Db      1321 AATGTGATTAATGATTAATCTCAAGAGAGAGAGACACTGTAATTCAGCAATTT 1380
Qy      1381 CCTGACACGAAAGTGAAGAGTATCAACAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
Db      1381 CCTGACACGAAAGTGAAGAGTATCAACAGAAATTTGCGAATTAATTTCTGACAAAGAA 1440
Qy      1441 AAGCAGATGCGAAATTAATCTCTGAAAAACAGAACCCAGAAACCTTAAGCTGACA 1500
Db      1441 AAGCAGATGCGAAATTAATCTCTGAAAAACAGAACCCAGAAACCTTAAGCTGACA 1500
Qy      1501 TCAGAGAAAGAGTCAAGAAAGCTTGAAGGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
Db      1501 TCAGAGAAAGAGTCAAGAAAGCTTGAAGGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
Qy      1561 CAAGAACCCAGAAATAAATGAATGATGATAGAGAGCTAGAAATTTTATGCTATCGAA 1620
Db      1561 CAAGAACCCAGAAATAAATGAATGATGATAGAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAAGAACCGAAGTACTCATGTCGGATTCGCCAGAAACCTGACTAATGCTGCC 1680
Db      1621 GAAATGAAGAACCGAAGTACTCATGTCGGATTCGCCAGAAACCTGACTAATGCTGCC 1680
Qy      1681 ACTGTGCGCAATGATGATGATTAATTCCTCAAGAGAGAGAGACACTGGAAGC 1740
Db      1681 ACTGTGCGCAATGATGATGATTAATTCCTCAAGAGAGAGAGACACTGGAAGC 1740
Qy      1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGATGACAGACAAATGATCTCAG 1800
Db      1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGATGACAGACAAATGATCTCAG 1800
Qy      1801 AAGCAATTTTGAAGAACGAGACACTGGAATTTACAGATGATGATTCATGAA 1860
Db      1801 AAGCAATTTTGAAGAACGAGACACTGGAATTTACAGATGATGATTCATGAA 1860
Qy      1861 GAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTCTCTAGTTGTAAGAA 1920
Db      1861 GAAAGCAGATGAGAGTGTGAAAAATGAATTTCTGAGCTTCTCTAGTTGTAAGAA 1920
Qy      1921 GAAAAAGACATCTTTCATGAAAAATAGTACGTTGCGGAGAAATTCCTAGTACAGCTG 1980
Db      1921 GAAAAAGACATCTTTCATGAAAAATAGTACGTTGCGGAGAAATTCCTAGTACAGCTG 1980
Qy      1981 GAGCTAGACACATGAAACATGACGAGCGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
Db      1981 GAGCTAGACACATGAAACATGACGAGCGCTAAAAAATTTTAAAAAATTTTAAAAA 2040

RESULT 3
AAI67213
ID AAI67213 standard; cDNA; 2040 BP.
XX
AC AAI67213;
XX
DT 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 3 encoding cDNA.
XX
KM Genetic subraction; DNA microarray analysis; polymerase chain reaction;
XX cancer; B305D; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..2016
FT CDS /*tag= a

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FT      /product= "B305D isoform C splice variant"
XX
XX      MO200175171-A2.
XX
XX      11-OCT-2001.
XX
XX      02-APR-2001; 2001WO-US010631.
XX
XX      03-APR-2000; 2000US-0194241P.
XX      20-JUL-2000; 2000US-0219862P.
XX      27-JUL-2000; 2000US-0221300P.
XX      18-DEC-2000; 2000US-0256592P.
XX
XX      (CORI-) CORIXA CORP.
XX
XX      Houghton RI, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
XX      WPI; 2001-626449/72.
XX      P-PSDB; AAG65978.
XX
XX      Identifying tissue (tumor)-specific polynucleotides overexpressed in
XX      tissue of interest as compared to control tissue, for detecting cancer
XX      cells in patient, comprises DNA microarray analysis or quantitative
XX      polymerase chain reaction.
XX
XX      Claim 4; Page 94-95; 127pp; English.
XX
XX      The invention relates to identifying tissue-specific polynucleotides (P)
XX      that involves performing a genetic subraction to identify pool of (P)
XX      from tissue of interest (TI), performing DNA microarray analysis to
XX      identify first subset of polynucleotides (SP1) at least 2-fold over
XX      expressed in TI, and performing quantitative polymerase chain reaction
XX      (PCR) analysis on SP1 to identify second subset of (P). The method is
XX      useful for determining the presence or absence of a cancer cell in a
XX      patient, monitoring the progression of cancer in a patient using a
XX      biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX      urine or a tumour biopsy sample. The methods are useful for determining
XX      the presence or absence of or monitoring progression of prostate, breast,
XX      colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
XX      gastric, kidney, bladder, pancreatic or endometrial cancer. The present
XX      sequence represents a cDNA encoding a B305D isoform C splice variant
XX
XX      Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 2040; DB 4; Length 2040;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1 ATGTGTGATGAGTTGATTCATGCGCGGCTGCTTCTGTGAAGAAAGCATTTGGTCTC 60
Db      1 ATGTGTGATGAGTTGATTCATGCGCGGCTGCTTCTGTGAAGAAAGCATTTGGTCTC 60
Qy      61 AGGAGCAAGATGAGGCAAGTGTGCTGCGCTTGCTTCCCTGCTGACGAGAGCGGCAAG 120
Db      61 AGGAGCAAGATGAGGCAAGTGTGCTGCGCTTGCTTCCCTGCTGACGAGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTTTGGAGAACCAACGACACTCTGCTATGAAGACATTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTTTGGAGAACCAACGACACTCTGCTATGAAGACATTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGACAGGAGGAGTGGCAAGACAGTG 240
Db      181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGACAGGAGGAGTGGCAAGACAGTG 240
Qy      241 GCGGCTTTCGAGACACGACGACTCTGTATGAAGACACTGAGAAACAAGATGGGCAAG 300
Db      241 GCGGCTTTCGAGACACGACGACTCTGTATGAAGACACTGAGAAACAAGATGGGCAAG 300
Qy      301 TGTGTGCGCACTGCTTCCCTGCTGACAGGAGGAGCGGCAAGACAGTGGCGCTTGG 360
Db      301 TGTGTGCGCACTGCTTCCCTGCTGACAGGAGGAGCGGCAAGACAGTGGCGCTTGG 360
Qy      361 GGAAGACTAGATGACAGTGCCTTCATGAGAGCCAGGTACCAAGTCGCTGGAGAAAGATCTG 420

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Db      361 GGAAGACTAGATGACAGTCCCTTCATGAGCCAGATCCAGTCCGTGGAGAAAGTCTG 420
Qy      421 GACAACTCCACAGAGCTCCGTGGTGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
Db      421 GACAACTCCACAGAGCTCCGTGGTGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
Qy      481 CTCAGGACACTGACGTGAAACAAGAGGCAAGCAAAAGAGGCTGCTACATCTGGCC 540
Db      481 CTCAGGACACTGACGTGAAACAAGAGGCAAGCAAAAGAGGCTGCTACATCTGGCC 540
Qy      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGCAAGAGATGCACTTAAT 600
Db      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGCAAGAGATGCACTTAAT 600
Qy      601 GTTCCTTGACAAACAAAAGAGACAGCTTGATTAAGCCGTACATGCGAAGAGATGAA 660
Db      601 GTTCCTTGACAAACAAAAGAGACAGCTTGATTAAGCCGTACATGCGAAGAGATGAA 660
Qy      661 TGTGGCTTAATGTGTGGAACAAGGCAATGCAATTCGAATTCAGATGATGGAAT 720
Db      661 TGTGGCTTAATGTGTGGAACAAGGCAATGCAATTCGAATTCAGATGATGGAAT 720
Qy      721 ACCACTCTGCACTACGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Db      721 ACCACTCTGCACTACGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Qy      781 TATGTGCTGATATCGAATCAAAAAACAAGATGGCTCAACAACCTGTTACTTGTGTA 840
Db      781 TATGTGCTGATATCGAATCAAAAAACAAGATGGCTCAACAACCTGTTACTTGTGTA 840
Qy      841 CATGAGCAAAAAACAGAACTCGTGAATTTTATTAAGAAAAAAGCGAATTTAAATGCA 900
Db      841 CATGAGCAAAAAACAGAACTCGTGAATTTTATTAAGAAAAAAGCGAATTTAAATGCA 900
Qy      901 CTGATATGATGAGAAAGACTGCTCATACTGCTGATAGTTGTTGATGAGCAAGTATA 960
Db      901 CTGATATGATGAGAAAGACTGCTCATACTGCTGATAGTTGTTGATGAGCAAGTATA 960
Qy      961 GTCAAGCTTCTAATTGAGCAAAATATATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db      961 GTCAAGCTTCTAATTGAGCAAAATATATGATCTTCTCAAGATCTATCTGAGACAG 1020
Qy      1021 GCCAAGAGATATGCTGTTCTAGTCTATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db      1021 GCCAAGAGATATGCTGTTCTAGTCTATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy      1081 AAAAGAAAAACAGATGCTAAATCTCTGCAAAAACAGAAATCCAGAAACAGATTAAG 1140
Db      1081 AAAAGAAAAACAGATGCTAAATCTCTGCAAAAACAGAAATCCAGAAACAGATTAAG 1140
Qy      1141 CTGACATCAGAGAGAAAGTCACAAAGTTCAAAAGGAGTAAATAGCAGCCAGAGAAA 1200
Db      1141 CTGACATCAGAGAGAAAGTCACAAAGTTCAAAAGGAGTAAATAGCAGCCAGAGAAA 1200
Qy      1201 ATGTCTCAAGAAACCAAGAAATTAATGAATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAAACCAAGAAATTAATGAATGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy      1261 AAGCAATGAAGTAAATATGAGGATTAATGAGAAACCTGATCTGCTGAGC 1320
Db      1261 AAGCAATGAAGTAAATATGAGGATTAATGAGAAACCTGATCTGCTGAGC 1320
Qy      1321 AATGTGATATGATTAATCTCAAGAGAAAGAGCAACCTGAATATGCAATTT 1380
Db      1321 AATGTGATATGATTAATCTCAAGAGAAAGAGCAACCTGAATATGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAAATGATTCTGATCAAAAGAA 1440
Db      1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAAATGATTCTGATCAAAAGAA 1440
Qy      1441 AAAAGATGCAAAATTAATCTCTGAAAAACAGCAACCAAGAACTTAAGCTGACA 1500

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Db      1441 AAAAGATGCAAAATTAATCTCTGAAAAACAGAAACCAAGAACTTAAGCTGACA 1500
Qy      1501 TCAAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATATGCGACGACAGAAAGATCT 1560
Db      1501 TCAAGAAAGAGTCAAAAGGCTTGAAGGCAAGTGAATATGCGACGACAGAAAGATCT 1560
Qy      1561 CAAGAACCAGAAATTAATGAAGATGATAGAGAGCTGAATATTTATGCTATCGAA 1620
Db      1561 CAAGAACCAGAAATTAATGAAGATGATAGAGAGCTGAATATTTATGCTATCGAA 1620
Qy      1621 GAATGAAGAACCAAGAAAGTACTATGTCGAAATTCAGAAAACTGATATGCTGAC 1680
Db      1621 GAATGAAGAACCAAGAAAGTACTATGTCGAAATTCAGAAAACTGATATGCTGAC 1680
Qy      1681 ACTGCTGGCAATGCTGATGATGATTAATCTCTCAAGAAAGAGCAACCTGAAAGC 1740
Db      1681 ACTGCTGGCAATGCTGATGATGATTAATCTCTCAAGAAAGAGCAACCTGAAAGC 1740
Qy      1741 CAGCAATTCCTGACACTGAGAAATGAAGATATCAAGTGAAGAAACAAATGATCTCAG 1800
Db      1741 CAGCAATTCCTGACACTGAGAAATGAAGATATCAAGTGAAGAAACAAATGATCTCAG 1800
Qy      1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAGATTTCTGATGAA 1860
Db      1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTAACAGATGAGATTTCTGATGAA 1860
Qy      1861 GAAAAGCAGATGAAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Db      1861 GAAAAGCAGATGAAAGTGTGAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Qy      1921 GAAAAAGCATCTTGCATGAAAAATGTAAGTTGCGGGAAGAAATGCCATGCTAAGACG 1980
Db      1921 GAAAAAGCATCTTGCATGAAAAATGTAAGTTGCGGGAAGAAATGCCATGCTAAGACG 1980
Qy      1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
Db      1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 4
AAS63809
ID AAS63809 standard; cDNA; 2040 BP.
XX
AC AAS63809;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #10.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX

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PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Rether MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX MPI: 2001-639232/73.
XX P-PSDB: AAU69779.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Claim 1, Page 350, 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polynucleotide of the invention
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTTGATTCATGACCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGGAGTTGATTCATGACCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60

QY 61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGACCGCAAG 120
DB 61 AGAGCAAGATGAGGCAAGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGACCGCAAG 120

QY 121 AACCAACGTGGGCACTTCTGAGACCAACGACGACTGCTGATGAAGACATCTCAGAGCAAG 180
DB 121 AACCAACGTGGGCACTTCTGAGACCAACGACGACTGCTGATGAAGACATCTCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCGGCACTGCTCCCTGCTGCAAGGAGAGTGGCAAGACGAGC 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTCCCTGCTGCAAGGAGAGTGGCAAGACGAGC 240

QY 241 GGCCTTCTGAGAGACCAACGACGACTGCTGATGAAGACATCTCAGAGCAAGTGGCAG 300
DB 241 GGCCTTCTGAGAGACCAACGACGACTGCTGATGAAGACATCTCAGAGCAAGTGGCAG 300

QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGAGCAGTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACGAGCAGTGG 360

QY 361 GGAAGACTAGAGTACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAAGATCTG 420
DB 361 GGAAGACTAGAGTACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAAGATCTG 420

QY 421 GACCACTTCAACGAGCTGCTGCTGAGGAGCCAGGTACAGTCCGTGGAAGATCTG 480
DB 421 GACCACTTCAACGAGCTGCTGCTGAGGAGCCAGGTACAGTCCGTGGAAGATCTG 480

QY 481 CTCAGGAGACATGACCTGAGCAAGAGACAGCAAAAGAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGAGACATGACCTGAGCAAGAGAGCAAGCAAAAGAGCTGCTTACATCTGGCC 540

QY 541 TCTGCAATGGGAAATTCAGAGTAAATCTCTGCTGGAAGAGATGTAAT 600
DB 541 TCTGCAATGGGAAATTCAGAGTAAATCTCTGCTGGAAGAGATGTAAT 600

QY 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGCTACATGCGAGAAAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGCTACATGCGAGAAAGATGA 660

DB 601 GTCTTGAACAACAAAAGAGACAGCTGTGATTAAGCGCTACATGCGAGAAAGATGA 660
QY 661 TGTGGTAAATGTTCTGGAACATGCACTGATCCAAATATCCAGATGATGAAT 720
DB 661 TGTGGTAAATGTTCTGGAACATGCACTGATCCAAATATCCAGATGATGAAT 720

QY 721 ACCACTGCACTACGCTATCTATGATGAAGATTAATATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTGCACTACGCTATCTATGATGAAGATTAATATGAGCCAAAGCACTGCTTA 780

QY 781 TATGCTGCTGATATGATCAAAAAACAGATGAGCTTCAACCACTGATCTTGATGA 840
DB 781 TATGCTGCTGATATGATCAAAAAACAGATGAGCTTCAACCACTGATCTTGATGA 840

QY 841 CATGACAAAAACACAAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGACAAAAACACAAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900

QY 901 CTGATATGATATGAGAGCACTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAGAGCACTGCTCATCTGCTGATGTTGTGATCAGCAAGTATA 960

QY 961 GTGACCTTCTTACCTTGAAGCAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTGACCTTCTTACCTTGAAGCAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020

QY 1021 GCCAAGAGTATGCTGTTCTTATGATCATCATGTAATTTGGCAGTTACTTCTGATAC 1080
DB 1021 GCCAAGAGTATGCTGTTCTTATGATCATCATGTAATTTGGCAGTTACTTCTGATAC 1080

QY 1081 AAGAAAAACAGATCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
DB 1081 AAGAAAAACAGATCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140

QY 1141 CTGACATCAAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATATGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATATGCCAGCAGAGAAA 1200

QY 1201 ATGTCTCAAGAACCAAAATTAATAGATGTTGATGAGAGTTGAAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATAGATGTTGATGAGAGTTGAAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATATGTTGGATTTACTAGAAAACTGACTAATGTTGTCAGTGGC 1320
DB 1261 AAGCATGAAAGTAAATATGTTGGATTTACTAGAAAACTGACTAATGTTGTCAGTGGC 1320

QY 1321 AATGTTGATTAATGATTAATTTCTCAAAAGAAAGACAGAACCTGAAATGACAAATT 1380
DB 1321 AATGTTGATTAATGATTAATTTCTCAAAAGAAAGACAGAACCTGAAATGACAAATT 1380

QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGTTCTGATCAAAAGAA 1440

QY 1441 AAAAGATGCAAAATTAATCTCTGAAAAACAGCAACCCAGAACAACTTAAAGCTGACA 1500
DB 1441 AAAAGATGCAAAATTAATCTCTGAAAAACAGCAACCCAGAACAACTTAAAGCTGACA 1500

QY 1501 TCAAGAGAAAGTCAAAAGGCTTGAAGGCAAGTAAATGTCAGCAGAGAGAAAGATCT 1560
DB 1501 TCAAGAGAAAGTCAAAAGGCTTGAAGGCAAGTAAATGTCAGCAGAGAGAAAGATCT 1560

QY 1561 CAAGAAACCAAAATTAATGAAGATGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAAACCAAAATTAATGAAGATGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620

QY 1621 GAAATGAGAGACAGAAAGTACTAGTCGATCCAGAAACCTGACTAATGATGTC 1680
DB 1621 GAAATGAGAGACAGAAAGTACTAGTCGATCCAGAAACCTGACTAATGATGTC 1680

QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740


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Db 1021 GCCAGAGATAGCTGTTCTGATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAAAATCTCTGAGAAAAGAGAAATCCAGAAAGATCTTAAAG 1140
Db 1081 AAGAGAAAAAGATGCTAAAAATCTCTGAGAAAAGAGAAATCCAGAAAGATCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGAGTGAATAATAGCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGAGTGAATAATAGCAGCAGAGAAA 1200
QY 1201 ATGCTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAGAAATGAAG 1260
Db 1201 ATGCTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGAGGATTACTAGAAAACCTGATATGCTGCTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATATGAGGATTACTAGAAAACCTGATATGCTGCTGCTGCG 1320
QY 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACACGAAAGTGAAGAGATCAAGAAATTTGCGAAATTTAGTTTCTGACTACAAAG 1440
Db 1381 CCTGACACGAAAGTGAAGAGATCAAGAAATTTGCGAAATTTAGTTTCTGACTACAAAG 1440
QY 1441 AAAAGATGCGCAAAATCTCTGAGAAACAGAAACCCAGAAACAAACTTAAAGCTGAGA 1500
Db 1441 AAAAGATGCGCAAAATCTCTGAGAAACAGAAACCCAGAAACAAACTTAAAGCTGAGA 1500
QY 1501 TCAGAGAGAGAGTCAAGAGAGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGAGTCAAGAGAGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 CAAAGACCGAAATTAATAGATGCTGATAGAGAGCTGAGAAATTTATGCTATCGAA 1620
Db 1561 CAAAGACCGAAATTAATAGATGCTGATAGAGAGCTGAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGAGAGAGTCTCATGTCGAGTTCCCGAGAAACCTGACTATAGTGGC 1680
Db 1621 GAAATGAAGAGAGAGAGTCTCATGTCGAGTTCCCGAGAAACCTGACTATAGTGGC 1680
QY 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGCACTGAGATGAAGAGATCAAGTGAAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAGCAATTTCTGCACTGAGATGAAGAGATCAAGTGAAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 AAGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 AAGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GAAAGACAGATGAAGTGTGTTGAAAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGACAGATGAAGTGTGTTGAAAAATGAATTTGAGCTTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATGATACGTTGCGGAGAGAAATTTGCCATGCTAAGCTG 1980
Db 1921 GAAAAAGACATCTTGATGAAAAATGATACGTTGCGGAGAGAAATTTGCCATGCTAAGCTG 1980
QY 1981 GAGCTTGAACACATGAAGATCTGAGAGCCAGCTTAAAAAAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGCTTGAACACATGAAGATCTGAGAGCCAGCTTAAAAAAGAGAGAGAGAGAGAGAG 2040
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RESULT 6
AAH85030
ID AAH85030 standard; cDNA, 2040 BP.
XX
AC AAH85030;
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XX
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #10.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN WO200134802-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US030904.
XX
PR 12-NOV-1999; 99US-00439313.
XX
PR 18-NOV-1999; 99US-00443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SJ, Jiang Y, Reed SG;
PI Kalos MD, Rector MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
XX MPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX
PS Claim 31; Page 248; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production. The
CC polypeptides, nucleic acids and antibodies from the present invention are
CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
CC region on chromosome 22q11.2 known as the cat eye syndrome region.
CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
Db 1 ATGTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
QY 61 AGGACCAAGATGGGAGAGTGGTGGCTGCTCCCTGCTGCAAGGAGAGCCGCAAG 120
Db 61 AGGACCAAGATGGGAGAGTGGTGGCTGCTCCCTGCTGCAAGGAGAGCCGCAAG 120
QY 121 AGCAAGTGGGCACTTTCTGAGAGACAGACGACTCTGCTATGAAGACATCTAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTTCTGAGAGACAGACGACTCTGCTATGAAGACATCTAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAAG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAAG 240
QY 241 GGGCGTTCTGAGAGACAGACGACTGCTATGAAGACATCTGAGAAAGATGGGCAAG 300
Db 241 GGGCGTTCTGAGAGACAGACGACTGCTATGAAGACATCTGAGAAAGATGGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCCGCAAGAGCAAGTGGGCGCTGG 360
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Db	301	TGTCGTCTCCACCTGCTTCCCTGCTGCGAGGGGGAGCGGCGAAGAGGTGGCGCTTGG	360
Oy	361	GGAGACTACGATGACAGTGCCTTCATGAGGCCACAGTACCACTGCCGTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGAGGCCACAGTACCACTGCCGTGAGAAAGATCTG	420
Oy	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGGTAAAGTCCGAGAAAGATCTCATGTCTATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGGTAAAGTCCGAGAAAGATCTCATGTCTATG	480
Oy	481	CTCAGGGGACACTGACGTGAACAAGAAGGACAAAGCAAAAGAGGACGTGCTCATCTGGCC	540
Db	481	CTCAGGGGACACTGACGTGAACAAGAAGGACAAAGGAGAGCTGCTCATCATCTGGCC	540
Oy	541	TCCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGCTGAGCAGACGATGCAACTTAAT	600
Db	541	TCCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGCTGAGCAGACGATGCAACTTAAT	600
Oy	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGATPAAAGGCCGTGACATGCCAGAAAGATGA	660
Db	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGATPAAAGGCCGTGACATGCCAGAAAGATGA	660
Oy	661	TGTGGCTTAATAGTTGCTGAGCAATGGGCACTGATCCAAATATTCAGAGATGATGGAAT	720
Db	661	TGTGGCTTAATAGTTGCTGAGCAATGGGCACTGATCCAAATATTCAGAGATGATGGAAT	720
Oy	721	ACCACCTGCGACCTACGCTATCTATPATAAGATAAATTAATGAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACCTGCGACCTACGCTATCTATPATAAGATAAATTAATGAGCCAAAGCACTGCTCTTA	780
Oy	781	TATGGTGTGATATTCGAATCAAAAAACAAGCATGGCCTCACACCATGTTACTTGGTGTGA	840
Db	781	TATGGTGTGATATTCGAATCAAAAAACAAGCATGGCCTCACACCATGTTACTTGGTGTGA	840
Oy	841	CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGGAAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGGAAATTTAAATGCA	900
Oy	901	CTGATATGATATGGAAGGACTGCTCATACCTTGCTGTATGTTGGATCAGCAAGATGA	960
Db	901	CTGATATGATATGGAAGGACTGCTCATACCTTGCTGTATGTTGGATCAGCAAGATGA	960
Oy	961	GTCAGCCCTTCTACTTGAGCAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCG	1020
Db	961	GTCAGCCCTTCTACTTGAGCAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCG	1020
Oy	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
Oy	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACCAAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACCAAGACTTAAG	1140
Oy	1141	CTGACATCAGAGAGAGTCACAAAAGTTCAAAGGCAAGTGAATAATAGCCAGAGAAAA	1200
Db	1141	CTGACATCAGAGAGAGTCACAAAAGTTCAAAGGCAAGTGAATAATAGCCAGAGAAAA	1200
Oy	1201	ATGTCTCAAGAACCGAATAATATPAGAGTGTGATAGAGGTTGAAGAAATATGAG	1260
Db	1201	ATGTCTCAAGAACCGAATAATATPAGAGTGTGATAGAGGTTGAAGAAATATGAG	1260
Oy	1261	AAGCATGAAATPAAATATGTTGGGAAATTTACTAABAAAACCTGATATGAGTGTCACTGGC	1320
Db	1261	AAGCATGAAATPAAATATGTTGGGAAATTTACTAABAAAACCTGATATGAGTGTCACTGGC	1320
Oy	1321	AATGTGTATTAATGATTAATCTCTCAAAAGAGACAGAACCTGTGAATAATCAGCAATTT	1380
Db	1321	AATGTGTATTAATGATTAATCTCTCAAAAGAGACAGAACCTGTGAATAATCAGCAATTT	1380
Oy	1381	CCTGACAAACGAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAAACGAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440

Db	1381	CCTGACAAACGAAATGTGAAGAGTATCACAGAAATTTGCAATTTAGTTCTGTACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATACTCTTCTGAAAAACGACACCAGAACAGAAGCTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATACTCTTCTGAAAAACGACACCAGAACAGAAGCTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAAGGTCAAAAGGCTTGAGAGGCAATGAAATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGGAAAGGTCAAAAGGCTTGAGAGGCAATGAAATGGCCAGCCAGAGAAAAGATCT	1560
Qy	1561	CAAGAACAGAAATTAATTAAGATGTGATAGAGAGCTAGAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACAGAAATTAATTAAGATGTGATAGAGAGCTAGAAATTTTATGGCTATCGAA	1620
Qy	1621	GAAATGAAGAAAGCACGAAGTACTCATGTGGAATTTCCAGAAAACTGACTAAATGTGTC	1680
Db	1621	GAAATGAAGAAAGCACGAAGTACTCATGTGGAATTTCCAGAAAACTGACTAAATGTGTC	1680
Qy	1681	ACTGCTGGCAATGGTGTATGATGATTAATTTCTTCCAAAGAAAGCAGAACACTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGATGATTAATTTCTTCCAAAGAAAGCAGAACACTGAAAGC	1740
Qy	1741	CAGCAATTTCTCGTACACTGAGAAATGAAGAGTATCACAGTACCGAACAAATGATCTCAG	1800
Db	1741	CAGCAATTTCTCGTACACTGAGAAATGAAGAGTATCACAGTACCGAACAAATGATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCGATTCAATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTCGATTCAATGAA	1860
Qy	1861	GAAAGCAGATAGAGTGTGTTGAAAAATGAATTCAGCTTCTCTTAACTGTAAGAAA	1920
Db	1861	GAAAGCAGATAGAGTGTGTTGAAAAATGAATTCAGCTTCTCTTAACTGTAAGAAA	1920
Qy	1921	GAAAAACAGATCTTGCATGAAAAATGACGTGCGGGAAGAAATTTGCCATGCTTAAGCTG	1980
Db	1921	GAAAAACAGATCTTGCATGAAAAATGACGTGCGGGAAGAAATTTGCCATGCTTAAGCTG	1980
Qy	1981	GAGCTTAGACAAATGAATCAATCAGAGCCAGCTTAAAAATTTTAAAAATTTTAAAAATTTT	2040
Db	1981	GAGCTTAGACAAATGAATCAATCAGAGCCAGCTTAAAAATTTTAAAAATTTTAAAAATTTT	2040
RESULT 7			
ACAS9617			
ID	ACAS9617 standard; cDNA; 2040 BP.		
XX	ACAS9617;		
AC	ACAS9617;		
XX	10-JUN-2003 (first entry)		
DT	10-JUN-2003 (first entry)		
XX	Prostate cancer therapy associated cDNA #360.		
DE	Prostate cancer therapy associated cDNA #360.		
XX	Prostate cancer; vaccine; gene therapy; cytosolic; fusion protein;		
KM	immunogen; cancer; prostate specific antigen; PSA;		
KM	prostatic acid phosphatase; PAP; prostate specific membrane antigen;		
KM	PSMA; gene; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	US2002192763-A1.		
PN	US2002192763-A1.		
XX	19-DEC-2002.		
PD	19-DEC-2002.		
XX	29-JUN-2001; 2001US-00895793.		
PF	29-JUN-2001; 2001US-00895793.		
XX	04-OCT-1999; 99US-0157455P.		
PR	04-OCT-1999; 99US-0157455P.		
XX	28-MAR-2001; 2001US-00822827.		
PR	28-MAR-2001; 2001US-00822827.		
XX	(XUJ/) XU J.		
PA	(DILL/) DILLON D C.		
PA	(MITC/) MITCHAM J L.		

PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUN/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SK, Wang A, Skelky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
 DR MPI; 2001-245062/25.
 XX P-PSDB; ABU71670.
 PT Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 XX
 PS Example 11; SEQ ID NO 375; 85bp; English.
 XX
 CC The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 3 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This sequence represents a prostate cancer
 CC therapy associated cDNA. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docid=US20020192763
 CC
 XX
 SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2040; DB 5; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGGTGGCGCTTGG 360
 DB |||||
 QY 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGGTGGCGCTTGG 360
 DB |||||
 QY 361 GGAGACTAGTACAGTGCCTTCAATGAGCCAGGTACACGCTCGTGGAGAAATCTTG 420
 DB |||||
 QY 361 GGAGACTAGTACAGTGCCTTCAATGAGCCAGGTACACGCTCGTGGAGAAATCTTG 420
 DB |||||
 QY 421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
 DB |||||
 QY 421 GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
 DB |||||
 QY 481 CTCAGGACACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGAGC 540
 DB |||||
 QY 481 CTCAGGACACTGACGTGAAACAAGAAAGCAAGCAAAAGAGAGCTGCTTACATCTGAGC 540
 DB |||||
 QY 541 TCTGCCAATGGGAATTGAGAAAGTAAAACTCTGCTGGACAGACGATGTCACTTAAT 600
 DB |||||
 QY 541 TCTGCCAATGGGAATTGAGAAAGTAAAACTCTGCTGGACAGACGATGTCACTTAAT 600
 DB |||||
 QY 601 GTCTTGGACAAACAAAAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
 DB |||||
 QY 601 GTCTTGGACAAACAAAAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
 DB |||||
 QY 661 TGTGGCTTAATGTGCTGGAAATGACATGCACTGATCCAAATATTCAGATGATGGAAT 720
 DB |||||
 QY 661 TGTGGCTTAATGTGCTGGAAATGACATGCACTGATCCAAATATTCAGATGATGGAAT 720
 DB |||||
 QY 721 ACCACTGTGACATGCTATCTATATGAAATGAAATTAATGAGCCAAAGACGTGCTTAA 780
 DB |||||
 QY 721 ACCACTGTGACATGCTATCTATATGAAATGAAATTAATGAGCCAAAGACGTGCTTAA 780
 DB |||||
 QY 781 TATGTGTCTGATATGGAATCAAAAACAAAGCATGAGCTCCACACACTGTACTTGGTGA 840
 DB |||||
 QY 781 TATGTGTCTGATATGGAATCAAAAACAAAGCATGAGCTCCACACACTGTACTTGGTGA 840
 DB |||||
 QY 841 CATGACAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
 DB |||||
 QY 841 CATGACAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
 DB |||||
 QY 901 CTGATATGATATGAAAGACATGCTCTCATATCTTGTGCTGATGTTGGATCAAGCAATAT 960
 DB |||||
 QY 901 CTGATATGATATGAAAGACATGCTCTCATATCTTGTGCTGATGTTGGATCAAGCAATAT 960
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATGATCTTCAAGATCTATCTGACAGAG 1020
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATGATCTTCAAGATCTATCTGACAGAG 1020
 DB |||||
 QY 961 GTACAGCTTCTATCTGAGAAAATTAATGATGATCTTCAAGATCTATCTGACAGAG 1020
 DB |||||
 QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 DB |||||
 QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
 DB |||||
 QY 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB |||||
 QY 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
 DB |||||
 QY 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAATGAAATTAAGCCAGCAAGAAA 1200
 DB |||||
 QY 1141 CTGACATCAGAGAAAGATCAAAAAGTTCAAAAGCAATGAAATTAAGCCAGCAAGAAA 1200
 DB |||||
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGATGAGAGGTTGAGAAAGAAATGAAG 1260
 DB |||||
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATGATGAGAGGTTGAGAAAGAAATGAAG 1260
 DB |||||
 QY 1261 AAGCATGAAAGTAAATATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAA 1320
 DB |||||
 QY 1261 AAGCATGAAAGTAAATATGATGAAATTAATGAGAAATTAATGAGAAATTAATGAGAA 1320
 DB |||||
 QY 1321 AATGTGATATGATTAATTTCTCAAGAGAAAGAGCAAACTGTAATGATGATCACTGCTG 1380
 DB |||||
 QY 1321 AATGTGATATGATTAATTTCTCAAGAGAAAGAGCAAACTGTAATGATGATCACTGCTG 1380
 DB |||||
 QY 1381 AATGTGATATGATTAATTTCTCAAGAGAAAGAGCAAACTGTAATGATGATCACTGCTG 1440
 DB |||||
 QY 1381 AATGTGATATGATTAATTTCTCAAGAGAAAGAGCAAACTGTAATGATGATCACTGCTG 1440
 DB |||||

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Db      1381  CTTGACACGAAAGTGAAGTATCACAGATTGGAAATTAGTTCTGACTCAAGAA 1440
Qy      1441  AACACATGCCAAATATCTTTCTGAAAAACAGCAACCCAGACAGACTTAAGCTGACA 1500
Db      1441  AACACATGCCAAATATCTTTCTGAAAAACAGCAACCCAGACAGACTTAAGCTGACA 1500
Qy      1501  TCAGAGGAAGTCACAAAGCTTGAAGGAGTGAATAATGGCCAGCCAGAGAAAGTCT 1560
Db      1501  TCAGAGGAAGTCACAAAGCTTGAAGGAGTGAATAATGGCCAGCCAGAGAAAGTCT 1560
Qy      1561  CAAAGAACAGAAATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTATGCTATGAA 1620
Db      1561  CAAAGAACAGAAATTAATTAAGATGCTGATAGAGAGCTAGAAAATTTATGCTATGAA 1620
Qy      1621  GAAATGAAGACGCGAAGTACTCATGTGGAATTCACAGAAAACCTGACTAATGTGTC 1680
Db      1621  GAAATGAAGACGCGAAGTACTCATGTGGAATTCACAGAAAACCTGACTAATGTGTC 1680
Qy      1681  ACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAGCAAGAACCTGAAGC 1740
Db      1681  ACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAGCAAGAACCTGAAGC 1740
Qy      1741  CAGCAATTTCTCTGACACTGAGATGAAGATATCAAGTACGAAACAAATGATCTCAG 1800
Db      1741  CAGCAATTTCTCTGACACTGAGATGAAGATATCAAGTACGAAACAAATGATCTCAG 1800
Qy      1801  AAGCAATTTTGAAGAACGAAACACTGGAATTAACAGATGATGATCTGATTCATGAA 1860
Db      1801  AAGCAATTTTGAAGAACGAAACACTGGAATTAACAGATGATGATCTGATTCATGAA 1860
Qy      1861  GAAAGCAGATAGAGGTTGAAAAAATTCAGCTTCTCTAGTTGTAAGAA 1920
Db      1861  GAAAGCAGATAGAGGTTGAAAAAATTCAGCTTCTCTAGTTGTAAGAA 1920
Qy      1921  GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAAATTCGATGTAAGCTG 1980
Db      1921  GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGAGAAATTCGATGTAAGCTG 1980
Qy      1981  GAGCTTGACACATGAATCACTCAGCGCCGCTTAAAAAATTTAAAAAATTTAAAAA 2040
Db      1981  GAGCTTGACACATGAATCACTCAGCGCCGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 8
ABL95180
ID      ABL95180 standard; cDNA; 2040 BP.
XX
AC      ABL95180;
XX
DT      19-JUL-2002 (first entry)
XX
DE      Human B305D splice variant cDNA sequence SEQ ID NO 375.
XX
KW      Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX      gene therapy; gene; ss.
XX
OS      Homo sapiens.
XX
PN      US200202248-A1.
XX
PD      21-FEB-2002.
XX
PF      12-JAN-2001; 2001US-00759143.
XX
PR      25-FEB-1997; 97US-00806099.
PR      01-AUG-1997; 97US-00904804.
PR      10-FEB-1998; 98US-00020956.
PR      25-FEB-1998; 98US-00030607.
PR      14-JUL-1998; 98US-00115453.
PR      23-SEP-1998; 98US-00159812.
PR      15-JAN-1999; 99US-00232149.
PR      09-APR-1999; 99US-00288946.

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PR      13-JUL-1999; 99US-00352616.
PR      12-NOV-1999; 99US-00439313.
PR      18-NOV-1999; 99US-00439386.
PR      14-JAN-2000; 2000US-00483672.
PR      27-MAR-2000; 2000US-00536857.
PR      09-MAY-2000; 2000US-00568100.
PR      12-MAY-2000; 2000US-00570737.
PR      13-JUN-2000; 2000US-00593793.
PR      27-JUN-2000; 2000US-00605783.
PR      10-AUG-2000; 2000US-00636215.
PR      29-AUG-2000; 2000US-00651236.
PR      06-SEP-2000; 2000US-00657279.
PR      02-OCT-2000; 2000US-00679426.
PR      10-OCT-2000; 2000US-00685166.
XX
XX      (XUJ/) XU J.
XX      (DILL/) DILLON D C.
XX      (MITC/) MITCHAM J L.
XX      (HARL/) HARLOCKER S L.
XX      (JIAN/) JIANG Y.
XX      (KALO/) KALOS M D.
XX      (FANG/) FANGER G R.
XX      (RETT/) RETTER M W.
XX      (STOL/) STOLK J A.
XX      (DAYC/) DAY C H.
XX      (VEDV/) VEDVICK T S.
XX      (CART/) CARTER D.
XX      (LISX/) LI S X.
XX      (WANG/) WANG A.
XX      (SKEI/) SKEIKY Y A W.
XX      (HEPL/) HEPLER W T.
XX      (HEND/) HENDERSON R A.
XX
XX      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
XX      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
XX      Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX      WPI; 2002-255649/30.
XX
XX      New prostate-specific polynucleotides for diagnosing and treating
XX      diseases, in particular prostate cancer, and as markers for the
XX      progression of cancer.
XX
XX      Claim 1; SEQ ID NO 375; 87bp; English.
XX
XX      The present invention provides prostate-specific coding sequences and
XX      their encoded proteins. These can be used in the diagnosis and treatment
XX      of cancers, particularly prostate cancer. The present sequence is a cDNA
XX      described in the invention
XX
XX      SQ      Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 2040; DB 6; Length 2040;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1 ATGGTGTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTCTC 60
Db      1 ATGGTGTGAGATTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTCTC 60
Qy      61 AGAGCAGATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
Db      61 AGAGCAGATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
Qy      121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGACACTCAGAGCAAG 180
Db      121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGACACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGTG 240
Db      181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCGTG 240
Qy      241 GCGGCTTCTGAGACCAAGCACTCTGCTATGAAAGACACTCAGAAACAAGATGGCAAG 300

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Db      241  GGGGCTTCTGGAGACCAAGACGACTCGTATGAACAACCTCAGAAACAAATGGGCAAG 300
Qy      301  TGGTGCTGCACTGTTCCCTGCTGTCAGAGGGGAGGGGCAAGGCAAGGTGGGCGCTTG 360
Db      301  TGGTGCTGCACTGTTCCCTGCTGTCAGAGGGGAGGGGCAAGGCAAGGTGGGCGCTTG 360
Qy      361  GGAAGCTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGGAGAAAGATCTG 420
Db      361  GGAAGCTAGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGGAGAAAGATCTG 420
Qy      421  GACAGCTCGACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
Db      421  GACAGCTCGACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG 480
Qy      481  CTCAGGAGACCTGACGTTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTACATCGGCC 540
Db      481  CTCAGGAGACCTGACGTTGAACAAGAAAGCAAGCAAAAGAGAGCTGCTACATCGGCC 540
Qy      541  TCTGCCAATGGGAATTCAAGAGTAGTAAACTCTGCTGGACAGAGATGCTCACTTAAT 600
Db      541  TCTGCCAATGGGAATTCAAGAGTAGTAAACTCTGCTGGACAGAGATGCTCACTTAAT 600
Qy      601  GTCTCTTGACACAAAAAAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGAAAGTGA 660
Db      601  GTCTCTTGACACAAAAAAGAGACAGCTCTGATTAAGGCGGTACAATGCCAGAAAGTGA 660
Qy      661  TGTGGCTAATGTTGTGGGAACATGGCACTGATCCAAATTTCCAAATAGATAGGAAT 720
Db      661  TGTGGCTAATGTTGTGGGAACATGGCACTGATCCAAATTTCCAAATAGATAGGAAT 720
Qy      721  ACCACTCTGCACTACGCTATCTAATAAGAAATAATTAATGGCCAAACACTGCTCTTA 780
Db      721  ACCACTCTGCACTACGCTATCTAATAAGAAATAATTAATGGCCAAACACTGCTCTTA 780
Qy      781  TATGTCCTGATATCGAATCAAAAAACAAGCATGCGCTCACCACTGTTACTTGGTGA 840
Db      781  TATGTCCTGATATCGAATCAAAAAACAAGCATGCGCTCACCACTGTTACTTGGTGA 840
Qy      841  CATGAGCAAAAAAGAGAGCGTGAATTTTAAATGAAGAAAAAAGCGAATTTAAATGCA 900
Db      841  CATGAGCAAAAAAGAGAGCGTGAATTTTAAATGAAGAAAAAAGCGAATTTAAATGCA 900
Qy      901  CTGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGTGGATCAGCAATGATA 960
Db      901  CTGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGTGGATCAGCAATGATA 960
Qy      961  GTGAGCTTCTACTTGAGCAAAAATATTGATGTAATCTTCTCAAGATCTATCTGACAG 1020
Db      961  GTGAGCTTCTACTTGAGCAAAAATATTGATGTAATCTTCTCAAGATCTATCTGACAG 1020
Qy      1021  GCCAGAGATATGCTGTTCTGATCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db      1021  GCCAGAGATATGCTGTTCTGATCATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy      1081  AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Db      1081  AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Qy      1141  CTGACATCAGAGAGAGTCACAAAGTTCAAGGACAGTGAATAATAGCCAGCCAGAAA 1200
Db      1141  CTGACATCAGAGAGAGTCACAAAGTTCAAGGACAGTGAATAATAGCCAGCCAGAAA 1200
Qy      1201  ATGTCTCAAGAACCAAGAAATTAAGATGCTGATAGAGAGGTTGAAGAAAGAAAG 1260
Db      1201  ATGTCTCAAGAACCAAGAAATTAAGATGCTGATAGAGAGGTTGAAGAAAGAAAG 1260
Qy      1261  AAGCATGAAGATATATGAGGATTAAGAAAACTGACTAATGCTGCTGCTGCTGCTG 1320
Db      1261  AAGCATGAAGATATATGAGGATTAAGAAAACTGACTAATGCTGCTGCTGCTGCTGCTG 1320
Qy      1321  AATGTGATATGATTAATTTCTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Db      1321  AATGTGATATGATTAATTTCTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380

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Db      1321  AATGTGATATGATTAATTTCTCAAGAGAGAGCAACCTGAAAAATCAGCAATTT 1380
Qy      1381  CCTGACACGAAAGAGAGATGACAGAAATTTGCGAATTTGCTTGTGACTACAAAGAA 1440
Db      1381  CCTGACACGAAAGAGAGATGACAGAAATTTGCGAATTTGCTTGTGACTACAAAGAA 1440
Qy      1441  AAACAGATGCCAAAAATCTCTCTGAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
Db      1441  AAACAGATGCCAAAAATCTCTCTGAAAAACAGCAACCCAGAACCAAGCTTAAAGCTGACA 1500
Qy      1501  TCAAGAGAAAGATGACAAAGGCTTTGAGGGCAGTGAATAATGCGCAGAGAAAAAGATCT 1560
Db      1501  TCAAGAGAAAGATGACAAAGGCTTTGAGGGCAGTGAATAATGCGCAGAGAAAAAGATCT 1560
Qy      1561  CAAGAACCGAAATTAATTAAGATGATGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620
Db      1561  CAAGAACCGAAATTAATTAAGATGATGATTAAGAGCTTGAAGAAATTTATGCTATCGAA 1620
Qy      1621  GAAATGAAGAGACAGAAAGTACTCATGTCGATTCGCCAGAAAACTGACTAATGGTGC 1680
Db      1621  GAAATGAAGAGACAGAAAGTACTCATGTCGATTCGCCAGAAAACTGACTAATGGTGC 1680
Qy      1681  ACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740
Db      1681  ACTGCTGCAATGATGATGATTAATTTCTTCAAGAGAGAGCAACCTGAAAGC 1740
Qy      1741  CAGCAATTTCTGACACTGAGATGAAGATGATCAAGTGAAGACAAATGATACTGAC 1800
Db      1741  CAGCAATTTCTGACACTGAGATGAAGATGATCAAGTGAAGACAAATGATACTGAC 1800
Qy      1801  AAGCAATTTTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTAAGAA 1860
Db      1801  AAGCAATTTTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTAAGAA 1860
Qy      1861  GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Db      1861  GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
Qy      1921  GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db      1921  GAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Qy      1981  GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATGATGATGATGATGATGATG 2040
Db      1981  GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATGATGATGATGATGATGATG 2040

RESULT 9
AAS9859
ID AAS9859 standard; cDNA; 2040 BP.
XX
AC AAS9859;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11g1 splice variant B11C-9,16.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN MO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016776.
XX
PR 24-MAY-2000; 2000US-00577505.
XX
PR 08-JUN-2000; 2000US-00580583.
XX
PR 26-OCT-2000; 2000US-00699295.
XX
PR 16-MAR-2001; 2001US-00810936.
XX

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(CORI-) CORIXA CORP.

Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW,
Wang A, Sheiky YAM, Harlocker SL, Day CH;

WPI; 2002-089919/12.
P-PSDB; AAU74379.

New breast tumor proteins and polynucleotides encoding them, useful for
treating and/or preventing cancer, particularly breast cancer, and for
eliciting humoral and/or cellular immune response.

Claim 1, Page 224-225; 245pb; English.

The invention relates to novel breast tumour polynucleotides and
polypeptides. The polypeptides and polynucleotides are useful in
pharmaceutical compositions for treating and/or preventing cancer,
particularly breast cancer, and for eliciting an immune response,
particularly humoral and/or cellular immune response. The polynucleotides
may be used as probes or primers for nucleic acid hybridisation, in the
design and preparation of ribozyme molecules for inhibiting expression of
tumour polypeptides and proteins, and in recombinant DNA molecules to
direct expression of a polypeptide in host cells. AAS9570-AAS9988
represent novel human breast cancer protein coding sequences and PCR
primers of the invention

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGTTGATTCATGCCGCTCTTCTGTGAGAACCATTTGCTTC 60
DB 1 ATGGTGTTGAGTTGATTCATGCCGCTCTTCTGTGAGAACCATTTGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTCGTCCGAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTCGTCCGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAACATCTAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAACATCTAGAGCAAG 180
QY 181 ATGGCAAGTGTGCTGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTCTG 240
DB 181 ATGGCAAGTGTGCTGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTCTG 240
QY 241 GGGCGTTCTGAGACCAAGCACTCTGTATGAAACATCTAGAGCAAGTGGGCAAG 300
DB 241 GGGCGTTCTGAGACCAAGCACTCTGTATGAAACATCTAGAGCAAGTGGGCAAG 300
QY 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGTTGG 360
DB 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGTTGG 360
QY 361 GGAACATAGATGACAGTCTTCTGAGACCAAGTACAGTCTGCTGAGAGATCTG 420
DB 361 GGAACATAGATGACAGTCTTCTGAGACCAAGTACAGTCTGCTGAGAGATCTG 420
QY 421 GACAAGTCTCAGAGCTGCTGCTGAGGGGTAAGTCTCCCAAGAAAGATCTCATCTG 480
DB 421 GACAAGTCTCAGAGCTGCTGCTGAGGGGTAAGTCTCCCAAGAAAGATCTCATCTG 480
QY 481 CTGAGGACATGACGCTGTAACAAGAGCAAGCAAGCAAGCAAGTCTTACATCTG 540
DB 481 CTGAGGACATGACGCTGTAACAAGAGCAAGCAAGCAAGCAAGTCTTACATCTG 540
QY 541 TCTGCAATGGAATTCAGAGTGAATAACTCTGCTGAGACAGAGATGTCAATTAA 600
DB 541 TCTGCAATGGAATTCAGAGTGAATAACTCTGCTGAGACAGAGATGTCAATTAA 600
QY 601 GTCTTGAACAAGAGAGACGCTGTGATTAAGGCGGTACATGCAAGAGATGTA 660

DB 601 GTCTTGAACAAGAGAGACGCTGTGATTAAGGCGGTACATGCAAGAGATGTA 660
QY 661 TGTGCGTTAATGTTGCTGAGACATGCGACATGATCCAAATATTCAGAGTATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGAGACATGCGACATGATCCAAATATTCAGAGTATGGAAT 720
QY 721 ACCACTCTGCACTAGGCTATCTATTAAGATTAATTAATGCGCAAGACATGCTCTTA 780
DB 721 ACCACTCTGCACTAGGCTATCTATTAAGATTAATTAATGCGCAAGACATGCTCTTA 780
QY 781 TATGCTGATGATGCAATCAAAAAACAAGATGCGCTCACACATGTTACTGGTGTGA 840
DB 781 TATGCTGATGATGCAATCAAAAAACAAGATGCGCTCACACATGTTACTGGTGTGA 840
QY 841 CATGACAAAAACAAGATGCGTGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAAACAAGATGCGTGAATTTTATCAAGAAAAACGAATTTAAATGCA 900
QY 901 CTGATATGATGAAAGATCTCTCATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATGAAAGATCTCTCATCTTGTCTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGATATTTGCAAGTATCTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGATATTTGCAAGTATCTTCTGATAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGAAATCCAGAACAACTTAAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGAAATCCAGAACAACTTAAAG 1140
QY 1141 CTGATCATGAGGAGAGATCAAAAGGTTCAAGGCAAGTAAATAGCAGCAGAGAAA 1200
DB 1141 CTGATCATGAGGAGAGATCAAAAGGTTCAAGGCAAGTAAATAGCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGATGATTAATGATTAATTCCTCAAGGAAAGACAGACACCTGAAATACAGCAATT 1380
DB 1321 AATGATGATTAATGATTAATTCCTCAAGGAAAGACAGACACCTGAAATACAGCAATT 1380
QY 1381 CCTGCAACGAAGATGAGAGATATCAGAAATTTGCAATTTGCTGACTACAAAGAA 1440
DB 1381 CCTGCAACGAAGATGAGAGATATCAGAAATTTGCAATTTGCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCGCAAAATTAATCTTCTGAAAAACAGCAACCAAGCAAGCAAGTAAAGCTGACA 1500
DB 1441 AAAACAGATGCGCAAAATTAATCTTCTGAAAAACAGCAACCAAGCAAGCAAGTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATGCAAAAGGTTGAGGCGAGTGAATAATGGCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGATGCAAAAGGTTGAGGCGAGTGAATAATGGCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 CAAGAACAGAAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 GAAATGAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 GAAATGAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740

Db 1681 ACTGCTGCAGATGATGATGATGATTAATTCCTCCAGAGAGACAGAACACCTGAAGC 1740
QY 1741 CAGCAATTCCTGCAGACTGAGATGAAGATATACAGATGACGAAATATATCTCG 1800
Db 1741 CAGCAATTCCTGCAGACTGAGATGAAGATATACAGATGACGAAATATATCTCG 1800
QY 1801 AAGCAATTTTGTGAAGAGACGACCTGGAATATTACAGATGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAGACGACCTGGAATATTACAGATGATTCGATTCATGAA 1860
QY 1861 GAAACACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTATGTTGAAGAA 1920
Db 1861 GAAACACAGATGAGAGTGTGTTGAAAAATGAAATTCGAGCTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGATCTGTGATGAAAAATAGTGTGCGGAGAGAAATTCGCTTAACATG 1980
Db 1921 GAAAAAGATCTGTGATGAAAAATAGTGTGCGGAGAGAAATTCGCTTAACATG 1980
QY 1981 GAGCTAGACATGAAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACATGAAATGAAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
RESULT 10
ACC95344
ID ACC95344 standard; cDNA; 2040 BP.
XX ACC95344;
AC ACC95344;
XX 28-AUG-2003 (first entry)
DT 28-AUG-2003 (first entry)
XX Prostate tumour specific cDNA sequence SEQ ID 375.
DE Prostate tumour specific cDNA sequence SEQ ID 375.
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KM Immune response; prostate cancer; ss.
OS Homo sapiens.
XX MO200289747-A2.
PN MO200289747-A2.
XX 14-NOV-2002.
PD 14-NOV-2002.
XX 09-MAY-2002; 2002MO-US014753.
PP 09-MAY-2002; 2002MO-US014753.
XX 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00852911.
XX 10-DEC-2001; 2001US-00012896.
PR 10-DEC-2001; 2001US-00012896.
XX (CORI-) CORIXA CORP.
PA (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghlon RL, Vinals Y De BaesioisC, Foy TM, Watanabe Y;
PI Deng T;
XX MPI; 2003-167130/16.
DR MPI; 2003-167130/16.
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX Example 11; Page 416; 691pp; English.
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 8; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGAGTATGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGTC 60
Db 1 ATGGTGTGAGAGTATGATTCATGCGGCTGCTCTTCTGTGAAGAAGCATTTGTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGAGGACCTTGTGAGACACAGACGACTGCTGATGAGACACTGAGGACG 180
Db 121 AGCAACGAGGACCTTGTGAGACACAGACGACTGCTGATGAGACACTGAGGACG 180
QY 181 ATGGGCAAGTGTGCGGCAAGTGTGCTGCTGCTGCAAGGAGAGTGGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCAAGTGTGCTGCTGCTGCAAGGAGAGTGGCAAGCTG 240
QY 241 GCGGCTTCTGAGACACAGACGACTGCTGCTGATGAGACACTGAGGACGAG 300
Db 241 GCGGCTTCTGAGACACAGACGACTGCTGCTGATGAGACACTGAGGACGAG 300
QY 301 TGTGCTGCTGACGCTTCCCTGCTGCAAGGAGAGCGGCAAGTGGCGCTTGG 360
Db 301 TGTGCTGCTGACGCTTCCCTGCTGCAAGGAGAGCGGCAAGTGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTGCCTTCAATGAGAGCCAGGATACAGCTCGTGAAGATCTG 420
Db 361 GGAAGCTACGATGACAGTGCCTTCAATGAGAGCCAGGATACAGCTCGTGAAGATCTG 420
QY 421 GAAAGCTTCACAGAGCTGCTGCTGAGGATTAAGTCCCAAGAGATTCATGCTCATG 480
Db 421 GAAAGCTTCACAGAGCTGCTGCTGAGGATTAAGTCCCAAGAGATTCATGCTCATG 480
QY 481 CTGAGGAGACCTGAGAGTGAAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTGAGGAGACCTGAGAGTGAAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCCAATGGGAATTCAGAGATGATTAACCTCTGCTGAGACAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGATGATTAACCTCTGCTGAGACAGATGCACTTAAT 600
QY 601 GTTCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTTCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGGCTATCTATAATGAGATTAATTAATGAGCACTGCTTGA 780
Db 721 ACCACTCTGCACTAGGCTATCTATAATGAGATTAATTAATGAGCACTGCTTGA 780
QY 781 TATGCTGCTGATATGATCAAAAAACAGATGAGCTTCAACCACTGTTACTTGTTGA 840
Db 781 TATGCTGCTGATATGATCAAAAAACAGATGAGCTTCAACCACTGTTACTTGTTGA 840
QY 841 CATGAGCAAAAAACAGATGAGCTTCAAAAAACAGATGAGCTTCAAAAAACAGATGAG 900
Db 841 CATGAGCAAAAAACAGATGAGCTTCAAAAAACAGATGAGCTTCAAAAAACAGATGAG 900
QY 901 CTGATATGATGAG 960
Db 901 CTGATATGATGAG 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACGAG 1020

[illegible]

ADAl1382;
06-NOV-2003 (first entry)
Human breast cancer specific cDNA B1C-9.16.
ss; gene; human; breast cancer; cytolethic; tumour; gene therapy.
Homo sapiens.
US2002165371-A1.
07-NOV-2002.
07-AUG-2001; 2001US-00924400.
11-JAN-1996; 96US-00585392.
10-JAN-1997; 97WO-US000485.
09-APR-1997; 97US-00838762.
11-DEC-1997; 97US-00991789.
17-APR-1998; 98US-0062451.
09-APR-1999; 99US-00289198.
28-OCT-1999; 99US-00429755.
23-MAR-2000; 2000US-00534825.
24-MAY-2000; 2000US-00575805.
26-JUN-2000; 2000US-00590583.
26-OCT-2000; 2000US-00699295.
16-MAR-2001; 2001US-00810936.
FRUD./ FRUDAKIS T N.
REED./ REED S G.
SMIT./ SMITH J M.
MISH./ MISHER L E.
DILL./ DILLON D C.
RETT./ RETTER M W.
WANG./ WANG A.
SKEI./ SKEIKY A W.
HARL./ HARLOCKER S L.
DAYC./ DAY C H.
LITSX./ LI S X.
DENG./ DENG T.
Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW, Wang A, Skelky YAW, Harlocker SL, Day CH, Li SX, Deng T; WPI; 2003-247262/24. P-PSDB; ADAl1385.
New breast tumor proteins nucleic acids encoding such proteins, useful in diagnosing, preventing and/or treating diseases such as cancer, particularly breast cancer, and as markers for detecting the presence of a cancer.
Claim 1; Page 141; 190pp; English.

QY 1861 GAAAGCAGATGAAAGTGTGAAAAAATGAATTCAGCTTCTCTAGTTGTAGAAA 1920
DB 1861 GAAAGCAGATGAAAGTGTGAAAAAATGAATTCAGCTTCTCTAGTTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGTGATGAAAAATAGTACGTTGCGGGAAGAAATTCCTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGTGATGAAAAATAGTACGTTGCGGGAAGAAATTCCTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAAATGACAGCCGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
DB 1981 GAGCTAGACACAATGAAATGACAGCCGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
RESULT 12
ADCI5355
ID ADCI5355 standard; DNA; 2040 BP.
XX ADCI5355;
AC
XX
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human breast tumour protein DNA, SEQ ID 303.
DE
XX
XX Cytostatic; Gene therapy; breast cancer; breast tumour protein; human;
KM ds.
XX
XX Homo sapiens.
OS
XX WO2003013431-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024917.
XX
XX 07-AUG-2001; 2001US-00924400.
XX PR 20-FEB-2002; 2002US-00079137.
XX PR 02-AUG-2002; 2002US-00212679.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH,
PI Kalos MD;
XX
XX WPI; 2003-342398/32.
XX
XX
XX New polynucleotide, useful for preparing a composition for diagnosing,
PT treating or preventing cancer.
PS
XX
XX Example 1; SEQ ID NO 303; 308bp; English.
CC The present invention relates to compositions and methods for the therapy
CC and diagnosis of cancer, particularly breast cancer. The method for
CC detecting the presence of a cancer in a patient comprises: obtaining a
CC biological sample from the patient; contacting the biological sample with
CC a binding agent that binds to the polypeptide; detecting in the sample an
CC amount of the polypeptide that binds to the binding agent; and comparing
CC the amount of the polypeptide to a predetermined cut-off value. Treating
CC breast cancer comprises administering a composition comprising breast
CC tumour proteins and nucleic acids, which stimulates and/or expands T cells
CC specific for the tumour protein. The present sequence was used to
CC illustrate the invention.
XX
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTTGTGAGACACAGACACTGTGTAATGAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTTGTGAGACACAGACACTGTGTAATGAGACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGGTGGCCGACCTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG 240
DB 181 ATGGCAAGTGGTGGCCGACCTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCGTG 240
QY 241 GCGCTTGTGAGACACAGACACTGTGTAATGAGACACTCAGAGCAAGTGGCAAG 300
DB 241 GCGCTTGTGAGACACAGACACTGTGTAATGAGACACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 GGAAGCTACAGATGACAGTGCCTTCATGAGAGCCAGGTACCACTCGTGGAGAGATCTG 420
DB 361 GGAAGCTACAGATGACAGTGCCTTCATGAGAGCCAGGTACCACTCGTGGAGAGATCTG 420
QY 421 GACAGCTTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGGATCTCATCTGCTAG 480
DB 421 GACAGCTTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGGATCTCATCTGCTAG 480
QY 481 CTCAGGGACACTGACGTGAAACAAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGAGC 540
DB 481 CTCAGGGACACTGACGTGAAACAAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGAGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGACATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGACATGTCACTTAAT 600
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGACATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGACATGTCACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGACAGCTGTGATAAAGGCGGTCAATGCCAGGAAGTGA 660
DB 601 GTCTTGAACAACAAAGAGAGACAGCTGTGATAAAGGCGGTCAATGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTGCTGGAATCATGCACTGATCAATATTCAGATGATGATGAAAT 720
DB 661 TGTGCTTAATGTGCTGGAATCATGCACTGATCAATATTCAGATGATGATGAAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTTGA 780
DB 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTTGA 780
QY 781 TATGCTGCTGATGATGATCAAAACAAAGCAATGCTCACAACACTGTTACTTGGTGA 840
DB 781 TATGCTGCTGATGATGATCAAAACAAAGCAATGCTCACAACACTGTTACTTGGTGA 840
QY 841 CATGACAAACAAACAGAGTGTGAAATTTTAAATCAAGAAAGGAAATTTAAATGCA 900
DB 841 CATGACAAACAAACAGAGTGTGAAATTTTAAATCAAGAAAGGAAATTTAAATGCA 900
QY 901 CTGATATGATGAGAGAGTGTGCTCATCTGCTGATATGTTGTGATACACAAAGTATA 960
DB 901 CTGATATGATGAGAGAGTGTGCTCATCTGCTGATATGTTGTGATACACAAAGTATA 960
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DB 961 GTACAGCTTCTACCTGAGCAAAATATGATGATCTTCCAGAGCTATCTGAGACAGAG 1020
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DB 1021 GCGAGAGATATGCTGTTCTAGTATCATCATATGTAATTTGCGAGTTACTTCTGACTAC 1080
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DB 1081 AAAGAAAAACAGATCTTAAATCTCTTGTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
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DB 1141 CTGATCATGAGGAAGATGACAAAGGTTCAAGGCAATGAAATATGACAGCAAGAAA 1200

Db 1141 CTGACATCAGAGGAAGTCCAGAAAGTTCAAAGCAGTGAATAATAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCGAATAATAGATGTGATAGAGAGTGAAGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCGAATAATAGATGTGATAGAGAGTGAAGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGAATTAATGTGGATTACTAGAAAACTGACTTAATGTGTCACTGTGC 1320
Db 1261 AAGCATGAAGAATTAATGTGGATTACTAGAAAACTGACTTAATGTGTCACTGTGC 1320
Oy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGCAGAACCTGAAATACGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGCAGAACCTGAAATACGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCAATTTGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCAATTTGTTCTGACTCAAGAA 1440
Oy 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTTCTGAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Oy 1501 TCAGAGAAAGAGTCCAAAGGCTTGAGGGGAGTGAATGGCCAGCCAGAGAAAAGATT 1560
Db 1501 TCAGAGAAAGAGTCCAAAGGCTTGAGGGGAGTGAATGGCCAGCCAGAGAAAAGATT 1560
Oy 1561 CAAGAACCAGAAATTAATAGATGTGATAGAGCTGAAATTTTATGTCTATCGAA 1620
Db 1561 CAAGAACCAGAAATTAATAGATGTGATAGAGCTGAAATTTTATGTCTATCGAA 1620
Oy 1621 GAATGAGAAAGACACGGAAGTACTCATGTGCAATTCCTCAAGAAACCTGACTAATGTGTC 1680
Db 1621 GAATGAGAAAGACACGGAAGTACTCATGTGCAATTCCTCAAGAAACCTGACTAATGTGTC 1680
Oy 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGCAGAACACCTGAAGC 1740
Db 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGCAGAACACCTGAAGC 1740
Oy 1741 CAGCAATTTCTGACATCGAGATGAAGATATCACAGTGAAGAACAAATGATCTCG 1800
Db 1741 CAGCAATTTCTGACATCGAGATGAAGATATCACAGTGAAGAACAAATGATCTCG 1800
Oy 1801 AAGCAATTTTGTGAAGACAGAACACTGGATATTAACAGATGAGATTTCTGATTCATGA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACACTGGATATTAACAGATGAGATTTCTGATTCATGA 1860
Oy 1861 GAAAAACGATAGAGTGTGTAATAATGAATTCCTGAGCTTTCTTGTGTGAAGAA 1920
Db 1861 GAAAAACGATAGAGTGTGTAATAATGAATTCCTGAGCTTTCTTGTGTGAAGAA 1920
Oy 1921 GAAAAAGACATCTGATGATAAATAGTAGTTGCCGGAAGAAATGGCCATGCTAGACTG 1980
Db 1921 GAAAAAGACATCTGATGATAAATAGTAGTTGCCGGAAGAAATGGCCATGCTAGACTG 1980
Oy 1981 GAGCTAGACACATGAATGAAATCATGAGCCAGCTTAATAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTAGACACATGAATGAAATCATGAGCCAGCTTAATAAAAAAAAAAAAAAAAAA 2040

RESULT 13
ADBI3825
ID ADBI3825 standard; cDNA; 2040 BP.
XX
AC ADBI3825;
XX
DT 18-DEC-2003 (first entry)
DE Human prostate specific cDNA B305 splice variant #10.
XX
XX Human prostate specific cDNA; cytosolic; immunostimulant;
KM gene therapy; cell therapy; vaccine; T-cell epitope;
KM class I major histocompatibility complex allele; MHC; prostate cancer;
KM tumour; antigen presenting cell.

XX Homo sapiens.
OS
XX US2003185830-A1.
PN
XX 02-OCT-2003.
PD
PF 12-NOV-2002; 2002US-00294025.
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00289946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00912896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
PI WPI: 2003-756193/71.
XX P-PsDB; ADBI3830.
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
XX response, or for treating or diagnosis cancer, preferably prostate
XX cancer.
XX
XX Example 11; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
XX 11-442 amino acids of ADBI3563 comprising a sequence ADBI487. The
XX peptides comprise a fragment ADBI3563 of that contain naturally processed
XX T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
XX cDNA. One of 648 disclosed as new. Also included are nucleic acids
XX encoding the proteins and peptides, expression vectors, a host cell
XX transformed with the vector, an isolated antibody (or antigen binding
XX fragment) that specifically binds to the protein or peptide, detecting
XX the presence of a cancer in a patient (comprising contacting a patient
XX sample with a binding agent that binds to the peptides or a polypeptide
XX appearing as ADBI3558, detecting the amount of polypeptide that binds to
XX the agent and comparing the amount of polypeptide to a predetermined cut-
XX off value to determine the presence of cancer), a fusion protein
XX comprising the peptides or proteins, stimulating or expanding T cells
XX specific for a tumour protein comprising contacting T cells with the
XX peptides or the isolated T cell population, treating prostate cancer in a
XX patient comprising administering a composition comprising the peptides,
XX nucleic acids, antibodies or compounds, determining the presence of a
XX cancer in a patient and treating prostate cancer in a patient comprising
XX incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated

CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPO at
CC seqdata.uspto.gov/sequence.html?docId=20030185830.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 10; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAAGCCATTGGCTC 60
DB 1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAAGCCATTGGCTC 60
QY 61 AGGAGCAAGTGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGTGGGCAAGTGTGCTGCCGTTGCTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGACATCAGAGACCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTCTGTATGAAGACATCAGAGACCAAG 180
QY 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACCAAGTGTG 240
DB 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACCAAGTGTG 240
QY 241 GGGGCTTCTGAGACACAGACGACTCTGTATGAAGACATCAGAGACCAAGTGTG 300
DB 241 GGGGCTTCTGAGACACAGACGACTCTGTATGAAGACATCAGAGACCAAGTGTG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGAGCAAGGAGTGGCGGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGAGCAAGGAGTGGCGGCTTGG 360
QY 361 GGAAGTACGATGACAGTGTCTCATGAGCCCAAGTACCAAGTCCGTGGAGAGATCTG 420
DB 361 GGAAGTACGATGACAGTGTCTCATGAGCCCAAGTACCAAGTCCGTGGAGAGATCTG 420
QY 421 GACCAAGTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTATG 480
DB 421 GACCAAGTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGAACAGTGAAGTGAAGACAGCAAGCAAGCAAGCAAGTCTCTCATCTGCGCC 540
DB 481 CTCAGGGAACAGTGAAGTGAAGACAGCAAGCAAGCAAGCAAGTCTCTCATCTGCGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGGAAGAGAGATGCAACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGGAAGAGAGATGCAACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAAGTGA 660
DB 601 GTCTTTGACAAACAAAAGAGAGACAGCTGTGATTAAGCCGTACAAATGCCAGAAAGTGA 660
QY 661 TGTGCTTAAATGTGTCTGGAACATGGCACTGATCCAAATTTCTCAAGATGATGAAT 720
DB 661 TGTGCTTAAATGTGTCTGGAACATGGCACTGATCCAAATTTCTCAAGATGATGAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAAGGCAAGAGACTGCTTGA 780
DB 721 ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATTAAGGCAAGAGACTGCTTGA 780
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QY 781 TATGTCGTGATATGCAATCAACAAAACAGCATAGGCTTACACACACTGTTACTGGTGA 840
DB 781 TATGTCGTGATATGCAATCAACAAAACAGCATAGGCTTACACACACTGTTACTGGTGA 840
QY 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGCAATTAATTAATGA 900
DB 841 CATGACAAAACAGCAAGTGTGAATTTTAAATCAAGAAAACGCAATTAATTAATGA 900
QY 901 CTGGATGATATGGAAGAAGCTGCTCATACTTGTGTAATGTTGATGATCAGCAATATA 960
DB 901 CTGGATGATATGGAAGAAGCTGCTCATACTTGTGTAATGTTGATGATCAGCAATATA 960
QY 961 GTTCAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATTAATCTGACAGC 1020
DB 961 GTTCAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATTAATCTGACAGC 1020
QY 1021 GCACAGATATAGCTGTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCACAGATATAGCTGTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTAAATAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGATCAACAAAGTTCAAAAGCGATGAATATGCCACAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGATCAACAAAGTTCAAAAGCGATGAATATGCCACAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCGAATAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAAGAACCGAATAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAGATTAATATGATGGAATTAATGAAAACCTGACTAATGATGATGATGATG 1320
DB 1261 AAGCATGAAGATTAATATGATGGAATTAATGAAAACCTGACTAATGATGATGATGATG 1320
QY 1321 AATGTGATTAATGATTAATTTCTTCAAGAAAGAGCAAAACCTGAAAATCGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTTCAAGAAAGAGCAAAACCTGAAAATCGCAATTT 1380
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DB 1381 CCTGCAAGAAAGGAAAGATATCAAGAAATTTGGGAAATTTGTTCTGACTACAAAGAA 1440
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DB 1441 AAAAGATGCCAAAATATCTCTTCTGAAAACAGCAACCCAGAAACAAGACTTAAGCTGACA 1500
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DB 1501 TGAAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAATGSCCAGCCAGAGAAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGATGATTAAGAGCTGAAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATGAAGATGATTAAGAGCTGAAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAACAGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAAGAACAGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTTCAAGGAAGAGCAAGCACTGAAAGC 1740
DB 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTTCAAGGAAGAGCAAGCACTGAAAGC 1740
QY 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCAAGTGAAGAACAAATATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCAAGTGAAGAACAAATATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAGATTTCTGATTCATGAA 1860
```


Db 661 TGTGCTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATATGCGCAAGACATGCTTTA 780
Db 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATATGCGCAAGACATGCTTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAAACAAGATGGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATCGAATCAAAAAACAAGATGGCTCACACACTGTTACTTGGTGA 840
Qy 841 CATGACCAAAAACAGCAAGTCGTGAATTTTATCATCAAGAAAAAGCAATTTTAAATGA 900
Db 841 CATGACCAAAAACAGCAAGTCGTGAATTTTATCATCAAGAAAAAGCAATTTTAAATGA 900
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Db 901 CTGATATGATATGGAAGGATGCTCTCATCTTCTGATATGTTGTGATGACGAAATGA 960
Qy 961 GTGAGCCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
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Db 1081 AAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCAGAAACAAGATTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGGAGTGAATTAAGCCAGCAAGAAAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAAAGGAGTGAATTAAGCCAGCAAGAAAA 1200
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Db 1201 ATGTCTCAAGAACAGAAATTAATGAAGATGATGATGAGAGGTTGAGAGAAATGAAG 1260
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Db 1261 AAGCATGAAGATTAATATGTTGGATTACTNAGAAAACCTGACTATGCTGCTGCGC 1320
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Db 1321 AATGATGATTAATGATTAATCTCTCAAAAGGAGAGAGCAACCTGAAATTCGCAATTT 1380
Qy 1381 CCTGACAAAGAGATGATCAAGAAATTTGGCAATTAATGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAGATGATCAAGAAATTTGGCAATTAATGTTCTGACTCAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGATTAAAGCTGAC 1500
Db 1441 AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGATTAAAGCTGAC 1500
Qy 1501 TCAGAGAGAGATGATCAAAAGGCTTGAAGGAGAGAGAAATGCGCAGCAAGAAAGATCT 1560
Db 1501 TCAGAGAGAGATGATCAAAAGGCTTGAAGGAGAGAGAAATGCGCAGCAAGAAAGATCT 1560
Qy 1561 CAAGAACCAGAAATTAATGAAGATGATGAGAGCTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAGAAATTAATGAAGATGATGAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAACTGACTTAAATGCTGAC 1680
Db 1621 GAAATGAAGAGACGGAAGTACTATGTCGATTTCCAGAAAACTGACTTAAATGCTGAC 1680
Qy 1681 ACTGCTGGCAATGCTGATGATTAATTTCCCAAGAGAGCAAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGCTGATGATTAATTTCCCAAGAGAGCAAGCAACCTGAAAGC 1740
Qy 1741 CAGCAATTTTCTGACATGAGATGAAGATATCAGATGACGAACAATGATTAATCTCAG 1800
Db 1741 CAGCAATTTTCTGACATGAGATGAAGATATCAGATGACGAACAATGATTAATCTCAG 1800

Qy 1801 AAGCAATTTTCTGAGAGACAGAACTGCAATTTTACAGATGATGATTCATGAA 1860
Db 1801 AAGCAATTTTCTGAGAGAGACAGAACTGCAATTTTACAGATGATGATTCATGAA 1860
Qy 1861 GAAAGCAGATGAGAGTGGTGAATTAATGATTTGAGCTTCTCTTGTGTAAGAA 1920
Db 1861 GAAAGCAGATGAGAGTGGTGAATTAATGATTTGAGCTTCTCTTGTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTGCATGAAATATGATGCTTGGGAGAAATTCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAATATGATGCTTGGGAGAAATTCATGCTAAGACTG 1980
Qy 1981 GAGCTTGAACAATGAACATGACGACCTGCTAAAAAATGAAAAAATGAAAAAATG 2040
Db 1981 GAGCTTGAACAATGAACATGACGACCTGCTAAAAAATGAAAAAATGAAAAAATG 2040

RESULT 15
AA06600
ID AA06600 standard; cDNA; 2040 BP.
XX
AC AA06600;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.
PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX
PS comprises an immunogenic portion of prostate tumor protein.
XX
PS Claim 50; Page 223-224; 263pp; English.

The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumor protein (PRP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AA066241 to AA06691 and CC AA082000 to AA082020 represent sequences used in the exemplification of the present invention

Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 U; 0 Other;

Query Match 99.9%; Score 2038.4; DB 3; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGAATTCATGCGCGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
 DB 1 ATGGTGGTGAAGTGAATTCATGCGCGCTGCTCTTCTGTGAAGAACATTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGGTCCCTGCTGCAAGGAGCCGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGGTCCCTGCTGCAAGGAGCCGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGGAAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
 DB 121 AGCAAGTGGGCACTTCTGGAAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
 DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
 QY 241 GGGGCTTCTGGAAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAGTGGCAAG 300
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 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGATGGGCGCTTGG 360
 DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGATGGGCGCTTGG 360
 QY 361 GGAAGACTACAGTACAGTGGCTTCAATGAGGCCAGGTACCACTCCGTGAGAGAGATCTG 420
 DB 361 GGAAGACTACAGTACAGTGGCTTCAATGAGGCCAGGTACCACTCCGTGAGAGAGATCTG 420
 QY 421 GACAACTCCACAGACTGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
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 QY 481 CTCAGGAGCACTGACGTGAACAAGAGACAAGCAAAAGAGACTGCTCTACACTGGCC 540
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 DB 601 GTCTTGAACAACAAAAGAGAGACGCTCTGATTAAGCCGTACAAATGCCAGAGAGATGAA 660
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 DB 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCGAATGATGGAAT 720
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 DB 721 ACCACTCTGCACTACGCTATCTATTAATGAATTAATTAAGCCAAAGCACTGCTCTTA 780
 QY 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
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 DB 841 CATGACCAAAAAAGCAAGTGGTGAATTTTAAATCAAGAAAAACGAAATTTAAATGGA 900
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 DB 901 CTGGATAGAATATGGAAGAGCTGCTCATACTTGTGATGTTGTGGATCAGCAAGTATA 960
 QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGGCAGTACTTCTGACTAC 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGGCAGTACTTCTGACTAC 1080
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 DB 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAACCAATTTAAG 1140
 QY 1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGCAAGTGAATTAATCCAGCAGAGAAA 1200
 DB 1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGCAAGTGAATTAATCCAGCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
 DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGTAAATATGTTGGAAATTAAGTGAAGAACTGACTAATGTTGCTCACTGGC 1320
 DB 1261 AAGCATGAAAGTAAATATGTTGGAAATTAAGTGAAGAACTGACTAATGTTGCTCACTGGC 1320
 QY 1321 AATGCTGATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAAAATCAGCAATTT 1380
 DB 1321 AATGCTGATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAAAATCAGCAATTT 1380
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 DB 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCGAGAGAAAGATTCACAAAGGCTTGAAGGCACTGAAAAATGGCCACGAGAGAAAAATCT 1560
 DB 1501 TCGAGAGAAAGATTCACAAAGGCTTGAAGGCACTGAAAAATGGCCACGAGAGAAAAATCT 1560
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 DB 1561 CAAGAACCGAATTAATTAAGATGATGATAGAGAGCTGAAATTTTATGCTATCGAA 1620
 QY 1621 GAAATGAAGAACAGGAAATGTAATGATGCGAATTTCCAGAAACCTGACTAATGCTGCC 1680
 DB 1621 GAAATGAAGAACAGGAAATGTAATGATGCGAATTTCCAGAAACCTGACTAATGCTGCC 1680
 QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGAAAGAGCAACCTGAAAGC 1740
 DB 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGAAAGAGCAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTGAAGCAAAATGATACTCAG 1800
 DB 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCAAGTGAAGCAAAATGATACTCAG 1800
 QY 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTAATTAACAGATGAGATTTCTGATTCATGAA 1860
 DB 1801 AAGCAATTTTGTGAAGAACAGAACCTGGAATTAATTAACAGATGAGATTTCTGATTCATGAA 1860
 QY 1861 GAAAAAGCATGAAAGTGGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
 DB 1861 GAAAAAGCATGAAAGTGGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1920
 QY 1921 GAAAAAGCATGAAAGTGGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1980
 DB 1921 GAAAAAGCATGAAAGTGGTGAAAAAATGAATTTCTGAGCTTTCTTATGTTGAAGAA 1980
 QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
 DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

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 Job time : 1224.95 secs

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OM nucleic - nucleic search, using sw model

Run on: December 17, 2005, 15:52:49 ; Search time 360.535 Seconds
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Title: US-09-924-400-303

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	3	US-09-439-313-375 Sequence 375, App
2	2040	100.0	2040	3	US-09-352-616A-375 Sequence 375, App
3	2040	100.0	2040	3	US-09-289-198-303 Sequence 303, App
4	2040	100.0	2040	3	US-09-636-215-375 Sequence 375, App
5	2040	100.0	2040	3	US-09-685-166A-375 Sequence 375, App
6	2040	100.0	2040	3	US-09-429-755-303 Sequence 303, App
7	2040	100.0	2040	3	US-09-679-426-375 Sequence 375, App
8	2040	100.0	2040	3	US-09-759-143-375 Sequence 375, App
9	2040	100.0	2040	3	US-09-651-236-375 Sequence 375, App
10	2040	100.0	2040	3	US-09-699-295-303 Sequence 303, App
11	2040	100.0	2040	3	US-09-534-825A-303 Sequence 303, App
12	2040	100.0	2040	3	US-09-657-279-375 Sequence 375, App
13	2040	100.0	2040	3	US-10-012-896-375 Sequence 375, App
14	1940	95.1	2000	3	US-09-439-313-374 Sequence 374, App
15	1940	95.1	2000	3	US-09-352-616A-374 Sequence 374, App
16	1940	95.1	2000	3	US-09-289-198-302 Sequence 302, App
17	1940	95.1	2000	3	US-09-636-215-374 Sequence 374, App
18	1940	95.1	2000	3	US-09-685-166A-374 Sequence 374, App
19	1940	95.1	2000	3	US-09-429-755-302 Sequence 302, App
20	1940	95.1	2000	3	US-09-679-426-374 Sequence 374, App
21	1940	95.1	2000	3	US-09-759-143-374 Sequence 374, App
22	1940	95.1	2000	3	US-09-651-236-374 Sequence 374, App
23	1940	95.1	2000	3	US-09-699-295-302 Sequence 302, App
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25	1940	95.1	2000	3	US-09-657-279-374 Sequence 374, App
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28	1147.6	56.3	1853	3	US-09-062-451-295 Sequence 295, App
29	1147.6	56.3	1853	3	US-09-352-616A-369 Sequence 369, App
30	1147.6	56.3	1853	3	US-09-289-198-295 Sequence 295, App
31	1147.6	56.3	1853	3	US-09-636-215-369 Sequence 369, App
32	1147.6	56.3	1853	3	US-09-685-166A-369 Sequence 369, App
33	1147.6	56.3	1853	3	US-09-429-755-295 Sequence 295, App
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36	1147.6	56.3	1853	3	US-09-651-236-369 Sequence 369, App
37	1147.6	56.3	1853	3	US-09-699-295-295 Sequence 295, App
38	1147.6	56.3	1853	3	US-09-534-825A-295 Sequence 295, App
39	1147.6	56.3	1853	3	US-09-657-279-369 Sequence 369, App
40	1147.6	56.3	1853	3	US-10-012-896-369 Sequence 369, App
41	1131.6	55.5	1155	3	US-09-439-313-373 Sequence 373, App
42	1131.6	55.5	1155	3	US-09-352-616A-373 Sequence 373, App
43	1131.6	55.5	1155	3	US-09-289-198-301 Sequence 301, App
44	1131.6	55.5	1155	3	US-09-636-215-373 Sequence 373, App
45	1131.6	55.5	1155	3	US-09-685-166A-373 Sequence 373, App

ALIGNMENTS

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RESULT 1
US-09-439-313-375
; Sequence 375, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kados, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42709
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGTTAGGATTCATTCGACCGGCTCTCTTCGTGAAGACATTGGTTC 60
1 ATGGCTGTTAGGATTCATTCGACCGGCTCTCTTCGTGAAGACATTGGTTC 60
Db 1 ATGGCTGTTAGGATTCATTCGACCGGCTCTCTTCGTGAAGACATTGGTTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTCTTCCTGCTGACGAGACGGCAAG 120
61 AGAGCAAGATGGGCAAGTGTGCTGCTCTTCCTGCTGACGAGACGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTCTTCCTGCTGACGAGACGGCAAG 120
QY 121 ACACAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGCACTCAGAGCAAG 180
121 ACACAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGCACTCAGAGCAAG 180
Db 121 ACACAGTGGGCACTTCTGAGACGACGACTCTGTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGTGTCGCCGACCTGCTCCCTCTGTGAGGGGAGTGGCAAGCACTG 240
181 ATGGGCAATGTGTCGCCGACCTGCTCCCTCTGTGAGGGGAGTGGCAAGCACTG 240
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Db	241	GGCGCTTCTGGAGACACAGAGAGCTCTGCTATGAAAGACCTCAGGAACAAGATGGGCAAG	300
Qy	301	TGGTGTCCGCACTGGCTTCCCTGCTGCAAG9999AAGCGGCAAGAGCAAGTGTGGGCGCTTGG	360
Db	301	TGGTGTCCGCACTGGCTTCCCTGCTGCTGCAAG9999AAGCGGCAAGAGCAAGTGTGGGCGCTTGG	360
Qy	361	GGAGACTACGATGACAGTGCCTTCAATGAGCCAGAGTACCAAGTCTGCTGGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCAATGAGCCAGAGTACCAAGTCTGCTGGAGAAAGATCTG	420
Qy	421	GACAAAGCTTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCTAATG	480
Db	421	GACAAAGCTTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCTAATG	480
Qy	481	CTCAGGGGACACTGAGCGTGAACAAGAAAGGACAAGCAAAAGAGAGACTGCTCATCTGCGCC	540
Db	481	CTCAGGGGACACTGAGCGTGAACAAGAAAGGACAAGCAAAAGAGAGACTGCTCATCTGCGCC	540
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Db	1021	GCCAGAGATATGCTGTTTCTAGTCAATCATCATGTAATTTGCGAGTATCTTCTGACTAC	1080
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Qy	1141	CTGACATCAGAGAAAGTCACAAAGTTCCAAAGCAGTGAANAATAGCCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGTCACAAAGTTCCAAAGCAGTGAANAATAGCCAGCCAGAGAAA	1200
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Qy	1261	AAGCATGAAGATTAATATGTTGGATTAATAGAAAACCTGAATATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGATTAATATGTTGGATTAATAGAAAACCTGAATATGTGTCACTGTGGC	1320

Qy	1321	AATGGTGTATATGGAATTAAATTCCTCAAGGAAGAGCGAACAACCTGAAAATACACAATTT	1380
Db	1321	AATGGTGTATATGGAATTAAATTTCTCTCAAGGAAGAGCGAACAACCTGAAAATACACAATTT	1380
Qy	1381	CTTGACACACGAAGAGTGAAGAGTATCAAGAAATTTTGGAAATTTGTTCTTGACTACAAAGAA	1440
Db	1381	CCTGACACACGAAGAGTGAAGAGTATCAAGAAATTTTGGAAATTTGTTCTTGACTACAAAGAA	1440
Qy	1441	AAACAGATGGCAAAATTAATCTCTTGGAAAACAGCAACCCAGAACAAAGACTTAAACCTGACA	1500
Db	1441	AAACAGATGGCAAAATTAATCTCTTGGAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTCACAAAGGCTTGAAGGACAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGGAAGAGTCACAAAGGCTTGAAGGACAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
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Qy	1621	GAATATGAAGAAAGACGGAAGTACTCATGTGCGAATTCCTCCAGAAAACCTGACTAAATGGTACC	1680
Db	1621	GAATATGAAGAAAGACGGAAGTACTCATGTGCGAATTCCTCCAGAAAACCTGACTAAATGGTACC	1680
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Db	1681	ACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAAAGAGACAGACACACTGAAAAGC	1740
Qy	1741	CAGCAATTTCTCTGACACTGAGAAATGAAGAGTATCAGAGTGCAGAACAAATATGATATCTCAG	1800
Db	1741	CAGCAATTTCTCTGACACTGAGAAATGAAGAGTATCAGAGTGCAGAACAAATATGATATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAAATATTAACAGATGAGATTCGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAAATATTAACAGATGAGATTCGATTCATGAA	1860
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Db	1861	GAAAGAGAGATGAGAGTGGTTGAAAATTAATCTCAGACTTCTCTTAGTGTATAGAAA	1920
Qy	1921	GAAGAAAGACATCTTGCATGAAAATATGATACGTTGGGAGAAAGAAATTTGCATGCTAAAGACTG	1980
Db	1921	GAAGAAAGACATCTTGCATGAAAATATGATACGTTGGGAGAAAGAAATTTGCATGCTAAAGACTG	1980
Qy	1981	GAGCTTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA	2040
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RESULT 2
US-09-352-616A-375
Sequence 375, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42768
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FaalSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-375

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Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGGATTCATGCGGCTGCTTCTGTGTAAGAAAGCCATTGGTCTC 60
DB 1 ATGGTGGTGAAGTGGATTCATGCGGCTGCTTCTGTGTAAGAAAGCCATTGGTCTC 60
QY 61 AGGAGCAATGGGCAAGTGGTGGCGTGGCTTCCCTGCTGCAAGGAGCCGCAAG 120
DB 61 AGGAGCAATGGGCAAGTGGTGGCGTGGCTTCCCTGCTGCAAGGAGCCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTCTGCTATGAAGACATCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAAGCAAGCACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCACTG 240
QY 241 GGGCGCTTCTGGAAGCAAGCACTCTGCTATGAAGACATCAGAGCAAGTGGGCAAG 300
DB 241 GGGCGCTTCTGGAAGCAAGCACTCTGCTATGAAGACATCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 GGAAGCTAGATGAGCAAGTGGCTTCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 GGAAGCTAGATGAGCAAGTGGCTTCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 GACAAAGCTTCAAGAGTGGCTTGGTGGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAAAGCTTCAAGAGTGGCTTGGTGGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAAGGACACTGAGTGGTAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
DB 481 CTCAAGGACACTGAGTGGTAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCAATGGGAAATTCAGAAATGATTAATCTCTGCTGCAAGCAAGATGCACTTAAT 600
DB 541 TCTGCAATGGGAAATTCAGAAATGATTAATCTCTGCTGCAAGCAAGATGCACTTAAT 600
QY 601 GTCTTGGACAAAGAAAGAGCAAGCTGCTGATTAAGGCGGTACATGCCAGGAAGTGA 660
DB 601 GTCTTGGACAAAGAAAGAGAGCAAGCTGCTGATTAAGGCGGTACATGCCAGGAAGTGA 660
QY 661 TGTGGCTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGAGTATGGAAT 720
DB 661 TGTGGCTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGAGTATGGAAT 720
QY 721 ACCACTGTCACATGCTATCTATATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTGTCACATGCTATCTATATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
QY 781 TATGGTGTGATATGGAATCAAGAAAGCAAGTGGCTCAACACTGTTACTTGGTGA 840
DB 781 TATGGTGTGATATGGAATCAAGAAAGCAAGTGGCTCAACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGGTGAATTTTATATGAAGAAAGCCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAAGCAAGTGGTGAATTTTATATGAAGAAAGCCGAATTTAAATGA 900
QY 901 CTGAGTATGATGGAAGAGCTGCTCATACTTGGCTGATGTTGGTGGATCAGCAAGTATA 960
DB 901 CTGAGTATGATGGAAGAGCTGCTCATACTTGGCTGATGTTGGTGGATCAGCAAGTATA 960
QY 961 GTCAAGCTTCTATCTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAAGC 1020
DB 961 GTCAAGCTTCTATCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAAGC 1020
QY 1021 GCCAAGAGTATGCTGTTCTTATGATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080

DB 1021 GCCAAGAGTATGCTGTTCTTATGATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATTCAGAAACAGACTTAAAG 1140
DB 1081 AAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATTCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGGAAGTCAAGAGCTTCAAGGCAAGTGAATTAAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTCAAGAGCTTCAAGGCAAGTGAATTAAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGGTTGAAGAAAGAAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGCTGATAGAGGTTGAAGAAAGAAAG 1260
QY 1261 AAGCATGAAGATTAATGTTGGATTACTAGAAAACTGACTAATGTTGTCATGCTGGC 1320
DB 1261 AAGCATGAAGATTAATGTTGGATTACTAGAAAACTGACTAATGTTGTCATGCTGGC 1320
QY 1321 AATGGTATTAATGATTAATTTCTTCAAGGAAAGACAGAAACCTGAAATCAGCAATTT 1380
DB 1321 AATGGTATTAATGATTAATTTCTTCAAGGAAAGACAGAAACCTGAAATCAGCAATTT 1380
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DB 1381 CCTGAACAAGAAAGTGAAGATATCAGAAATTTGGAAATTTGATCTTACAAAGAA 1440
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DB 1441 AAACAGATGCCAAAAATCTCTTCTGAAAAAGCAAGCAAGCAAGCAAGCAAGCAAG 1500
QY 1501 TCAAGGAAAGATCAAGAGCTTGAAGGCAAGTGAATGGCAAGCAAGAAAGATCT 1560
DB 1501 TCAAGGAAAGATCAAGAGCTTGAAGGCAAGTGAATGGCAAGCAAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATGAAGTGGTATGAGAGCTAGAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATTAATGAAGTGGTATGAGAGCTAGAAATTTTATGCTATCGAA 1620
QY 1621 GAATGAAGAAAGCAAGAAATGATCTGATGCGATTCAGAAAGCAAGCAAGCAAGCAAG 1680
DB 1621 GAATGAAGAAAGCAAGAAATGATCTGATGCGATTCAGAAAGCAAGCAAGCAAGCAAG 1680
QY 1681 ACTGCTGCAATGTTGATGATGATTAATTTCTTCAAGGAAAGCAAGCAAGCAAGCAAG 1740
DB 1681 ACTGCTGCAATGTTGATGATGATTAATTTCTTCAAGGAAAGCAAGCAAGCAAGCAAG 1740
QY 1741 CAGCAATTTCTGCAAGCAAGTGAAGTATCAAGTGAAGCAAGCAAGCAAGCAAGCAAG 1800
DB 1741 CAGCAATTTCTGCAAGCAAGTGAAGTATCAAGTGAAGCAAGCAAGCAAGCAAGCAAG 1800
QY 1801 AAGCAATTTTGAAGAAAGCAAGCAAGTGAATTAATCAAGATGATGATGATGATGATGAT 1860
DB 1801 AAGCAATTTTGAAGAAAGCAAGCAAGTGAATTAATCAAGATGATGATGATGATGATGAT 1860
QY 1861 GAAAAAGCAATGAAAGTGGTGAAGAAATGAATTTGAGCTTCTTATGTTGAAGAA 1920
DB 1861 GAAAAAGCAATGAAAGTGGTGAAGAAATGAATTTGAGCTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCAATTTGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 GAAAAAGCAATTTGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 GAGCTAGACAAATGAACATCAGAGCAAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAG 2040
DB 1981 GAGCTAGACAAATGAACATCAGAGCAAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAG 2040

RESULT 3
US-09-289-198-303
; Sequence 303, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:

OY	1261	AAGCATGGAAGTAATAAATGTGGATTACTAGAAA	CTGACTAAATAGTGTCACTGTGGC	1320
Db	1261	AAGCATGGAAGTAATAATGTGGATTACTAGAAA	CTGACTAAATAGTGTCACTGTGGC	1320
OY	1321	AATGTGATTAATTGATTTAATTCCTCAAAAGAA	GAGCAGAACACCTGAAATCAGCAATTT	1380
Db	1321	AATGTGATTAATTGATTTAATTCCTCAAAAGAA	GAGCAGAACACCTGAAATCAGCAATTT	1380
OY	1381	CCTGCAACGAAAGTAGAAGATATCACGAATTTG	CGAATTGATTTCTGACTACAAAGAA	1440
Db	1381	CCTGCAACGAAAGTAGAAGATATCACGAATTTG	CGAATTGATTTCTGACTACAAAGAA	1440
OY	1441	AAACGATAGCCAAATTA	CTCTTGCAAAAACGCAACCCAGAACAAAGATTA	1500
Db	1441	AAACGATAGCCAAATTA	CTCTTGCAAAAACGCAACCCAGAACAAAGATTA	1500
OY	1501	TCAGAGAAAGAGTCA	CAAAAGCCTTGAGGCAAGTGAATATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGAAAGAGTCA	CAAAAGCCTTGAGGCAAGTGAATATGGCCAGCCAGAGAAAAGATCT	1560
OY	1561	CAAGAACAGAAATTAATTAAGATAGTATAGAG	ACTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACAGAAATTAATTAAGATAGTATAGAG	ACTAGAAAATTTTATGGCTATCGAA	1620
OY	1621	GAAATGAAGAAAGACACGGAAGTACTATGTCC	GCATTC	1680
Db	1621	GAAATGAAGAAAGACACGGAAGTACTATGTCC	GCATTC	1680
OY	1681	ACTGTGGCAATGATGATGATGATTTAATTCCT	CCAGAAAGAGAGCAACCTGGAAGC	1740
Db	1681	ACTGTGGCAATGATGATGATGATTTAATTCCT	CCAGAAAGAGAGCAACCTGGAAGC	1740
OY	1741	CAGCAATTTCTGACACTGAGATGAAGAGTATCA	CACTGACGAACAAATGATCTCAG	1800
Db	1741	CAGCAATTTCTGACACTGAGATGAAGAGTATCA	CACTGACGAACAAATGATCTCAG	1800
OY	1801	AAGCAATTTTGTGAAGAAACAGAACCTGGAAT	ATTATCACGATGAGATTTCTGATCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAAACAGAACCTGGAAT	ATTATCACGATGAGATTTCTGATCATGAA	1860
OY	1861	GAAAAAGCAGATGAGATGAGTGA	AAAAATGAAATTTGAGCTTTCTTATGTTTGAAGAA	1920
Db	1861	GAAAAAGCAGATGAGATGAGTGA	AAAAATGAAATTTGAGCTTTCTTATGTTTGAAGAA	1920
OY	1921	GAAAAAGCATCTTTCATGAAATATGATCGTTG	CGGGAAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAGCATCTTTCATGAAATATGATCGTTG	CGGGAAGAAATTTGCCATGCTAAGACTG	1980
OY	1981	GAGCTTAGACACATGAAACATAGAGCCAGGCT	TA	2040
Db	1981	GAGCTTAGACACATGAAACATAGAGCCAGGCT	TA	2040

RESULT 5
US-09-685-166A-375

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlockee, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kelos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reutter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

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1  APPLICANT:  Mang, Aijun
2  APPLICANT:  Skeiky, Kasir A.W.
3  APPLICANT:  Hepler, William
4  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
5  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
6  FILE REFERENCE:  210121.427C21
7  CURRENT APPLICATION NUMBER:  US/09/685,166A
8  CURRENT FILING DATE:  2000-10-10
9  NUMBER OF SEQ ID NOS:  898
10 SOFTWARE:  FastSeq for Windows Version 3.0
11 SEQ ID NO 375
12 LENGTH:  2040
13 TYPE:  DNA
14 ORGANISM:  Homo sapien
15 US-09-685-166A-375

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Query Match	100.0%;	Score 2040;	DB 3;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	ATGGTGGTTGAGTTGATTCACATGCGCGGTGCTCTTCGTGTAACAAGCACTTGGCTTC	60
Db	1	ATGGTGGTTGAGTTGATTCACATGCGCGGTGCTCTTCGTGTAACAAGCACTTGGCTTC	60
OY	61	AGAGCAAGATGGGCAAGTGGTGGTCTGCCGTTGCTTCCCCTGTCGAGGAGAGCGCAAG	120
Db	61	AGAGCAAGATGGGCAAGTGGTGGTCTGCCGTTGCTTCCCCTGTCGAGGAGAGCGCAAG	120
OY	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACACTTGTCTATGAAACACTCAGAGGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACACTTGTCTATGAAACACTCAGAGGCAAG	180
OY	181	ATGGGCAAGTGGTGGCGGCACCTGCTTCCCTGCTGCAGAGGAGGTGGCAAGCAACTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACCTGCTTCCCTGCTGCAGAGGAGGTGGCAAGCAACTG	240
OY	241	GGCGCTTCTGAGACACACGACGACTCTGTATGAAGACACTCAGGAACAAGTGGCAAG	300
Db	241	GGCGCTTCTGAGACACACGACGACTCTGTATGAAGACACTCAGGAACAAGTGGCAAG	300
OY	301	TGTGTCTGCCACTGCTTCCCTGCTGTGAGGGGGAACGGCCAAAGCAAGTGGGCGCTTGG	360
Db	301	TGTGTCTGCCACTGCTTCCCTGCTGTGAGGGGGAACGGCCAAAGCAAGTGGGCGCTTGG	360
OY	361	GGAAGCTACATGACAGTGCCTTTCATGAGGCCACAGGTACCAAGTCCGTGSAAGATCTG	420
Db	361	GGAAGCTACATGACAGTGCCTTTCATGAGGCCACAGGTACCAAGTCCGTGSAAGATCTG	420
OY	421	GACAACTCCACAGAGTCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG	480
Db	421	GACAACTCCACAGAGTCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATCGTCATG	480
OY	481	CTCAGGGGCACTGACGTGTAACAAGAAAGACAAGAAAGAGGACGTCTCTAATCTGGGC	540
Db	481	CTCAGGGGCACTGACGTGTAACAAGAAAGACAAGAAAGAGGACGTCTCTAATCTGGGC	540
OY	541	TCTGCGCAATGGGAATTCAAGAGTAGTAAAACTCTGCTGSAACAGACGATGCAACTTAAT	600
Db	541	TCTGCGCAATGGGAATTCAAGAGTAGTAAAACTCTGCTGSAACAGACGATGCAACTTAAT	600
OY	601	GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGAGCGGTACATATGCCAGGAAGTGA	660
Db	601	GTCCTTGAACAACAAAAGAGACAGCTCTGATTAAGAGCGGTACATATGCCAGGAAGTGA	660
OY	661	TGTGGGTAAATGTTGCTGGAAACATGGCACTGATCCAAATATTCACAGATGAGATGGAAT	720
Db	661	TGTGGGTAAATGTTGCTGGAAACATGGCACTGATCCAAATATTCACAGATGAGATGGAAT	720
OY	721	ACCACTGCACTACGCTATCTATATATGAAGATTAATTATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTACGCTATCTATATGAAGATTAATTATGGCCAAAGCACTGCTCTTA	780
OY	781	TATGTGCTGATATTCGAATCAAAAAACAGCATGGCCTTCACACCACTGTATCTTGGTGA	840

DB 781 TATGGTGTGATATGCAATCAAAAAACAGCAGTGGCTCAGACCACTGTTACTTGGTGTG 840
QY 841 CATGACCAAAAAACAGCAAGTCGTGAAATTTTATATAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGACCAAAAAACAGCAAGTCGTGAAATTTTATATAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGGACTGCTCATATCTGCTGTATGTTGTGGATCAGCAATATAT 960
DB 901 CTGGATAGATATGGAAGGACTGCTCATATCTGCTGTATGTTGTGGATCAGCAATATAT 960
QY 961 GTGAGCCTTCTACTTGGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
DB 961 GTGAGCCTTCTACTTGGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTTACTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
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DB 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGCAGTGAATAAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAGAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAGAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGTTGGATTTACTAGAAAACTGACTATATGCTGCTGCTGCTG 1320
DB 1261 AAGCATGAAGATTAATGTTGGATTTACTAGAAAACTGACTATATGCTGCTGCTGCTG 1320
QY 1321 AATGTGATTAATGATTTAATCTCTCAAGAGAGAGAGCAACCTGAAATACGCAATTT 1380
DB 1321 AATGTGATTAATGATTTAATCTCTCAAGAGAGAGAGCAACCTGAAATACGCAATTT 1380
QY 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGAAATGATTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGAAATGATTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATATCTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
DB 1441 AAAACAGATGCCAAATATCTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGAC 1500
QY 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATGGCCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTCACAAAGGCTTGAGGGCAGTGAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGATGATGAGAGCTAGAAAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGATGATGAGAGCTAGAAAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAGAGAGCAGGAAGTACTCATGTGCGATTCAGAAAACTGACTAATGTGTCC 1680
DB 1621 GAAATGAGAGAGCAGGAAGTACTCATGTGCGATTCAGAAAACTGACTAATGTGTCC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAGAGATCAAGTACGAGCAAAATGATGATCTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAGAGATCAAGTACGAGCAAAATGATGATCTGAG 1800
QY 1801 AAGCAATTTTGTGAGAGAGAGCACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAGAGAGAGCACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAGCAGATGAATGTTGAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
DB 1861 GAAAGCAGATGAATGTTGAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920

DB 1861 GAAAGCAGATGAATGTTGAAAAATGAATTTCTGAGCTTTCTTTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGATGAAAAATGATGATGCTGGGAGAGAAATTTGCCATGCTAG 1980
DB 1921 GAAAAAGACATCTTGATGATGAAAAATGATGATGCTGGGAGAGAAATTTGCCATGCTAG 1980
QY 1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTTAAAAATTTTTTTTTTTTTTTTTTTT 2040
DB 1981 GAGCTAGACACAAATGAAATCATGAGCCAGCTTAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Prudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
FILE REFERENCE: 1999-10-28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATGATGATGATTCATGCGGCTGCTCTTGTGAGAGAGCAATTTGCTTC 60
DB 1 ATGTGTTGATGATGATGATTCATGCGGCTGCTCTTGTGAGAGAGCAATTTGCTTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGCAAGCAAGCTGCTATGAGACACTCAGAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGAGCAAGCAAGCTGCTATGAGACACTCAGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCAAGT 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTCTGCAAGGAGAGTGGCAAGAGCAAGT 240
QY 241 GCGGCTTCTGAGAGCAAGCAAGCTCTGCTATGAGAGCACTCAGAGAAAGATGGCAAG 300
DB 241 GCGGCTTCTGAGAGCAAGCAAGCTCTGCTATGAGAGCACTCAGAGAAAGATGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGAGTACAGTCTTCAATGAGAGCCAGATACAGTCCGTGAGAAAGTCTG 420
DB 361 GGAGACTAGATGAGTACAGTCTTCAATGAGAGCCAGATACAGTCCGTGAGAAAGTCTG 420
QY 421 GACAACTTCCAGAGAGCTGCTGCTGAGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
DB 421 GACAACTTCCAGAGAGCTGCTGCTGAGAGTAAAGTCCCAAGAAAGATCTCATGCTGATG 480
QY 481 CTCAGAGACACTGAGTGAACAAAGAGCAAGCAAGAGAGCAAGTCTTACATCTGCTGC 540
DB 481 CTCAGAGACACTGAGTGAACAAAGAGCAAGCAAGAGAGCAAGTCTTACATCTGCTGC 540


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Db 481 CTCAGGACCTGACGTGAACAAGAGACAAAGCAAAAGAGACTGCTCTACCTGACC 540
QY 541 TCTGCAATGGGAAATTCAGAGATGATAAATCTCTGCTGGAACAGCATGTCAACTTAAT 600
Db 541 TCTGCAATGGGAAATTCAGAGATGATAAATCTCTGCTGGAACAGCATGTCAACTTAAT 600
QY 601 GTCTTTCAGCAACAAAAGAGAGACAGCTGTATTAAGCCGTACATGCCAGAAAGATGAA 660
Db 601 GTCTTTCAGCAACAAAAGAGAGACAGCTGTATTAAGCCGTACATGCCAGAAAGATGAA 660
QY 661 TGTGCTTATGTGTCTGGACATGGCATGTATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCTTATGTGTCTGGACATGGCATGTATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTTAAATGAAGATTAATGGCCAAAGACCTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTTAAATGAAGATTAATGGCCAAAGACCTGCTTA 780
QY 781 TATGCTGTGATTCGAATCAAAAACAAAGCATGGCTGACACACTGTACTTGGTGA 840
Db 781 TATGCTGTGATTCGAATCAAAAACAAAGCATGGCTGACACACTGTACTTGGTGA 840
QY 841 CATGACCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATGATATGGAAGAGACTGCTCATCTGTATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGATGATATGGAAGAGACTGCTCATCTGTATGTTGTGGATCAGCAAGTATA 960
QY 961 GTTCAGCTTCTACTTGGAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGACAG 1020
Db 961 GTTCAGCTTCTACTTGGAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGACAG 1020
QY 1021 GCCAGAGATATGCTCTTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGATAC 1080
Db 1021 GCCAGAGATATGCTCTTTCTAGTCAATCATGATTAATTTGCCAGTTACTTCTGATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTCTGAAAAACAGCAATCCAAACAAAGCTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTCTGAAAAACAGCAATCCAAACAAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATTAAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATTAAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGAGGAGTTACTAGAAAACCTGATTAATGCTGCTGAC 1320
Db 1261 AAGCATGAAGTAAATATGAGGAGTTACTAGAAAACCTGATTAATGCTGCTGAC 1320
QY 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATACGAATTT 1380
Db 1321 AATGTGATATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATACGAATTT 1380
QY 1381 CCTGACAGAGAGAGAGATGATCAAGAAATTTGCGAATTAATTTCTGATCAAAAGAA 1440
Db 1381 CCTGACAGAGAGAGAGATGATCAAGAAATTTGCGAATTAATTTCTGATCAAAAGAA 1440
QY 1441 AAACAGATGCAAAATATCTCTGAAAAACAGCAACCCAGAACTTAAGCTGAGAC 1500
Db 1441 AAACAGATGCAAAATATCTCTGAAAAACAGCAACCCAGAACTTAAGCTGAGAC 1500
QY 1501 TCAGAGAGAGAGTCAACAAAGCTTGAAGGCGAGTGAATTAAGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAACAAAGCTTGAAGGCGAGTGAATTAAGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAAGAACCAAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAAGAACCAAGAAATTAATAGATGATGATGAGAGCTGAGAAATTTTATGCTATCGAA 1620
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QY 1621 GAAATGAAGAGACAGAAAGTACTCATGTCGATTCGGAATTCAGAAACCTGATATGTC 1680
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QY 1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATTAATTTCTCCAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCACAGTACGAAACAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCACAGTACGAAACAAATGATCTCAG 1800
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Db 1801 AAGCAATTTTGGAGAGACAGAAACCTGGAATATTACAGATGATGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAAGTGTGAAAAAATGAATTTCTGACCTTCTTATGTTAGAA 1920
Db 1861 GAAAAGCAGATGAAAGTGTGAAAAAATGAATTTCTGACCTTCTTATGTTAGAA 1920
QY 1921 GAAAAAGCATTTGATGATGAAAAATGATGATGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGCATTTGATGATGAAAAATGATGATGCGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAACATGAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
Db 1981 GAGCTAGACACAAATGAACATGAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 7
US-09-679-426-375
Sequence 375, Application US/09679426
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCTTGAAGTTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGATCTC 60
Db 1 ATGTGCTTGAAGTTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGATCTC 60
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QY 61 AGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGAGGAGAGCGGCAAG 120
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Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACAAGAGCTGTCTATGAGACACTCAGAGCAAG 180
| | | | |
Db 121 AGCAAGTGGGCACTTCTGAGACAAGAGCTGTCTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGACAAGT 240
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Db 181 ATGGGCAATGGTGGCCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGACAAGT 240
QY 241 GGGCTTCTGAGACAAGAGCTGTCTATGAGACAAGAGTGGGCAAG 300
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Db 241 GGGCTTCTGAGACAAGAGCTGTCTATGAGACAAGAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGTGGGCAAGTGG 360
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Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGTGGGCAAGTGG 360
QY 361 GGAAGCTAGATGACAGTGTCTATGAGAGCCAGGTAACAGTCCGTGAGAAATCTG 420
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Db 361 GGAAGCTAGATGACAGTGTCTATGAGAGCCAGGTAACAGTCCGTGAGAAATCTG 420
QY 421 GACAAGCTCAGAGAGCTGTGAGGAGTAAAGTCCAGAAAGATCTCATGCTGATG 480
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Db 421 GACAAGCTCAGAGAGCTGTGAGGAGTAAAGTCCAGAAAGATCTCATGCTGATG 480
QY 481 CTCAGGAGACATGACCTGAGACAAGAGACAAGCAAAAGAGAGCTCTCTACATCTG 540
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Db 481 CTCAGGAGACATGACCTGAGACAAGAGACAAGCAAAAGAGAGCTCTCTACATCTG 540
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QY 601 GTTCCTGACAACAAAAGAGAGAGCTGTGATTAAGCCGTAAAGCCAGAGAAATGTA 660
| | | | |
Db 601 GTTCCTGACAACAAAAGAGAGAGCTGTGATTAAGCCGTAAAGCCAGAGAAATGTA 660
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Db 661 TGTGCTTAATGTGTGAGACAAGGACATGATCCAAATATTCAGATGATGTAAT 720
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Db 721 ACCACTCTGACACTGCTATCTATTAATGAAGATTAATGAGCAAGCACTGCTTA 780
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| | | | |
Db 781 TATGCTGCTGATTCGATCAATCAAAAGCAAGCATGAGCTTCACTTGGTGA 840
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Db 841 CATGAGCAAAAACAGAGAGCTGTGAATTTTAAATCAAGAAAAGCAATTTAAATGA 900
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| | | | |
Db 901 CTGAGATGATGAGAGAGAGCTGTCTCATCTGCTGATGTTGAGATCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
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Db 961 GTACAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGAGAG 1020
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Db 1021 GCCAGAGATGATGCTTTCTAGTCAATCATCATGATTAATTTGCAAGTAACTTTGAGTAC 1080
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Db 1081 AAAAGAAAAACAGATGCTAAATATCTTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
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Db 1141 CTGACATCAGAGAGAGATCAAAAGTTCAAAAGGAGAGTGAATAAGCCAGCAAGAAA 1200
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Db 1201 ATGTCTCAAGAAACAGAAAATTAATAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGAGTTACTGAAAACTGATTAAGTGTCTACTGTGGC 1320
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Db 1261 AAGCATGAAAGTAAATATGATGAGTTACTGAAAACTGATTAAGTGTCTACTGTGGC 1320
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| | | | |
Db 1321 AATGTGATTAATGATTAATCTTCAAGAGAGAGCAAGCACTGAAATCAGCAATTT 1380
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Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTAATTTCTGATCAAAAGAA 1440
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| | | | |
Db 1441 AAAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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| | | | |
Db 1501 TCAGAGAAAGATCAAAAGGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATCT 1560
QY 1561 CAAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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Db 1561 CAAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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Db 1621 GAAATGAGAGAGAGAGAGAGTCTCATGTGCGATTTCCAGAAAACCTGATTAATGATGAT 1680
QY 1681 ACTGCTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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Db 1681 ACTGCTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1800
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Db 1801 AAGCAATTTTGTGAAGACAGAACTGTGAATTTTACAGATGATGATGATGATGATGAT 1860
QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTGAATGTAAGAA 1920
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Db 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTTCTTGAATGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1980
| | | | |
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040
| | | | |
Db 1981 GAGCTAGACACATGAAACATGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT 2040

RESULT 8
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuhui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

```
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Derrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yaelir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C23
/ CURRENT APPLICATION NUMBER: US/09/759,143
/ NUMBER OF SEQ ID NOS: 934
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-09-759-143-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  ATGGTGGTGAAGTGAATTCATGCGGGCTGCTTTGTGAGAAAGCATTTGGTCTC 60
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DB      61  AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGTGCGAGGAGAGCGCAAG 120
QY      121  AGCAAGTGGGCACTTCTGAGACCAAGAGACTCTGCTATGAAAGCACTCAGAGCAAG 180
DB      121  AGCAAGTGGGCACTTCTGAGACCAAGAGACTCTGCTATGAAAGCACTCAGAGCAAG 180
QY      181  ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGTGCGAGGAGGAGTGGCAAGCAAGCTG 240
DB      181  ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGTGCGAGGAGGAGTGGCAAGCAAGCTG 240
QY      241  GGGGCTTCTGGAGACCAAGAGACTCTGCTATGAAAGCACTCAGAAACAAGATGGCAAG 300
DB      241  GGGGCTTCTGGAGACCAAGAGACTCTGCTATGAAAGCACTCAGAAACAAGATGGCAAG 300
QY      301  TGGTGTGCGCACTGCTTCCCTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB      301  TGGTGTGCGCACTGCTTCCCTGTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY      361  GGAAGCTAGAGTGAAGTGGCTTCAATGAGGCCAGGTAACAGTCCGTGGAAGAAATCTG 420
DB      361  GGAAGCTAGAGTGAAGTGGCTTCAATGAGGCCAGGTAACAGTCCGTGGAAGAAATCTG 420
QY      421  GACAACTCCACAGAGCTGCTGGTGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
DB      421  GACAACTCCACAGAGCTGCTGGTGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY      481  CTGAGGAGCACTGACGTGAACAAGAAAGGACAAACAAAGAGAGAGCTCTCACTGGCC 540
DB      481  CTGAGGAGCACTGACGTGAACAAGAAAGGACAAACAAAGAGAGAGCTCTCACTGGCC 540
QY      541  TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGAGCAAGAGATGCACTTAAT 600
DB      541  TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGTGAGCAAGAGATGCACTTAAT 600
QY      601  GTCTTGAACAACAAAAGAGAGAGCTTGAATAAGGCGTACATGCGCAGAAAGATGA 660
DB      601  GTCTTGAACAACAAAAGAGAGAGAGCTTGAATAAGGCGTACATGCGCAGAAAGATGA 660
QY      661  TGTGCTTAATGTTGTGTGGAACATGGCACTGATCAAAATATTCAGATGAGTGAAT 720
DB      661  TGTGCTTAATGTTGTGTGGAACATGGCACTGATCAAAATATTCAGATGAGTGAAT 720
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QY      721  ACCAGCTGCACTAGCTATCTATATGAAAGTAAATTAATGGCCAAAGCACTGCTTA 780
DB      721  ACCAGCTGCACTAGCTATCTATATGAAAGTAAATTAATGGCCAAAGCACTGCTTA 780
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DB      781  TATGGTGTGATATGAAATCAAAAAACAAGATGGCTCACACACTGTTACTTGGTGA 840
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DB      901  CTGATATGATGAAAGAGCTGCTCACTCTGCTGATATGTTGTGATCAGCAAGTATA 960
QY      961  GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
DB      961  GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
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DB      1021  GCCAAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGATC 1080
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DB      1081  AAAGAAAAACAGATGCTAAATCTCTGAAAACAGCAATCCAGAACAAAGCTTAAAG 1140
QY      1141  CTGATCATGAGAAAGAGTCAAAAGGCTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
DB      1141  CTGATCATGAGAAAGAGTCAAAAGGCTTCAAGGCAAGTAAATAGCCAGCAGAGAAA 1200
QY      1201  ATGTCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGTTGAAAGAAATGAA 1260
DB      1201  ATGTCTCAAGAACCGAAATTAATAGATGGTGTATAGAGAGTTGAAAGAAATGAA 1260
QY      1261  AAGCATGAAAGTAATATGTTGGATTTAATGAGAAACCTGATGATGTTGCTGCTGGC 1320
DB      1261  AAGCATGAAAGTAATATGTTGGATTTAATGAGAAACCTGATGATGTTGCTGCTGGC 1320
QY      1321  AATGGTGAATATGATTAATTTCTCAAGAAAGAGCAGAACCACTGAATAGCAATTT 1380
DB      1321  AATGGTGAATATGATTAATTTCTCAAGAAAGAGCAGAACCACTGAATAGCAATTT 1380
QY      1381  CTTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTCTGACTACAAAG 1440
DB      1381  CTTGACAAAGAAAGTGAAGATATCAAGAAATTTGCGAATTAAGTTCTGACTACAAAG 1440
QY      1441  AAACAGATGCCAAAATACCTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGAC 1500
DB      1441  AAACAGATGCCAAAATACCTCTGAAAACAGCAACCCAGAACAAAGCTTAAAGCTGAC 1500
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QY      1561  CAAGAACCAAGAAATTAATAGATGGTGTATAGAGAGCTAGAAATTTTATGCTATCGAA 1620
DB      1561  CAAGAACCAAGAAATTAATAGATGGTGTATAGAGAGCTAGAAATTTTATGCTATCGAA 1620
QY      1621  GAAATGAAGAACAGAGAGTCTCATGTCGAAATTTCCAGAAACCTGACTAATGGTGC 1680
DB      1621  GAAATGAAGAACAGAGAGTCTCATGTCGAAATTTCCAGAAACCTGACTAATGGTGC 1680
QY      1681  ACTGCTGCAATGATGATGATTAATTTCTCAAGAGAAAGAGAGCAACTGTAAGC 1740
DB      1681  ACTGCTGCAATGATGATGATTAATTTCTCAAGAGAAAGAGAGCAACTGTAAGC 1740
QY      1741  CAGCAATTTCTGACATGAGATGAAAGATATCAAGTGAAGAACAAATATGATCTCAG 1800
DB      1741  CAGCAATTTCTGACATGAGATGAAAGATATCAAGTGAAGAACAAATATGATCTCAG 1800
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QY	1801	1AGCAATTTTGTGAAGAACAGAACCTGGAAATATTACACGATGATCTGTATTCATGAA	1860
DB	1801	AAGCAATTTTGTGAAGAACAGAACCTGGAAATATTACACGATGATCTGTATTCATGAA	1860
QY	1861	GAAGAAGCAATGAGTGGTTGAAAAAAATGAAATTCGTAGCTTTCTTATGTTGTAAGAA	1920
DB	1861	GAAGAAGCAATGAGTGGTTGAAAAAAATGAAATTCGTAGCTTTCTTATGTTGTAAGAA	1920
QY	1921	GAAGAAGCAATCTTGCATGAAATATGATCGTTGCGGGAAGAAATTCAGCTTAAGACTG	1980
DB	1921	GAAGAAGCAATCTTGCATGAAATATGATCGTTGCGGGAAGAAATTCAGCTTAAGACTG	1980
QY	1981	GAGCTAGACCAATGAAATCATGAGCCGCACTTAAAAAAAAAAAAAAAAAAAAAAAAA	2040
DB	1981	GAGCTAGACCAATGAAATCATGAGCCGCACTTAAAAAAAAAAAAAAAAAAAAAAAAA	2040
RESULT 9			
	US-09-651-236-375		
	/ Sequence 375, Application US/09651236		
	/ Patent No. 6818751		
	/ GENERAL INFORMATION:		
	/ APPLICANT: Xu, Jiangchun		
	/ APPLICANT: Dillon, Davin C.		
	/ APPLICANT: Mitcham, Jennifer L.		
	/ APPLICANT: Harlocker, Susan L.		
	/ APPLICANT: Jiang, Yuyu		
	/ APPLICANT: Henderson, Robert A.		
	/ APPLICANT: Kalos, Michael D.		
	/ APPLICANT: Fanger, Gary R.		
	/ APPLICANT: Retter, Marc W.		
	/ APPLICANT: Stolk, John A.		
	/ APPLICANT: Day, Craig H.		
	/ APPLICANT: Vedwick, Thomas S.		
	/ APPLICANT: Carter, Derrick		
	/ APPLICANT: Li, Samuel		
	/ APPLICANT: Wang, Aijun		
	/ APPLICANT: Skeiky, Yaeli A.W.		
	/ APPLICANT: Hepler, William		
	/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND		
	/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER		
	/ FILE REFERENCE: 210121.42718C18		
	/ CURRENT APPLICATION NUMBER: US/09/651.236		
	/ CURRENT FILING DATE: 2000-08-29		
	/ NUMBER OF SEQ ID NOS: 865		
	/ SOFTWARE: FastSeq for Windows Version 3.0		
	/ SEQ ID NO 375		
	/ LENGTH: 2040.		
	/ TYPE: DNA		
	/ ORGANISM: Homo sapien		
	US-09-651-236-375		
	Query Match	100.0%; Score 2040;	DB 3; Length 2040;
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2040; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	1	ATGGGTGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTAAGAAAGCATTTGGTCTC	60
DB	1	ATGGGTGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTAAGAAAGCATTTGGTCTC	60
QY	61	AGAGCAAGATGAGGCAAGTGTGTGTCGCGTGTCTTCCCTGCTCAGGAGAGCGGCAAG	120
DB	61	AGAGCAAGATGAGGCAAGTGTGTGTCGCGTGTCTTCCCTGCTCAGGAGAGCGGCAAG	120
QY	121	AGCAACGTGGGCACTTCTGAGAACCAAGCACTCTGTTATGAAGACCTCAGAGCAAG	180
DB	121	AGCAACGTGGGCACTTCTGAGAACCAAGCACTCTGTTATGAAGACCTCAGAGCAAG	180
QY	181	ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTCAGGAGAGGCAAGCAAGCAAGTGT	240
DB	181	ATGGGCAAGTGTGTGCGGCACTGCTTCCCTGCTCAGGAGAGGCAAGCAAGCAAGTGT	240
QY	241	GAGCGTCTTGAGAACCAAGCAAGCACTCTGTTATGAAGACCTCAGAGCAAGTGTGGCAAG	300

Db	241	GGCGCTTCTGAGACCAAGCAACTCTGTATGAAACACTCAGAAACMAATGGGCAAG	300
Oy	301	TGTTGCTCCACATGCTTCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGTGGGCGTTGG	360
Db	301	TGTGTCTCCACTGCTTCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Oy	361	GAAGACTACATGACAGTGCCTTCAATGAGGCCAGGTACCACTGTCGTGAGAAATCTG	420
Db	361	GAAGACTACATGACAGTGCCTTCAATGAGGCCAGGTACCACTGTCGTGAGAAATCTG	420
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Db	421	GACAACTTCCACAGAGCTGCTGGTGGGTAAAGTCCACAGAAAGATCTCATGTGCATG	480
Oy	481	CTCAGGGGCACTGACGTGAACAAAGAGGCAAGGAAAGAGAGACCTGCTCATCTGGCC	540
Db	481	CTCAGGGGCACTGACGTGAACAAAGAGGCAAGGAAAGAGAGACCTGCTCATCTGGCC	540
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Db	541	TCTGCCAATGGGAATTCAGAAAGTAAATCTCGCTGACAGACGATGCAACTTAAT	600
Oy	601	GTCCTTGACAAACAAAAGAGGACGCTCTGTAAAGCCGTACATGCGAGAAAGATGA	660
Db	601	GTCCTTGACAAACAAAAGAGGACGCTCTGTAAAGCCGTACATGCGAGAAAGATGA	660
Oy	661	TGTGGTTAATGTTGCTGGGAACATGGGACGTGATCCAAATNTCCAGATGATAGSAAAT	720
Db	661	TGTGGTTAATGTTGCTGGGAACATGGGACGTGATCCAAATNTCCAGATGATAGSAAAT	720
Oy	721	ACCACTCTGCACCTACGCTATCTATATAGAGATTAATTAATGSCCAAGACCTGCTTA	780
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Oy	781	TATGGTGTGATATCGAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGT	840
Db	781	TATGGTGTGATATCGAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGT	840
Oy	841	CATAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAAGGAAATTTTAAATGCA	900
Db	841	CATAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAAGGAAATTTTAAATGCA	900
Oy	901	CTGATATGATATGGAAGGACTGCTCTCAACTTCTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGACTGCTCTCAACTTCTGTATGTTGTGATCAGCAAGTATA	960
Oy	961	GTCAGCCTTCTACTTGAACAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGC	1020
Db	961	GTCAGCCTTCTACTTGAACAAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGC	1020
Oy	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATATATTTGCCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATATATTTGCCAGTTACTTCTGACTAC	1080
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Db	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTCTGAAGAACAGCATCAGAACAAAGCTTAAG	1140
Oy	1141	CTGACATCAGAGGAAGTCAAAAGTTCAAGGCAAGTGAATAATAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGTCAAAAGTTCAAGGCAAGTGAATAATAGCCAGAGAA	1200
Oy	1201	ATGTCTCAAGAACAGAAATTAATTAAGATGTGTATAGAGAGTTGAAGAAATGAG	1260
Db	1201	ATGTCTCAAGAACAGAAATTAATTAAGATGTGTATAGAGAGTTGAAGAAATGAG	1260
Oy	1261	AAGCATGAAGTATATATGCGGATTTACTGAAGAACCTGATATGAGTGCACGTGGCC	1320
Db	1261	AAGCATGAAGTATATATGCGGATTTACTGAAGAACCTGATATGAGTGCACGTGGCC	1320
Oy	1321	AATGTGATATATGATTTAATTTCTCAAGAGGAAGCAACACTGAAAATTCAGCAATTT	1380

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Qy 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTCTGATCAAGAGAA 1440
Db 1381 CCTGACAGAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATTCTGATCAAGAGAA 1440
Qy 1441 AAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAAATATCTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA 1500
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Db 1501 TCAGAGAGAGATCACAAAAGCTTGAAGGCAATGAAAAATGCGCAAGCAAGAAAAGATCT 1560
Qy 1561 CAAGAACCAGAAATTAATAAGATGGTATAGAGAGCTAAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACCAGAAATTAATAAGATGGTATAGAGAGCTAAGAAATTTATGCTATCGAA 1620
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Qy 1681 ACTGCTGGCAATGTGTATGATGATTAATTCCTCAAGAGAGAGCAACCTGAAAC 1740
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Qy 1741 CAGCAATTTCTCTGACCTGAGAAATGAAGATATCAAGTGAAGCAAAATGATCTGAC 1800
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Qy 1861 GAAACACATAGAAATGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTGAAGAA 1920
Db 1861 GAAACACATAGAAATGTGTGAAAAATGAATTTCTGAGCTTCTTGTGTGAAGAA 1920
Qy 1921 GAAAAAGACATCTTGATGATGAATAGTACGTTGCGGGAAGAAATTCAGATCTAAGAC 1980
Db 1921 GAAAAAGACATCTTGATGATGAATAGTACGTTGCGGGAAGAAATTCAGATCTAAGAC 1980
Qy 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 10
US-09-699-295-303
Sequence 303, Application US/09699295
Patent No. 6828431
GENERAL INFORMATION:
APPLICANT: Prudakie, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misner, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaser A.W.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST AND OTHER TYPES OF CANCER
FILE REFERENCE: 210121.419C10
CURRENT APPLICATION NUMBER: US/09/699,295
CURRENT FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 326
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-699-295-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGTGTGATTAATGATTAATTCCTCAAGAGAGAGCAACCTGAAAAATGCAATTT 60
Qy 61 AGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 120
Db 61 AGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 120
Qy 121 AGCAAGCTGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 180
Db 121 AGCAAGCTGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGAT 180
Qy 181 ATGGGCAAGTGTGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 240
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Qy 241 GGGGCTTCTGAG 300
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Qy 301 TGGTCTGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 GGAAGCTAGATGAG 420
Db 361 GGAAGCTAGATGAG 420
Qy 421 GACAGAGCTGAG 480
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Qy 481 CTGAG 540
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Qy 721 ACCACTGCACTGAG 780
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Qy 841 CATGAG 900
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Qy 901 CTGAGATGATGAG 960
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Qy 961 GTGAGCTTCTGAG 1020
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RESULT 11
US-09-534-825A-303
; Sequence 303, Application US/09534825A
; Patent No. 6861506

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John W.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534,825A
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-534-825A-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCTGTTGAGGTTGATTCATGCGGCTCCTCTTCTGTGAAGAGCATTTGGTCTC 60
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Db 661 TGTGCTTAATGTTGTGAGAACATGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTCTGACCTAGCTATCTAATATGAAGTAAATTAATGGCCAAAGCACTGCTCTTA 780
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Db      1201  ATGTCTCAAGAACCCAGAAATTAATAGATGATGATAGAGAGTTGAAGAAATGAAG 1260
Qy      1261  AAGCATGAAAGTAAATATGATGAGATTACTAGAAAACTTGAATGATGCTGCTGAC 1320
Db      1261  AAGCATGAAAGTAAATATGATGAGATTACTAGAAAACTTGAATGATGCTGCTGAC 1320
Qy      1321  AATGTGATTAATGATTAATCTCTCAAGAGAAAGCAACCTGAAATTCAGCAATTT 1380
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Db      1381  CCTGACAAAGAAAGTAAAGATTCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGA 1440
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Db      1441  AAAAGATGCCAAATATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db      1501  TCGAGAGAAAGATCAAAAAGCTTGAAGGAGTGAAGAAATGCGCAGCAGAGAAATGCT 1560
Qy      1561  CAAGAACCAAGAAATTAATAGATGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
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Qy      1621  GAAATGAAGAGACCGAAGTACTCATGTCGAAATTCAGAAAACTGACTAATGCTGACC 1680
Db      1621  GAAATGAAGAGACCGAAGTACTCATGTCGAAATTCAGAAAACTGACTAATGCTGACC 1680
Qy      1681  ACTGCTGGCAATGATGATGATTAATTTCTTCAAGAGAGCAAGCACTGGAAGC 1740
Db      1681  ACTGCTGGCAATGATGATGATTAATTTCTTCAAGAGAGCAAGCACTGGAAGC 1740
Qy      1741  CAGCAATTTCTTCACTGAGATGAAGATATCAAGTACCAAAATGATCTCAG 1800
Db      1741  CAGCAATTTCTTCACTGAGATGAAGATATCAAGTACCAAAATGATCTCAG 1800
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RESULT 12
US-09-657-279-375
; Sequence 375, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedic, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGTGATGATGATGATGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGGTTC 60
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Qy      121  AGCAACGTGGGCACTTTGAGAGACACAGCACTCTGCTATGAAGACATTCAGAGCAAG 180
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Qy      181  ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGACAGGAGGAGTGGCAAGCAAGT 240
Db      181  ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGACAGGAGGAGTGGCAAGCAAGT 240
Qy      241  GCGGCTTCTGAGACACAGCACTCTGCTATGAAGACATTCAGAGCAAGATGGGCAAG 300
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DB 1921 GAAAAAGCATTTGATGATGAAGAAATGATGATGCTGCGGAGAGAAATTTGCCATGAGACTG 1980
QY 1981 GAGCTAGACACAAATGAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 1981 GAGCTAGACACAAATGAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 13
US-10-012-896-375
Sequence 375, Application US/10012896
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yahir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Manzanabe, Yoshihiro

```

; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAAGCCATTGGTCTC 60
DB      1 ATGGTGGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAAGCCATTGGTCTC 60

QY      61 AGGAGCAAAATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120
DB      61 AGGAGCAAAATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCGAGAGCGGCAAG 120

QY      121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAACACTCAGAGCAAG 180
DB      121 AGCAAGTGGGCACTTCTGAGACACAGACACTCTGTATGAAACACTCAGAGCAAG 180

QY      181 ATGGGCAAGTGTGCGGCACTGCTTCCCCTGTGCAAGGGAGTGGCAAGCAACGTG 240
DB      181 ATGGGCAAGTGTGCGGCACTGCTTCCCCTGTGCAAGGGAGTGGCAAGCAACGTG 240

QY      241 GGGGCTTTGAGAGACACACACACTCTGTATGAAACACTCAGAGCAAGTGGCAAG 300
DB      241 GGGGCTTTGAGAGACACACACACTCTGTATGAAACACTCAGAGCAAGTGGCAAG 300

QY      301 TGGTGTGCGCACTGCTTCCCCTGTGCAAGGGAGTGGCAAGCAAGTGGGCGCTTGG 360
DB      301 TGGTGTGCGCACTGCTTCCCCTGTGCAAGGGAGTGGCAAGCAAGTGGGCGCTTGG 360

QY      361 GGAAGTACGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAGAAAGTCTG 420
DB      361 GGAAGTACGATGACAGTGTCTTCAATGAGCCCAAGGTACCACTGCTGGAGAAAGTCTG 420

QY      421 GACAACTCCACAGAGCTGTGCTGGAGCCCAAGGTACCACTGCTGGAGAAAGTCTG 480
DB      421 GACAACTCCACAGAGCTGTGCTGGAGCCCAAGGTACCACTGCTGGAGAAAGTCTG 480

QY      481 CTCAGGGAACACTGACGTGAACAAGAGACAAAGAGAGAGCTGCTTACATCTGGCC 540
DB      481 CTCAGGGAACACTGACGTGAACAAGAGAGACAAAGAGAGAGCTGCTTACATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAGATGTCAACTTAAT 600
DB      541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGGAACAGATGTCAACTTAAT 600

QY      601 GTCTTGAACAACAAAAAGAGAGACAGCTGTGATAAGCCGTACAAATGCCAGGAAGTGA 660
DB      601 GTCTTGAACAACAAAAAGAGAGACAGCTGTGATAAGCCGTACAAATGCCAGGAAGTGA 660

QY      661 TGTGCGTTAATGTTGCTGAACATGGACATGATCCAAATTTCTCAGATGATGGAAT 720
DB      661 TGTGCGTTAATGTTGCTGAACATGGACATGATCCAAATTTCTCAGATGATGGAAT 720

QY      721 ACCACTCTGCACTACGTATCTATTAATGAGATTAATTAATGAGCAAGACATGCTCTTA 780
DB      721 ACCACTCTGCACTACGTATCTATTAATGAGATTAATTAATGAGCAAGACATGCTCTTA 780

QY      781 TATGAGTGTATATCGAATTAACAAAAACAGATGAGCTTCAACCACTGTTACTTGGTGA 840
DB      781 TATGAGTGTATATCGAATTAACAAAAACAGATGAGCTTCAACCACTGTTACTTGGTGA 840
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QY      841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB      841 CATGAGCAAAAAACAGAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900

QY      901 CTGATATGATATGAAAGACTGCTCTCATCTGCTGTATGTTGTGATCAGCAAGTATA 960
DB      901 CTGATATGATATGAAAGACTGCTCTCATCTGCTGTATGTTGTGATCAGCAAGTATA 960

QY      961 GTACGCTTCTATCTTGAGCAAAATATATGATATCTTCCAGATCTATCTGGAACAGAG 1020
DB      961 GTACGCTTCTATCTTGAGCAAAATATATGATATCTTCCAGATCTATCTGGAACAGAG 1020

QY      1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTTCTATGATCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080

QY      1081 AAAGAAAAACAGATCTAAATAATCTTCTGAAAAACGCAATCCAGAACAAAGACTTAAG 1140
DB      1081 AAAGAAAAACAGATCTAAATAATCTTCTGAAAAACGCAATCCAGAACAAAGACTTAAG 1140

QY      1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGAAA 1200
DB      1141 CTGACATCAGAGAAAGAGTCAAAAGGTTCAAAAGGCAAGTAAATAGCCAGCAAGAAA 1200

QY      1201 ATGCTCAAGAACACAGAAATTAATAGGATGAGTGAAGAAGGTTGAAGAAATGAAG 1260
DB      1201 ATGCTCAAGAACACAGAAATTAATAGGATGAGTGAAGAAGGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAGATTAATATGTGGATTAATAGAAAACTGACTAATGTGTCTACTGTGCG 1320
DB      1261 AAGCATGAAGATTAATATGTGGATTAATAGAAAACTGACTAATGTGTCTACTGTGCG 1320

QY      1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGACAGAAACCTGAAATATGCAATTT 1380
DB      1321 AATGTGATTAATGATTAATTTCTCAAGAGAAAGACAGAAACCTGAAATATGCAATTT 1380

QY      1381 CCTGACAAAGGAGGAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
DB      1381 CCTGACAAAGGAGGAGATATCAAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440

QY      1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
DB      1441 AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500

QY      1501 TCAGAGAAAGAGTCAAAAGGCTTTGAGGCAATGAAAAATGGCCACCCAGAGAAAAAGTCT 1560
DB      1501 TCAGAGAAAGAGTCAAAAGGCTTTGAGGCAATGAAAAATGGCCACCCAGAGAAAAAGTCT 1560

QY      1561 CAAGAACAGAAATTAATAGATGATGATAGAGAGCTGAAATTTTATGTGCTATCGAA 1620
DB      1561 CAAGAACAGAAATTAATAGATGATGATAGAGAGCTGAAATTTTATGTGCTATCGAA 1620

QY      1621 GAAATGAAGAACACGAAAGTACTCATGTGCGATTCGCCAGAAACCTGACTAATGGTGGC 1680
DB      1621 GAAATGAAGAACACGAAAGTACTCATGTGCGATTCGCCAGAAACCTGACTAATGGTGGC 1680

QY      1681 ACTGCTGGCAATGTGTGATGATGATTAATTTCTTCCAGAGAAAGCAAGAACACTGAAAGC 1740
DB      1681 ACTGCTGGCAATGTGTGATGATGATTAATTTCTTCCAGAGAAAGCAAGAACACTGAAAGC 1740

QY      1741 CAGCAATTTCTGACACTGAGAAATGAAGATGATCAAGTGAAGAACAAATGATCTCGAG 1800
DB      1741 CAGCAATTTCTGACACTGAGAAATGAAGATGATCAAGTGAAGAACAAATGATCTCGAG 1800

QY      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATGAGA 1860
DB      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATGAGA 1860

QY      1861 GAAAGACAGATGAAGTGTGTAATAATGAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
DB      1861 GAAAGACAGATGAAGTGTGTAATAATGAATTTCTGAGCTTTCTTATGTTGTAAGAAA 1920
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QY 1561 CAGAAACAGAAATAAATAGATGATGATAGAGAGAGTAAATTTATGCTATCGAA 1620
DB 1548 -----AGAGTGAGAAATTTATGCTATCGAA 1575
QY 1621 GAAATGAGAGACGAGAGTACTCATGTCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
DB 1576 GAAATGAGAGACGAGAGTACTCATGTCGATTTCCAGAAAACCTGACTAATGCTGCC 1635
QY 1681 ACTGTCGCAATGATGATGATGATTTAATTCCTCAAGAGAGAGAGACACTGAAAGC 1740
DB 1636 ACTGTCGCAATGATGATGATGATTTAATTCCTCAAGAGAGAGAGACACTGAAAGC 1695
QY 1741 CAGCAATTTCTCTGACACTGAGAAATGAAAGATATCAAGTACGAGCAAAATGATCTGAC 1800
DB 1696 CAGCAATTTCTCTGACACTGAGAAATGAAAGATATCAAGTACGAGCAAAATGATCTGAC 1755
QY 1801 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTCATGAA 1860
DB 1756 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTCATGAA 1815
QY 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGAAA 1920
DB 1816 GAAAGCAGATAGAGTGTGTAAGAAATGAAATTTCTGAGCTTCTCTAGTTGTAAGAAA 1875
QY 1921 GAAAAAGACATCTTGATGATAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1980
DB 1876 GAAAAAGACATCTTGATGATAAATAGTACGTTGCGGAGAAATTCATGCTAAGACTG 1935
QY 1981 GAGCTGACACATGAAACATCAAGGACGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1936 GAGCTGACACATGAAACATCAAGGACGCTAATAAAAAAAAAAAAAAAAAAAAAA 1995

RESULT 15

US-09-352-616A-374
/ Sequence 374, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillion, Davin C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Jiang, Yiqui
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352.616A
/ NUMBER OF SEQ ID NOS: 472
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 95.1%; Score 1940; DB 3; Length 2000;
Best Local Similarity 97.8%; Pred. No. 0;

Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGATGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCAATTTGCTC 60
DB 1 ATGATGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAAGCAATTTGCTC 60
QY 61 AGAGCAAGATGAGCAAGTGTGCTGCTGTTCTTCCCTGCTGCAAGGAGAGCGCAAG 120
DB 61 AGAGCAAGATGAGCAAGTGTGCTGCTGTTCTTCCCTGCTGCAAGGAGAGCGCAAG 120
QY 121 AGGACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAACACTCAGAGCAAG 180
DB 121 AGGACGTGGGCACTTCTGAGACCAAGCACTGCTATGAAACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240

DB 181 ATGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGT 240
QY 241 GGGCGCTTCTGAGACCAAGCACTTCTGTATGAAAGCACTCAGAGCAAGATGGCAAG 300
DB 241 GGGCGCTTCTGAGACCAAGCACTTCTGTATGAAAGCACTCAGAGCAAGATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGAGTGGCGCTTGG 360
QY 361 GAGACTAGATGACAGTGCCTTCAATGAGCCAGATCAAGTCCGTGAGAAAGATCTG 420
DB 361 GAGACTAGATGACAGTGCCTTCAATGAGCCAGATCAAGTCCGTGAGAAAGATCTG 420
QY 421 GACAGCTTCAAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
DB 421 GACAGCTTCAAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTGAGGGAACATGAGCTGCAAGAAAGCAAGCAAAAGAGAGACTGCTACATCTGGCC 540
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DB 601 GTCTTGTGACACAAAGAGAGACAGCTCTGATTAAGGCGGTCAATGCCAGAAATGAA 660
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QY 721 ACCACTGTCACATGCTATCTATATGAAATTAATGAGCAAGCACTGCTTTA 780
DB 721 ACCACTGTCACATGCTATCTATATGAAATTAATGAGCAAGCACTGCTTTA 780
QY 781 TATGTCGTGATATGATCAAAACCAAGCATGCTTCAACCATGTTACTTGTGAT 840
DB 781 TATGTCGTGATATGATCAAAACCAAGCATGCTTCAACCATGTTACTTGTGAT 840
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DB 841 CATGACAAAAACAGAAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATATGATGAGAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATGAGAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
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DB 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGCAAGTACTATCTGACAG 1080
QY 1081 AAGAGAAAAACAGATGTAATAATCTCTTGTGAAAACAGATTCAGAAACAAGCTTAAAG 1140
DB 1081 AAGAGAAAAACAGATGTAATAATCTCTTGTGAAAACAGATTCAGAAACAAGCTTAAAG 1140
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DB 1141 CTGACATCAGAGAGAGTCAAAAGCTTCAAGGCAAGTGAATATGCCAGAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGATGATGAGAGTGAAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGATGATGAGAGTGAAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGGAATTAATGAGAAACCTGATTAATGATGATGCTGCGC 1320

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Db      1321 AATGGTGAATAATGATTAATTTCTCAAGAGAGAGACACCTGAAATCGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGGCAATTAGTTCTGACTACAAAGAA 1440
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Qy      1501 TCAGAGGAAGATGTCAAAGAGCTTGAAGGCACTGAAATGGCCAGAGAAAAAGATCT 1560
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Qy      1561 CAAGAACAGAAATAATAGATGGTATAGAGAGCTAGAAAAATTTATGGCTATCGAA 1620
Db      1548 -----AGAGCTAGAAATTTTATGGCTATCGAA 1575
Qy      1621 GAATGAGAAGACGGAAGTACTCATGTCGATTCGAGAAAACTGACTAATGCTGCC 1680
Db      1576 GAATGAGAAGACGGAAGTACTCATGTCGATTCGAGAAAACTGACTAATGCTGCC 1635
Qy      1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGACGAAACCTGGAAGC 1740
Db      1636 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGACGAAACCTGGAAGC 1695
Qy      1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTACGAAACAAATGATCTCAG 1800
Db      1696 CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTACGAAACAAATGATCTCAG 1755
Qy      1801 AAGCAATTTTGTGAAGACAGAACACTGGAATATTACAGATGAGATTCGATTCATGAA 1860
Db      1756 AAGCAATTTTGTGAAGACAGAACACTGGAATATTACAGATGAGATTCGATTCATGAA 1815
Qy      1861 GAAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTAGTTGTAAAGAA 1920
Db      1816 GAAAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTCTTAGTTGTAAAGAA 1875
Qy      1921 GAAAAAGCAGATGATGAATAATAGTAGTTGCCGGAAGAAATGCCATGCTAAGACTG 1980
Db      1876 GAAAAAGCAGATGATGAATAATAGTAGTTGCCGGAAGAAATGCCATGCTAAGACTG 1935
Qy      1981 GAGCTAGACACATGAAAAATCATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
Db      1936 GAGCTAGACACATGAAAAATCATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 1995
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OM nucleic - nucleic search, using sw model

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Title: US-09-924-400-303

Perfect score: 2040

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Searched: 9793542 seqs, 413468905 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2040	100.0	2040	US-09-780-669-375	Sequence 375, App
4	2040	100.0	2040	US-09-810-936-303	Sequence 303, App
5	2040	100.0	2040	US-09-822-827-375	Sequence 375, App
6	2040	100.0	2040	US-09-429-755-303	Sequence 303, App
7	2040	100.0	2040	US-09-924-400-303	Sequence 303, App
8	2040	100.0	2040	US-09-895-793-375	Sequence 375, App
9	2040	100.0	2040	US-09-895-814-375	Sequence 375, App
10	2040	100.0	2040	US-10-012-896-375	Sequence 375, App
11	2040	100.0	2040	US-10-010-940-375	Sequence 375, App
12	2040	100.0	2040	US-10-212-679-303	Sequence 303, App
13	2040	100.0	2040	US-10-144-678A-375	Sequence 375, App
14	2040	100.0	2040	US-10-033-527-7	Sequence 7, App11
15	2040	100.0	2040	US-10-294-025-375	Sequence 375, App
16	2040	100.0	2040	US-10-079-137B-303	Sequence 303, App
17	1940	95.1	2000	US-09-825-301-6	Sequence 6, App11
18	1940	95.1	2000	US-09-759-143-374	Sequence 374, App
19	1940	95.1	2000	US-09-780-669-374	Sequence 374, App
20	1940	95.1	2000	US-09-810-936-302	Sequence 302, App
21	1940	95.1	2000	US-09-822-827-374	Sequence 374, App
22	1940	95.1	2000	US-09-429-755-302	Sequence 302, App
23	1940	95.1	2000	US-09-924-400-302	Sequence 302, App

24	1940	95.1	2000	3	US-09-895-793-374	Sequence 374, App
25	1940	95.1	2000	3	US-09-895-814-374	Sequence 374, App
26	1940	95.1	2000	5	US-10-012-896-374	Sequence 374, App
27	1940	95.1	2000	5	US-10-010-940-374	Sequence 374, App
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36	1147.6	56.3	1853	3	US-09-810-936-295	Sequence 295, App
37	1147.6	56.3	1853	3	US-09-822-827-369	Sequence 369, App
38	1147.6	56.3	1853	3	US-09-429-755-295	Sequence 295, App
39	1147.6	56.3	1853	3	US-09-924-400-295	Sequence 295, App
40	1147.6	56.3	1853	3	US-09-895-793-369	Sequence 369, App
41	1147.6	56.3	1853	3	US-09-895-814-369	Sequence 369, App
42	1147.6	56.3	1853	5	US-10-012-896-369	Sequence 369, App
43	1147.6	56.3	1853	5	US-10-010-940-369	Sequence 369, App
44	1147.6	56.3	1853	6	US-10-212-679-295	Sequence 295, App
45	1147.6	56.3	1853	6	US-10-144-678A-369	Sequence 369, App

ALIGNMENTS

RESULT 1
US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US20020009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesch, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fering, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FaSTSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-7

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best local similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGGTTGATTCAGGCGGCTCTTCTGTGAAGAGCAATTGGTCTC 60
1 ATGGTGTGAGGTTGATTCAGGCGGCTCTTCTGTGAAGAGCAATTGGTCTC 60
Db 1 ATGGTGTGAGGTTGATTCAGGCGGCTCTTCTGTGAAGAGCAATTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAGGAGCGGCAAG 120
61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAGGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACGACGACTGTGTAAGACACTTCAGAGCAAG 180
121 AGCAACGTGGGCACTTCTGAGACGACGACTGTGTAAGACACTTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACGACGACTGTGTAAGACACTTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAAGTGTG 240
181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAAGTGTG 240
Db 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAAGTGTG 240
QY 241 GGGCGTTTGGAGACACAGACGACTGTGTAAGAGCACTGAGAAAGATGGGCAAG 300
241 GGGCGTTTGGAGACACAGACGACTGTGTAAGAGCACTGAGAAAGATGGGCAAG 300

Db 241 GGCGCTTCTGAGACCAAGCACTCTGCTATGAAGACATCAAGAAACAGATGGGCAAG 300
Qy 301 TGGTGTGCGCACTGCTTCCCTGCTGTCAGAGGGAGAGCGCAAGGATGGGCGCTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGTCAGAGGGAGAGCGCAAGGATGGGCGCTTGG 360
Qy 361 GGAGACTAGAGTACAGTGCCTTCATGAGGCCAGGTACACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTAGAGTACAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
Qy 421 GACAACTCCCAAGAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 480
Db 421 GACAACTCCCAAGAGTGCCTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 480
Qy 481 CTCAAGGACACTGACGTGACCAAGAAAGCAAGCAAAAGAGAGAGTCTTCAATCTGACC 540
Db 481 CTCAAGGACACTGACGTGACCAAGAAAGCAAGCAAAAGAGAGAGTCTTCAATCTGACC 540
Qy 541 TGTGCGCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGAGATGCACTTAA 600
Db 541 TGTGCGCAATGGGAATTCAGAAATGTAATACTCTGCTGAGACAGAGATGCACTTAA 600
Qy 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGGCGGTACATGCCAGAAATGAA 660
Db 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGGCGGTACATGCCAGAAATGAA 660
Qy 661 TGTGCGCAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGCAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTAATAAGAAATTAATTAAGCCCAAGCACTGCTTAA 780
Db 721 ACCACTCTGCACTACGCTATCTAATAAGAAATTAATTAAGCCCAAGCACTGCTTAA 780
Qy 781 TATGCTGCTGATATGCAATCAAAACCAAGCATGGCTCAACACTGTTACTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAACCAAGCATGGCTCAACACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATCAAGAAACCAAGATTTAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTCTGGAATTTTATCAAGAAACCAAGATTTAATGA 900
Qy 901 CTGATATGATGAAAGAGCTGCTCATATCTGCTGATATGTTGATGAGCAAGTAA 960
Db 901 CTGATATGATGAAAGAGCTGCTCATATCTGCTGATATGTTGATGAGCAAGTAA 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGCAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCGAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCGAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAATACTCTTCTGAAAACAGCAATCCAGAACAGCTTAA 1140
Db 1081 AAAAGAAAAACAGATGCTAAATACTCTTCTGAAAACAGCAATCCAGAACAGCTTAA 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGCAAGTAAATGCCAGCAGAGAA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATAGATGGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATAGATGGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGATGATTAATTAAGAAACCTGACTATGCTGCTGAC 1320
Db 1261 AAGCATGAAAGTAAATATGATGATTAATTAAGAAACCTGACTATGCTGCTGAC 1320
Qy 1321 AATGCTGATTAATGATTAATCTTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380

Qy 1381 CTTGACCAAGAAAGTGAAGAGTATCAGAAATTTTGGAAATTTGTTGACTACAAAGAA 1440
Db 1381 CTTGACCAAGAAAGTGAAGAGTATCAGAAATTTTGGAAATTTGTTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAAGCTTAAAGTGA 1500
Db 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAAAGCTTAAAGTGA 1500
Qy 1501 TCAGAGAAAGTCAAAAGGCTTGAAGGCAAGTGAATAATGGCAGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGTCAAAAGGCTTGAAGGCAAGTGAATAATGGCAGCCAGAGAAAGATCT 1560
Qy 1561 CAAGAACCAAGAAATTAATAGATGATGATGAGAGCTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATAGATGATGATGAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAAACAGCAAGTATCTGATGCGAATTCAGAAACCTGACTAATGATGCC 1680
Db 1621 GAAATGAAGAAACAGCAAGTATCTGATGCGAATTCAGAAACCTGACTAATGATGCC 1680
Qy 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGCAACACTGAAAGC 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTTCTCCAGAGAGAGCAACACTGAAAGC 1740
Qy 1741 CAGCAATTTCTGCACTGAGATGAAAGTATCAAGTGAACGAAACAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGCACTGAGATGAAAGTATCAAGTGAACGAAACAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAACAGAACATGGAATATTAACAGATGATGATGATGATGA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACATGGAATATTAACAGATGATGATGATGATGA 1860
Qy 1861 GAAAGCAAGATGAAAGTGTGAAAAATGAATTTGAGCTTCTCTTAAGTGAAGAA 1920
Db 1861 GAAAGCAAGATGAAAGTGTGAAAAATGAATTTGAGCTTCTCTTAAGTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTGCATGAAAAATGTAAGTGGCGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGCATGAAAAATGTAAGTGGCGGAGAAATTTGCCATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAACATCAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTAGACACATGAACATCAGAGCCAGCTTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 2
US-09-759-143-375
Sequence 375, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTGTTGAGGTGATTCATGCGGCTCTTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGGTGTGAGGTGATTCATGCGGCTCTTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AAGAGCAAGTGGGCAAGTGTGCTCCGTTGCTCCCTGTGACAGGACGGCAAG 120
DB 61 AAGAGCAAGTGGGCAAGTGTGCTCCGTTGCTCCCTGTGACAGGACGGCAAG 120
QY 121 AAGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAAGCACTCAGAGCAAG 180
DB 121 AAGCAAGTGGGCACTTCTGAGACCAAGCACTCTGTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGTGACAGGAGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGTGACAGGAGGAGTGGCAAGCACTG 240
QY 241 GCGGCTTCTGAGACCAAGCACTCTGTATGAAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCACTCTGTATGAAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGTGACAGGAGGAGTGGCAAGTGGTGG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGTGACAGGAGGAGTGGCAAGTGGTGG 360
QY 361 GGAAGCTAGATGACAGTGCCTTCATGAGCCCAAGTACCACTCCGTGGAAGATCTG 420
DB 361 GGAAGCTAGATGACAGTGCCTTCATGAGCCCAAGTACCACTCCGTGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGAGCACTGACCTGGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGAGCACTGACCTGGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGACAGAGATGTCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGACAGAGATGTCACTTAAT 600
QY 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGACAGAGATGTCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGTAATACTCTGCTGACAGAGATGTCACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGCAAGCTCTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660
DB 601 GTCTTGAACAACAAAGAGAGCAAGCTCTGATTAAGGCGGTACAAATGCCAGGAAGATGA 660
QY 661 TGTGCGTATGTTGTGTAACAAGCACTGATCCAAATATTCAGATGATGTAAGAAAT 720
DB 661 TGTGCGTATGTTGTGTAACAAGCACTGATCCAAATATTCAGATGATGTAAGAAAT 720
QY 721 ACCACTCTGCACTACCTCTATCTAATATGAAGATTAATGAGCCAAAGCACTGCTTAA 780
DB 721 ACCACTCTGCACTACCTCTATCTAATATGAAGATTAATGAGCCAAAGCACTGCTTAA 780
QY 781 TATGAGTGTGATTCGAATCAAAACAAAGATGGCTCAACACACTGTTACTTGGTGA 840
DB 781 TATGAGTGTGATTCGAATCAAAACAAAGATGGCTCAACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAACGAAATTTAAATGCA 900
QY 901 CTGAGTAGATATGGAAGAGCTGCTCATATCTTGTATGTTGTGATCAGCAAGTATA 960

DB 901 CTGAGTAGATATGGAAGAGCTGCTCATATCTTGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTCAAGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
DB 961 GTCAAGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTGATCATCATATGTAATTTGCCAGTACTTCTGATC 1080
DB 1021 GCCAGAGATATGCTGTTTCTGATCATCATATGTAATTTGCCAGTACTTCTGATC 1080
QY 1081 AAAAGAAAAACAGATGTAAATAATCTCTGAAAAACAGATCCAGAAACAAGCTTAAG 1140
DB 1081 AAAAGAAAAACAGATGTAAATAATCTCTGAAAAACAGATCCAGAAACAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAAAGAGTCACAAAGGTTCAAAAGGAGTAAATAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAAAGAGTCACAAAGGTTCAAAAGGAGTAAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAAACAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAAACAGAAATTAATAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGAGGATTAATGAGAAACCTGAACTAATGTTGCACTGCTGC 1320
DB 1261 AAGCATGAAGATTAATGAGGATTAATGAGAAACCTGAACTAATGTTGCACTGCTGC 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAAAGAGAGAGCAACCTGAAATACGAATTT 1380
DB 1321 AATGTGATTAATGATTAATTCCTCAAAAGAGAGAGCAACCTGAAATACGAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGATATCACAAATTTTGGAAATGTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAACGAAAGTGAAGATATCACAAATTTTGGAAATGTTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAATATCTCTGAAAAACAGAAACCCAGAAACAAGCTTAAGAGTGA 1500
DB 1441 AAAAGATGCCAAATATCTCTGAAAAACAGAAACCCAGAAACAAGCTTAAGAGTGA 1500
QY 1501 TCAGAGGAAGAGTCACAAAGGCTTGAAGGCACTGAAATGAGCCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTCACAAAGGCTTGAAGGCACTGAAATGAGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGCTAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGCTAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAACCAAGAGATCTCATGTGGAATCCCAAGAAACCTGACTAATGGTGC 1680
DB 1621 GAAATGAAGAACCAAGAGATCTCATGTGGAATCCCAAGAAACCTGACTAATGGTGC 1680
QY 1681 ACTGTGCAATGTGATGATGATTAATCTCTCCAAAGAGAGCAGAAACCTGAAAGC 1740
DB 1681 ACTGTGCAATGTGATGATGATTAATCTCTCCAAAGAGAGCAGAAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTGAAGAAACAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGAGTATCACAGTGAAGAAACAATGATACTCAG 1800
QY 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTAATACAGATGAGATTTGATTCATGAA 1860
DB 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTAATACAGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAGAGATGAGATGATGATGATTAATGATTTCTGAGCTTCTTATGTTGTAAGAA 1920
DB 1861 GAAAGAGATGAGATGATGATGATTAATGATTTCTGAGCTTCTTATGTTGTAAGAA 1920
QY 1921 GAAAAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 GAAAAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 GAGCTAGACAAATGAAACATAGAGCCAGCTTAAGAAAAAAGAAAAAAGAAAAA 2040

Db 1981 GAGCTAGACATGAAACATCAGACGACGCTAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 3
US-09-780-669-375
Sequence 375, Application US/09780669
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTATTCATGCGCGGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTTATTCATGCGCGGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60

QY 61 AGGAGCAAGTGGGCAAGTGGTGTGCTGCGGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGTGGGCAAGTGGTGTGCTGCGGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120

QY 121 AGCAAGTGGGCACTTCTGAGACACGACGACGACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACGACGACGACTCTGTATGAAGACACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240

QY 241 GGGGCTTGGAGACACGACGACGACTGCTATGAAGACACTCAGAGCAAGGAGTGGCAAG 300
DB 241 GGGGCTTGGAGACACGACGACGACTGCTATGAAGACACTCAGAGCAAGGAGTGGCAAG 300

QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGAGTGGCGCTTGG 360
DB 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGAGTGGCGCTTGG 360

QY 361 GGAAGCTAGATGACAGTGGCTTCTCATGAGGCCAGGTACCAAGTCCGTGGAAGAGTCTG 420
DB 361 GGAAGCTAGATGACAGTGGCTTCTCATGAGGCCAGGTACCAAGTCCGTGGAAGAGTCTG 420

QY 421 GACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAAAGATCTACGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAAAGATCTACGTCATG 480

QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540

QY 541 TGTGCAATGGGAATTCCGAAGTAAACCTCCGCTGGAAGAGAGATGTCATCTTAAT 600
DB 541 TGTGCAATGGGAATTCCGAAGTAAACCTCCGCTGGAAGAGAGATGTCATCTTAAT 600

QY 601 GTCTTGAACAACAAG 660
DB 601 GTCTTGAACAACAAG 660

QY 661 TGTGCGTTAATGTTGCTGGAAATGAGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAAATGAGCACTGATCCAAATATTCAGATGATGGAAT 720

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DB 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGCGCAAGACCTGCTTGA 780

QY 781 TATGGTGTGATATGATGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TATGGTGTGATATGATGATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

QY 841 CATGAGCAAAAG 900
DB 841 CATGAGCAAAAG 900

QY 901 CTGATATGATATGAG 960
DB 901 CTGATATGATATGAG 960

QY 961 GTGACGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGACGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGCGAGTTACTTCTGATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATATTTGCGAGTTACTTCTGATAC 1080

QY 1081 AAAAGAAAAAGATCTAAATCTCTTCTGAAAAAGAGATCCAGAAACAAGCTTAAAG 1140
DB 1081 AAAAGAAAAAGATCTAAATCTCTTCTGAAAAAGAGATCCAGAAACAAGCTTAAAG 1140

QY 1141 CTGACATCAG 1200
DB 1141 CTGACATCAG 1200

QY 1201 ATGTCTCAAGAACAGAAATTAAGATGATGATGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAAGATGATGATGAGAGAGAGAGAGAGAGAGAGAG 1260

QY 1261 AAGCATGAAGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 AAGCATGAAGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320

QY 1321 AATGATGATTAATGATTAATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGATGATTAATGATTAATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

QY 1381 CCTGCAACGAAAGTGAAGAGATATCAGAAATTTGCAATTAATGATTTGATCTTCAAGAG 1440
DB 1381 CCTGCAACGAAAGTGAAGAGATATCAGAAATTTGCAATTAATGATTTGATCTTCAAGAG 1440

QY 1441 AAACAGATGCCAAATATCTTTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAACAGATGCCAAATATCTTTCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1500

QY 1501 TCAGAGAGAGAGATCAAAAGGCTTGAAGGCAAGTGAATGGCAGCAGAGAGAGAGATCT 1560

Db 1501 TCAGAGGAGAGATGCAAAAGGCTTGAAGGCAAGTGAATTCGCGACGACGAGAAATCT 1560
Qy 1561 CAAGAACCAAGAAATTAATAGATGATAGAGAGCTAGAAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATAGATGATAGAGAGCTAGAAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAAGAGACGGAAGTACTCATGTCGAAATTCGCGAAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAAGAGACGGAAGTACTCATGTCGAAATTCGCGAAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGACCACTGAAAG 1740
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGACCACTGAAAG 1740
Qy 1741 CAGCAATTTCTGCACTGAGAAATGAGATCACAGTACGAGCAAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGCACTGAGAAATGAGATCACAGTACGAGCAAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAGAAAGAGACACTGGAATTTACAGATGAGATTCGATTCAGAA 1860
Db 1801 AAGCAATTTTGTGAGAAAGAGACACTGGAATTTACAGATGAGATTCGATTCAGAA 1860
Qy 1861 GAAAAGCAGATAGAGTGGTGAATAATGAAATTCAGCTTCTCTTATGTTGTAAGAA 1920
Db 1861 GAAAAGCAGATAGAGTGGTGAATAATGAAATTCAGCTTCTCTTATGTTGTAAGAA 1920
Qy 1921 GAAAAAGACATCTTGATGAGAAATAGTACGTTGCGGAGAAATTCAGTCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGAGAAATAGTACGTTGCGGAGAAATTCAGTCTAAGACTG 1980
Qy 1981 GAGCTGAGACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTGAGACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 4
US-09-810-936-303
Sequence 303, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda B.
APPLICANT: Dillon, Davin C.
APPLICANT: Rector, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF INHERITED AND ACQUIRED FORMS OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-303

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAGCAATTTGCTTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAGAGCAATTTGCTTC 60
Qy 61 AGAGAGAAATGAGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120

Db 61 AGAGAGAAATGAGGCAAGTGGTCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGAGCAAGAGCACTGCTATGAGAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGCAAGAGCACTGCTATGAGAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAATGATGCTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCACTG 240
Db 181 ATGGGCAATGATGCTGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCACTG 240
Qy 241 GGGGCTTCTGAGAGCAAGAGCACTGCTATGAGAGCACTCAGAGCAAGATGGCAAG 300
Db 241 GGGGCTTCTGAGAGCAAGAGCACTGCTATGAGAGCACTCAGAGCAAGATGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Qy 361 GAGAGTACAGATGACAGTGTCTTCAATGAGAGCCAGGTACCACTGCTGAGAGATCTG 420
Db 361 GAGAGTACAGATGACAGTGTCTTCAATGAGAGCCAGGTACCACTGCTGAGAGATCTG 420
Qy 421 GACAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCGAGAAAGGATCTCATGCTATG 480
Db 421 GACAGCTCCAGAGAGCTGCTGAGGAGTAAAGTCCCGAGAAAGGATCTCATGCTATG 480
Qy 481 CTGAGGACATGACGTGAAAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTGAGGACATGACGTGAAAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TCTGCAATGGAATTTCAAGATGATTAATCTCTGCTGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TCTGCAATGGAATTTCAAGATGATTAATCTCTGCTGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 GTGCTTGAACAACAAAG 660
Db 601 GTGCTTGAACAACAAAG 660
Qy 661 TGTGCTTAATGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 TGTGCTTAATGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 721 ACCACTGCTGACATGCTATCTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 ACCACTGCTGACATGCTATCTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 TATGCTGCTGATGAG 840
Db 781 TATGCTGCTGATGAG 840
Qy 841 CATGAGCAAAAG 900
Db 841 CATGAGCAAAAG 900
Qy 901 CTGATGATGATGAG 960
Db 901 CTGATGATGATGAG 960
Qy 961 GTGAGCTTCTGAG 1020
Db 961 GTGAGCTTCTGAG 1020
Qy 1021 GCCAGAGATGATGCTGTTCTGATCATCATGATCATGATGATGATGATGATGATGAT 1080
Db 1021 GCCAGAGATGATGCTGTTCTGATCATCATGATCATGATGATGATGATGATGATGAT 1080
Qy 1081 AAAAG 1140
Db 1081 AAAAG 1140
Qy 1141 CTGACATGAG 1200


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Db      1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAAGGATGAAATATGACCGACGAGAGAAA 1200
Qy      1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGGTGTAAGAGAAATGAAG 1260
Db      1201 ATGTCTCAAGAACCAAGAAATTAATAGATGTGATAGAGAGGTGTAAGAGAAATGAAG 1260
Qy      1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACTATATGTGTCTGCTGCGC 1320
Db      1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACCTGACTATATGTGTCTGCTGCGC 1320
Qy      1321 AATGTGATATATGATTAATTTCTTCAAGAGAGAGCAACACCTGATAATGCAATTT 1380
Db      1321 AATGTGATATATGATTAATTTCTTCAAGAGAGAGCAACACCTGATAATGCAATTT 1380
Qy      1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAAATTTGTTCTGATCAAGAA 1440
Db      1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAAATTTGTTCTGATCAAGAA 1440
Qy      1441 AAACAGATGCAAAATATCTTCTGAAAACAGCAACCCAGAACCAAGCTTAAAGCTGAC 1500
Db      1441 AAACAGATGCAAAATATCTTCTGAAAACAGCAACCCAGAACCAAGCTTAAAGCTGAC 1500
Qy      1501 TCAGAGAAAGATCAAAAGGCTTGAAGGAGTGAATATGCGCAAGCAAGAAAGATTT 1560
Db      1501 TCAGAGAAAGATCAAAAGGCTTGAAGGAGTGAATATGCGCAAGCAAGAAAGATTT 1560
Qy      1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGATGAAATTTTATGCTATCGAA 1620
Db      1561 CAAGAACCAAGAAATTAATAGATGTGATAGAGATGAAATTTTATGCTATCGAA 1620
Qy      1621 GAAATGAAAGAGCAAGAAATTAATAGATGTGATAGAGATGAAATTTTATGCTATCGAA 1680
Db      1621 GAAATGAAAGAGCAAGAAATTAATAGATGTGATAGAGATGAAATTTTATGCTATCGAA 1680
Qy      1681 ACTGCTGCAATGTGTATGATGATTAATTTCTTCAAGAGAGCAAGCAAGCTTGAAGC 1740
Db      1681 ACTGCTGCAATGTGTATGATGATTAATTTCTTCAAGAGAGCAAGCAAGCTTGAAGC 1740
Qy      1741 CAGCAATTTCTGCACTGAGATGAAAGTATCAAGTGAAGCAAAATGATATCTGAG 1800
Db      1741 CAGCAATTTCTGCACTGAGATGAAAGTATCAAGTGAAGCAAAATGATATCTGAG 1800
Qy      1801 AAGCAATTTTGTGAAGAGCAAGCACTGATATTAACAGATGATGATTTCTGATTCATGA 1860
Db      1801 AAGCAATTTTGTGAAGAGCAAGCACTGATATTAACAGATGATGATTTCTGATTCATGA 1860
Qy      1861 GAAAGCAATGATAGATGTGTTGAAAAATGAATTTCTGAGCTTTCTTATGTTGTAAGAA 1920
Db      1861 GAAAGCAATGATAGATGTGTTGAAAAATGAATTTCTGAGCTTTCTTATGTTGTAAGAA 1920
Qy      1921 GAAAAAGACATCTTGATGAAAAATGATGAGTTGCGGGAAGAAATTCATGCTAAGACG 1980
Db      1921 GAAAAAGACATCTTGATGAAAAATGATGAGTTGCGGGAAGAAATTCATGCTAAGACG 1980
Qy      1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
Db      1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

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; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGTGTTGAGATGATTCATGCGGCTGCTTCTGTGTAAGAACGATTTGGTCTC 60
Db      1 ATGTGTTGAGATGATTCATGCGGCTGCTTCTGTGTAAGAACGATTTGGTCTC 60
Qy      61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTTCCCTGCTGCAAGGAGCGGCAAG 120
Qy      121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Db      121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAG 180
Qy      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
Db      181 ATGGGCAAGTGTGCTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCACTG 240
Qy      241 GGGGCTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
Db      241 GGGGCTTCTGAGACCAAGCAAGCACTGCTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
Qy      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Db      301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
Qy      361 GGAAGCTACGATGACAGTGTCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
Db      361 GGAAGCTACGATGACAGTGTCTTCAATGAGAGCCAGATACAGTCCGTGGAAGATCTG 420
Qy      421 GACAAAGCTCACAAGAGCTGCGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCGATG 480
Db      421 GACAAAGCTCACAAGAGCTGCGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCGATG 480
Qy      481 CTCAAGGGAACCTGACGTGAACAAGAGGCAAGCAAGAAAGAGCTCTTACATCTGCGC 540
Db      481 CTCAAGGGAACCTGACGTGAACAAGAGGCAAGCAAGAAAGAGCTCTTACATCTGCGC 540
Qy      541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGGAAGAGATGTCACTTAAT 600
Db      541 TCTGCAATGGGAATTCAGAAATGATTAATCTCTGCTGGAAGAGATGTCACTTAAT 600
Qy      601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTACAAATGCGCAGAGATGA 660
Db      601 GTCTTGAACAACAAAGAGAGCAGCTCTGATTAAGGCGGTACAAATGCGCAGAGATGA 660
Qy      661 TGTGCTTAATGTGCTGGAACATGCACTGATTAAGGCGGTACAAATGCGCAGAGATGA 720
Db      661 TGTGCTTAATGTGCTGGAACATGCACTGATTAAGGCGGTACAAATGCGCAGAGATGA 720
Qy      721 ACCACTCTGCACTAGCTATCTATATGAAATTAATTAAGGCCAAGACCTGCTCTTA 780
Db      721 ACCACTCTGCACTAGCTATCTATATGAAATTAATTAAGGCCAAGACCTGCTCTTA 780
Qy      781 TATGTGCTGATATGAAATCAAAAAACAAGATGAGCTTCAAGCACTGTTACTGGTGA 840
Db      781 TATGTGCTGATATGAAATCAAAAAACAAGATGAGCTTCAAGCACTGTTACTGGTGA 840
Qy      841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAATGA 900
Db      841 CATGAGCAAAAAACAGAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAATGA 900
Qy      901 CTGATATGATGAAAGATGCTCTCATCTTCTGATGTTGTTGATCAGCAAGTATA 960
Db      901 CTGATATGATGAAAGATGCTCTCATCTTCTGATGTTGTTGATCAGCAAGTATA 960

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RESULT 5
US-09-822-827-375
; Sequence 375, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: us/09/822.827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375

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QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCTCAAGATCTATCGAGACAG 1020
DB 961 GTTACGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCGAGACAG 1020
QY 1021 GCCAGAGATGCTGTTCTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATGCTGTTCTTCTAGTCAATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAG 1140
DB 1081 AAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAAGTTCAAGGAGTGAATAAGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAAATAAAGATGATGATAGAGAGTTGAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAAATAAAGATGATGATAGAGAGTTGAGAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 CCTGACAAAGAAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAAAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGTGAAGAAATGAGGAGGAGGAGGAGGAGGAG 1560
DB 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGTGAAGAAATGAGGAGGAGGAGGAGGAGGAG 1560
QY 1561 CAGAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 CAGAGAACAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GAAATGAGAGAGAGTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 GAAATGAGAGAGAGTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ACTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 ACTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 CAGCAATTTCTGACACTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 CAGCAATTTCTGACACTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGATGATGATGATGATGATGAT 1860
DB 1801 AAGCAATTTTGTGAAGACAGAACTGGAATATTAACAGATGATGATGATGATGATGATGAT 1860
QY 1861 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
DB 1861 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1921 GAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 1921 GAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 GAGCTGAGACAAATGAAATCATGAGCCAGCTTAAATGATGATGATGATGATGATGATGAT 2040
DB 1981 GAGCTGAGACAAATGAAATCATGAGCCAGCTTAAATGATGATGATGATGATGATGATGAT 2040

RESULT 6
US-09-429-755-303
Sequence 303, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-303
Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAT 60
DB 1 ATGAT 60
QY 61 AG 120
DB 61 AG 120
QY 121 AGCAAG 180
DB 121 AGCAAG 180
QY 181 ATGAG 240
DB 181 ATGAG 240
QY 241 GAG 300
DB 241 GAG 300
QY 301 TGTGCT 360
DB 301 TGTGCT 360
QY 361 GAG 420
DB 361 GAG 420
QY 421 GAG 480
DB 421 GAG 480
QY 481 CTGAG 540
DB 481 CTGAG 540
QY 541 TGTGCT 600
DB 541 TGTGCT 600
QY 601 GTCTTGAACAAAG 660
DB 601 GTCTTGAACAAAG 660
QY 661 TGTGCT 720

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Db 661 TGGCCCTTATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTGTGACCTAATCTTATTAAGATTAATTAATGAGCAAGACGCTCTTA 780
Db 721 ACCACTGTGACCTAATCTTATTAAGATTAATTAATGAGCAAGACGCTCTTA 780
Qy 781 TATGTGTGATATCGAATCAAAAAAAGCATGGCTCAGACACTGTTACTTGATGA 840
Db 781 TATGTGTGATATCGAATCAAAAAAAGCATGGCTCAGACACTGTTACTTGATGA 840
Qy 841 CATGACCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAATGA 900
Db 841 CATGACCAAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAATGA 900
Qy 901 CTGATAGATATGGAAGAGAGCTGCTCATATCTGCGTATGTTGATGATCAGAACTTA 960
Db 901 CTGATAGATATGGAAGAGAGCTGCTCATATCTGCGTATGTTGATGATCAGAACTTA 960
Qy 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAATAATCTCTCGAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTCGAAAACAGCAATCCAGAACAGCTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGATCACAAAAGTTCAAAAGCATGTAATATGAGCCAGAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGATCACAAAAGTTCAAAAGCATGTAATATGAGCCAGAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATGATGAGATTAATCAAGAAACCTGATATGCTGCTGCTGAC 1320
Db 1261 AAGCATGAAGATTAATGATGAGATTAATCAAGAAACCTGATATGCTGCTGCTGAC 1320
Qy 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT 1380
Db 1321 AATGTGATATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAATCAGCAATTT 1380
Qy 1381 CCTGACACGAAGAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAGAA 1440
Db 1381 CCTGACACGAAGAGATATCAAGAAATTTGCGAATTTAGTTCTGACTCAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAAAGCTTAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGATCACAAAAGCTTGAAGGAGAGTAATGGCCAGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGATCACAAAAGCTTGAAGGAGAGTAATGGCCAGCCAGAGAAAGATCT 1560
Qy 1561 CAGAAACAGAAATTAATTAAGATGATGATGAGAGCTAGAAAAATTTATGCTATCGAA 1620
Db 1561 CAGAAACAGAAATTAATTAAGATGATGATGAGAGCTAGAAAAATTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAGAGAGAGATCTCATATGCTGAGTTCCCGAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAGAGAGAGATCTCATATGCTGAGTTCCCGAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGCAATGATGATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAAG 1740
Db 1681 ACTGCTGCAATGATGATGATTAATCTCTCAAGAGAGAGAGCAACCTGAAAG 1740
Qy 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCAGATGACAGCAAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCAGATGACAGCAAAATGATCTCAG 1800
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Db 1741 CAGCAATTTCTGACATGAGAAATGAAGATATCAGATGACAGCAAAATGATATCTCAG 1800
Qy 1801 AAGCAATTTTGAAGAGACAGAACCTGGAATTAATACGATGATCTGATTAAGAA 1860
Db 1801 AAGCAATTTTGAAGAGACAGAACCTGGAATTAATTAACGATGATCTGATTAAGAA 1860
Qy 1861 GAAAAGCAGATGAAGTGTGAAAAAATGAATTCGAGCTTCTCTTAAGTTGAAGAA 1920
Db 1861 GAAAAGCAGATGAAGTGTGAAAAAATGAATTCGAGCTTCTCTTAAGTTGAAGAA 1920
Qy 1921 GAAAAAGCATCTTGCATGAATAATGATACCTTGCGGAGAAATTCCTGTAAGACTG 1980
Db 1921 GAAAAAGCATCTTGCATGAATAATGATACCTTGCGGAGAAATTCCTGTAAGACTG 1980
Qy 1981 GAGCTGACACATGAATGATGAGCCAGCTTAAGAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTGACACATGAATGATGAGCCAGCTTAAGAAAAAATGAAAAAATGAAAAA 2040
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RESULT 7

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US-09-924-400-303
; Sequence 303, Application US/09924400
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda B.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C12
; CURRENT APPLICATION NUMBER: US/09/924,400
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-924-400-303
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Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ATGGTGTGATGATGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
Db 1 ATGGTGTGATGATGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGCTTC 60
Qy 61 AAGAGCAAGATGGGCAAGTGTGCTGCGCTTCTCTCTGTCAGAGGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGGCAAGTGTGCTGCGCTTCTCTCTGTCAGAGGAGAGCGGCAAG 120
Qy 121 AAGCAAGTGGGCAAGTGTGCTGCGCTTCTCTCTGTCAGAGGAGAGCGGCAAG 180
Db 121 AAGCAAGTGGGCAAGTGTGCTGCGCTTCTCTCTGTCAGAGGAGAGCGGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGCTG 240
Qy 241 GCGGCTTCTGAGAGACAGACGATCTGCTATGAAGACACTAGAGAAAGATGGCAAG 300
Db 241 GCGGCTTCTGAGAGACAGACGATCTGCTATGAAGACACTAGAGAAAGATGGCAAG 300
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OY	301	IGGAGTCCACATGGCTTCCCTGCTGACAGGGGGAGCGCAAGCAAGATGGTGGCTTGG	360
Db	301	TGGTGTCTCCACTGCTTCCCTGCTGACAGGGGGAGCGCAAGCAAGATGGTGGCTTGG	360
OY	361	GGAGACTACGATGACATGCTCTTCATGAGAGCCAGGTACCACTGCTCTGAGAAAGATCTG	420
Db	361	GGAGACTACGATGACATGCTCTTCATGAGAGCCAGGTACCACTGCTCTGAGAAAGATCTG	420
OY	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGTCTATG	480
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATGTCTATG	480
OY	481	CTCAGGGGACATGAGGTGAACAAGAAAGACAAGCAAAAGAGACTGCTCTACATCTGGCC	540
Db	481	CTCAGGGGACATGAGGTGAACAAGAAAGACAAGCAAAAGAGACTGCTCTACATCTGGCC	540
OY	541	TCTGCGCAATGGGAATTCAGAAAGTAAACCTCCGCTGGAACAGACATGTCAACTTAT	600
Db	541	TCTGCGCAATGGGAATTCAGAAAGTAAACCTCCGCTGGAACAGACATGTCAACTTAT	600
OY	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGCCAGAAAGATGA	660
Db	601	GTCTCTTGACAAACAAAAGAGACAGCTCTGTATAAAGCCGTACAAATGCCAGAAAGATGA	660
OY	661	TGTGGTTAAAGTTGCTGGAAACATGGCACTATCCAAATTTCCAGATGATATGGAAT	720
Db	661	TGTGGTTAAAGTTGCTGGAAACATGGCACTATCCAAATTTCCAGATGATATGGAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATTAATAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATTAATAGATAAATTAATGGCCAAAGCACTGCTCTTA	780
OY	781	TATGTGTCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTATCTTGCTGTA	840
Db	781	TATGTGTCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTATCTTGCTGTA	840
OY	841	CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTCACTACTTGCTGATATGTTGGATTCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTCACTACTTGCTGATATGTTGGATTCAGCAAGTATA	960
OY	961	GTTCAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
Db	961	GTTCAGCCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTTACTTTCTGACTAC	1080
OY	1081	AAAAAAGAAACAGATGCTTAAATATCTCTCTGAAAACAGCAATCCAGAACAAAGCTTAAAG	1140
Db	1081	AAAAAAGAAACAGATGCTTAAATATCTCTCTGAAAACAGCAATCCAGAACAAAGCTTAAAG	1140
OY	1141	CTGACATCAGAGGAAGTCACAAAAGTTTCAAAGGCAAGTGAATAATAGCCACAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAGTCACAAAAGTTTCAAAGGCAAGTGAATAATAGCCACAGAGAAA	1200
OY	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGTATGAGAGTTGAAGAAATGAAG	1260
Db	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGTATGAGAGTTGAAGAAATGAAG	1260
OY	1261	AAGCATGAAATTAATATGTTGGGATTTACTAAGAAACCTGACTAATGGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAATTAATATGTTGGGATTTACTAAGAAACCTGACTAATGGTGTCACTGTGGC	1320
OY	1321	AATGGTGAATATGATTAATTTCTCAAGAGAGCAGAACACTGGAATAATCAAGCAATTT	1380
Db	1321	AATGGTGAATATGATTAATTTCTCAAGAGAGCAGAACACTGGAATAATCAAGCAATTT	1380
OY	1381	CCTGACAAAGAAATGGAAGATATCACAAATTTGCCAATTAATGTTTCTGACTACAAAGAA	1440

Db	1381	CTTGACACACAAAAGTGAAGGCTATCACAGAAATTTGGCAATTAGTTCTTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATAATCTCTTCTGAAAACAGCAACCCAGAACCAAGA CTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATAATCTCTTCTGAAAACAGCAACCCAGAACCAAGA CTAAGAGCTGACA	1500
Qy	1501	TCGAGGAAAGATCACAAAGGCTTGGGGGAGTGAAATGGCCAGCCAGAGAAAGATCT	1560
Db	1501	TCGAGGAAAGATCACAAAGGCTTGGGGGAGTGAAATGGCCAGCCAGAGAAAGATCT	1560
Qy	1561	CAAGAACACAGAAATAAATAAGATGCTGATAGAGAGCTAAGAAATTTTATGCTATCGAA	1620
Db	1561	CAAGAACACAGAAATAAATAAGATGCTGATAGAGAGCTAAGAAATTTTATGCTATCGAA	1620
Qy	1621	GAATGGAAGAAAGACGGGAAGTACCTCAGTGGAGATTCGCCAATAAACCTGACTAATGAGGCC	1680
Db	1621	GAATGGAAGAAAGACGGGAAGTACCTCAGTGGAGATTCGCCAATAAACCTGACTAATGAGGCC	1680
Qy	1681	ACTGCTGGCAATGGTGTGATGATTAATTCCTCCAAAGAAAGACAGAACACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTGATGATTAATTCCTCCAAAGAAAGACAGAACACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTCTGACACTGAGAATGGAAGATATACAGATGACCAACAAATGATATCTCAG	1800
Db	1741	CAGCAATTTCTCTGACACTGAGAATGGAAGATATACAGATGACCAACAAATGATATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAGAAACAGAACACTGGAATATTAACAGCATGAGATTCGTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAGAAACAGAACACTGGAATATTAACAGCATGAGATTCGTGATTCATGAA	1860
Qy	1861	GAAGAGAGATTAAGTGTGTGAAAAATGAATTCGAGCTTCTCTTAATGTGAAGAA	1920
Db	1861	GAAGAGAGATTAAGTGTGTGAAAAATGAATTCGAGCTTCTCTTAATGTGAAGAA	1920
Qy	1921	GAAGAAAGACATCTTGACATGAAAAATAGTACGTTCCGGGAAGAAATGGCATGCTAAGACTG	1980
Db	1921	GAAGAAAGACATCTTGACATGAAAAATAGTACGTTCCGGGAAGAAATGGCATGCTAAGACTG	1980
Qy	1981	GAGCTGACACATGGAACATCAGAGCCGCTTAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTGACACATGGAACATCAGAGCCGCTTAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 8
US-09-895-793-375
Sequence 375, Application US/99895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Ajun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghnon, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

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FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match      100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTGTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGAGTGTGAGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGCTGCTCTTCTGTGAAGAGCATTTGGTCTC 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGAGCTCTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGAGCTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGAGGCAAGTGTGCGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACG 240
DB 181 ATGAGGCAAGTGTGCGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGACG 240
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DB 241 GGGGCTTCTGAGAGACCAAGCAAGCTCTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGGCGGCAAGAGCATTTGGTCTG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGGCGGCAAGAGCATTTGGTCTG 360
QY 361 GGAAGATTAAGATGACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGTGAGAGATCTG 420
DB 361 GGAAGATTAAGATGACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGTGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGAGGAGTAAAGTCCCGGAGAAAGATCTCATCTGAGC 480
DB 421 GACAACTCCACAGAGCTGCTGTGAGGAGTAAAGTCCCGGAGAAAGATCTCATCTGAGC 480
QY 481 CTCAGGAGCACTGACGTGAACAAAGAGACAGCAAGCAAGAGAGCTGCTCATCTGAGC 540
DB 481 CTCAGGAGCACTGACGTGAACAAAGAGACAGCAAGCAAGAGAGCTGCTCATCTGAGC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGAGACAGAGATGCTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGCTGAGACAGAGATGCTCACTTAAT 600
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DB 601 GTCTTGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
QY 721 ACCACTCTGACATAGCTATCTATTAATGAAGATTAATTAAGCCCAAGAGAGAGAGAG 780
DB 721 ACCACTCTGACATAGCTATCTATTAATGAAGATTAATTAAGCCCAAGAGAGAGAGAG 780
QY 781 TATGAGTGTGATTAATGAGATCAAAAGATGAGCTACACACATGTTACTTGGTGA 840
DB 781 TATGAGTGTGATTAATGAGATCAAAAGATGAGCTACACACATGTTACTTGGTGA 840
QY 841 CATGACCAAAAGACAGAGAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGACCAAAAGACAGAGAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
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DB 841 CATGACCAAAAGACAGAGAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CTGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GTGAGCTTCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GTGAGCTTCTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GCGAGAGATATGCTGTTTCTAGATCATCATATGTAATTTGCGAGTACTTCTGATAC 1080
DB 1021 GCGAGAGATATGCTGTTTCTAGATCATCATATGTAATTTGCGAGTACTTCTGATAC 1080
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DB 1081 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
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DB 1141 CTGACATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 ATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 ATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 AAGCATGAAAGATTAATGATGAGATTTACTGAGAAAGCTGATTAATGATGATCTG 1320
DB 1261 AAGCATGAAAGATTAATGATGAGATTTACTGAGAAAGCTGATTAATGATGATCTG 1320
QY 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
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DB 1561 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 ACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 CAGCAATTTCTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 AAGCAATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 AAGCAATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1921 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
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QY 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
DB 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 9
US-09-814-375
; Sequence 375, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugui
; APPLICANT: Kaios, Michael D.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Horal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carleota
; APPLICANT: Roy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PaeSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-814-375

Query Match 100.0%; Score 2040; DB 3; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGCCATTGTTCTTC 60
DB 1 ATGCTGTTGAGGTTGATTCATGCGGCTGCTCTTCTGTGAAGCCATTGTTCTTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAAGGAGACGGCAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAAGGAGACGGCAG 120

QY 121 AGCAAGTGTGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGTGGCACTTCTGGAAGCAAGCACTCTGTATGAAGCACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGCTGCGCACTGCTTCCCTGTGTGCAAGGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCTGCGCACTGCTTCCCTGTGTGCAAGGGGAGTGGCAAGCAAGCTG 240

QY 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGGAGGCAAG 300
DB 241 GGGCTTCTGAGAGCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGGAGGCAAG 300

QY 301 TGTGTCTGCACTGCTTCCCTGTGTGCAAGGGGAGGCAAGGAGGAGGCTGCTTGG 360
DB 301 TGTGTCTGCACTGCTTCCCTGTGTGCAAGGGGAGGCAAGGAGGAGGCTGCTTGG 360

QY 361 GGAAGCTACATGACATGCTCTTATGAGCCCAAGTACACGCTCCGTGAGAAAGATCTG 420
DB 361 GGAAGCTACATGACATGCTCTTATGAGCCCAAGTACACGCTCCGTGAGAAAGATCTG 420

QY 421 GACAACTCCACAGACCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480
DB 421 GACAACTCCACAGACCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480

QY 481 CTCAGGAGCACTGACCTGAAAGCAAGAGCAAGCAAGAGAGCTGCTTCAATCTGGCC 540
DB 481 CTCAGGAGCACTGACCTGAAAGCAAGAGCAAGCAAGAGAGCTGCTTCAATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAAGATGATTAATCTCTGTGACAGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAAGATGATTAATCTCTGTGACAGAGATGCACTTAAT 600

QY 601 GTCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGCCGTACATGCGAGAAAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGCAGCTGTGATTAAGCCGTACATGCGAGAAAGATGAA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGAGAAAT 720

QY 721 ACCACTCTGCACTACCTCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTTGA 780
DB 721 ACCACTCTGCACTACCTCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTTGA 780

QY 781 TATGCTGTGATGATGAAATCAAAAACAAAGCATGGCTCAACCTGTTACTGTGATGA 840
DB 781 TATGCTGTGATGATGAAATCAAAAACAAAGCATGGCTCAACCTGTTACTGTGATGA 840

QY 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAGAAAACAGCAATTTAAATGCA 900
DB 841 CATGACAAAACAGCAAGTGTGAAATTTTAAATCAGAAAACAGCAATTTAAATGCA 900

QY 901 CTGATGATGATGAAAGAGCTGCTCATACTGCTGTATGTTGTGATCAGCAATGTA 960
DB 901 CTGATGATGATGAAAGAGCTGCTCATACTGCTGTATGTTGTGATCAGCAATGTA 960

QY 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB 961 GTGAGCTTCTAATTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020

QY 1021 GCCAGAGATAGCTGTTTCTAGTCATCATGATTAATTTGCACTTCTGCACTAC 1080
DB 1021 GCCAGAGATAGCTGTTTCTAGTCATCATGATTAATTTGCACTTCTGCACTAC 1080

QY 1081 AAAAGAAAACAGATGCTAAATCTCTTGTGAAAACAGCAATTCAGAAACAGCTTAAAG 1140
DB 1081 AAAAGAAAACAGATGCTAAATCTCTTGTGAAAACAGCAATTCAGAAACAGCTTAAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAAAAGCTTCAAGGAGTGAATTCAGAGCAAGGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAGCTTCAAGGAGTGAATTCAGAGCAAGGAAA 1200

QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATAGATGTGATGAGAGGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATGATGAGATTAATCTAGAAAACCTGACTAATGTGTCACTGCTGGC 1320
DB 1261 AAGCATGAAAGTAAATGATGAGATTAATCTAGAAAACCTGACTAATGTGTCACTGCTGGC 1320

QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAATGACCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACCTGAAAATGACCAATTT 1380

QY 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGATCAAAAGAA 1440
DB 1381 CCTGCAACGAAAGTGAAGATATCAAGAAATTTGCAATTTGTTCTGATCAAAAGAA 1440


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QY 1441 AACGATGCCAAATACTCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGCTGACA 1500
DB 1441 AACGATGCCAAATACTCTTCTGAAAAACAGAACCCAGAAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATCACAAGGCTTGAAGGCTGAGAAATGGCCAGCAGAGAAAAGATCT 1560
DB 1501 TCAGAGGAAGATCACAAGGCTTGAAGGCTGAGAAATGGCCAGCAGAGAAAAGATCT 1560
QY 1561 CAAGAACCGAATATAAGATGATAGAGAGCTGAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAACCGAATATAAGATGATAGAGAGCTGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGACACGGAAGTACTATGCGAATTTCCAGAAAACCTGACTATGCTGCC 1680
DB 1621 GAAATGAAGACACGGAAGTACTATGCGAATTTCCAGAAAACCTGACTATGCTGCC 1680
QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGACGAAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCCAGAGAGACGAAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAAGATTCACAGTGAAGAACAAATGATCTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAAGATTCACAGTGAAGAACAAATGATCTGAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTCATGA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACACTGGAATATTACAGATGAGATTTCTGATTCATGA 1860
QY 1861 GAAAAAGCATGAAAGTGGTGAATAAATGAATTTCTGAGCTTTCTTTAGTTGAAGAA 1920
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QY 1921 GAAAAAGCATGCTGCAATAAATAGTACGTTGCGGGAAGAAATGGCCATGCTAAGACTG 1980
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QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
DB 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTT 2040
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RESULT 10
US-10-012-896-375
; Sequence 375, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepley, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Manteana, Yoshinori
; APPLICANT: Mescher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
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; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-375

Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGAGTGAATTCATAGCGGCTGCTCTTCGTGAAGAAGCATTTGCTTC 60
DB 1 ATGGTGTGAGAGTGAATTCATAGCGGCTGCTCTTCGTGAAGAAGCATTTGCTTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGAGAGCGGCAAG 120
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DB 361 GGAAGCTAGATGAGAGGCTTCAATGAGCCCAAGTACAGTCCGTGGAAGAATCTG 420
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DB 421 GACAAGCTCCACAGAGCTGCTGCTGAGGTAAGTCCCAAGAAAGATCTCATGCTGATG 480
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DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAAAGAGGACTCTTACATCTGGCC 540
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DB 541 TCTGCCATTTGGGAATTTCAAGATTAATTAATCTCTGCTGGAAGAGATGTCATTAAT 600
QY 601 GTCTTTGACCAACAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCCAGAGATGA 660
DB 601 GTCTTTGACCAACAAAGAGAGCAGCTCTGATTAAGGCGGTACATGCCAGAGATGA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATTCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGCACTGATTCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTATATGAAGTAATTAATGGCCAAAGACATGCTCTTA 780
DB 721 ACCACTCTGCACTAGCTATCTATATGAAGTAATTAATGGCCAAAGACATGCTCTTA 780
QY 781 TATGCTGCTGATATGAATCAAAAAAGAGATGAGCTCAGCAGCTGTTACTTGGTGA 840
DB 781 TATGCTGCTGATATGAATCAAAAAAGAGATGAGCTCAGCAGCTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
DB 841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
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QY 901 CTGATAGATATGAAAGGAGCTGCTCATATCTGCTGATGTTGTGGATCAGCAAGTATTA 960
DB 901 CTGATAGATATGAAAGGAGCTGCTCATATCTGCTGATGTTGTGGATCAGCAAGTATTA 960
QY 961 GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGACG 1020
DB 961 GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGACG 1020
QY 1021 GCCAGAGATGCTGCTGTTCTAGCTCATCATGATGATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATGCTGCTGTTCTAGCTCATCATGATGATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAGAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAG 1140
DB 1081 AAGAGAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCTCAAGCAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAAAGGTTCAAGGAGTGAATAATAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGATCACAAAAGGTTCAAGGAGTGAATAATAGCCAGCAGAGAAA 1200
QY 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAGAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGAGGATTAATGAGAAACCTGACTAATGCTGCTGCG 1320
DB 1261 AAGCATGAAAGTAAATATGAGGATTAATGAGAAACCTGACTAATGCTGCTGCG 1320
QY 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
DB 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGAGATGATCAAGAAATTTGCAATTAATTTCTGACTAAGAA 1440
DB 1381 CCTGACAAAGAGAGATGATCAAGAAATTTGCAATTAATTTCTGACTAAGAA 1440
QY 1441 AAAAGATGCTCAAAATCTCTTCTGAAAACAGCAACCCAGCAAGCTTAAAGCTGACA 1500
DB 1441 AAAAGATGCTCAAAATCTCTTCTGAAAACAGCAACCCAGCAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGATCAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAGATCAAAAGGCTTGAAGGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATGAGTGTGATGAGAGCTGAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATGAGTGTGATGAGAGCTGAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAAGACCGAAGTACTCATGTCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAAAGACCGAAGTACTCATGTCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGAATGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGCTGGAATGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAAGTATCAAGTACGAAACCAATGATATCTGAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAAGTATCAAGTACGAAACCAATGATATCTGAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATTTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAGACAGATGAGATGTTGAAAAATGAAATTTCTGAGCTTCTCTTGTGTAGAAA 1920
DB 1861 GAAAGACAGATGAGATGTTGAAAAATGAAATTTCTGAGCTTCTCTTGTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGTGATGAAAAATGATGCGTTGCGGAGAAATTCATGCTTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGTGATGAAAAATGATGCGTTGCGGAGAAATTCATGCTTAAGACTG 1980

QY 1981 GAGCTAGACACATGAAATGATGAGCAGCTTAAATGAAAAATGAAAAATGAAAAATG 2040
DB 1981 GAGCTAGACACATGAAATGATGAGCAGCTTAAATGAAAAATGAAAAATGAAAAATG 2040

RESULT 11
US-10-010-940-375
; Sequence 375, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-375

Query Match 100.0%; Score 2040; DB 5; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTTGATTCATATGCGGCTGCTTCTGTGAAGCAAGCATTGTGCTC 60
DB 1 ATGCTGTTGAGGTTGATTCATATGCGGCTGCTTCTGTGAAGCAAGCATTGTGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGACAAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGACAAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCTG 240
QY 241 GCGGCTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGCAAGTGGGCGCTG 360
DB 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGCGCAAGCAAGTGGGCGCTG 360
QY 361 GGAAGCTAGATGACAGTCTTCAATGAGCCCAAGTACCACTGCTGAGAGATCTG 420
DB 361 GGAAGCTAGATGACAGTCTTCAATGAGCCCAAGTACCACTGCTGAGAGATCTG 420
QY 421 GACAACTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAACTTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACATGAGTGAACAAGAGCAAGCAAGAAAGAGAGCTGCTTAATCTGCTG 540
DB 481 CTCAGGAGACATGAGTGAACAAGAGCAAGCAAGAAAGAGAGCTGCTTAATCTGCTG 540

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QY 541 TCTGCCAATGGGAATTGAGAAAGTAAAACTCTGCTGGAGACAGATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTGAGAAAGTAAAACTCTCTGAGACAGAGATGTCACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGA 660
DB 601 GTCTCTTGACAAACAAAAGAGACAGCTGTATTAAGCCGTACAAATGCCAGGAAGATGA 660
QY 661 TGTGCGTTAATGTGTGGAAACATGGCACTGATCCAAATATTCCAAATGATGGAAT 720
DB 661 TGTGCGTTAATGTGTGGAAACATGGCACTGATCCAAATATTCCAAATGATGGAAT 720
QY 721 ACCACTGTCACCTACCTATCTTATTAAGAAATTAATGAGCCAAAGCATGCTCTTA 780
DB 721 ACCACTGTCACCTACCTATCTTATTAAGAAATTAATGAGCCAAAGCATGCTCTTA 780
QY 781 TATGTGTGATATTCGAATCAAAAAAACAAGCATGGCTCAGACACTGTACTTGTGTA 840
DB 781 TATGTGTGATATTCGAATCAAAAAAACAAGCATGGCTCAGACACTGTACTTGTGTA 840
QY 841 CATGAGCAAAAAACAGAAAGTCTGGAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGAAAGTCTGGAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGGACCTGCTCATTACTGTGTATGTTGTGGATCAGCAATATA 960
DB 901 CTGGATAGATATGGAAGGACCTGCTCATTACTGTGTATGTTGTGGATCAGCAATATA 960
QY 961 GTCAAGCTTCTACTTGGACAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGAG 1020
DB 961 GTCAAGCTTCTACTTGGACAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGATATGCTCTTCTAGTCAATCATATGTAATTTGGCAGTTACTTCTGCTAC 1080
DB 1021 GCCAGAGATATGCTCTTCTAGTCAATCATATGTAATTTGGCAGTTACTTCTGCTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
DB 1081 AAAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCAGAAACAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGGAGTGAATAATAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGGAGTGAATAATAGCCAGCCAGAGAA 1200
QY 1201 ATCTCTCAAGAACCAAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATCTCTCAAGAACCAAAATTAATTAAGATGTGATAGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGAATTACTAGAAAACTGACTAATGTTGCTGCTGAG 1320
DB 1261 AAGCATGAAGATTAATATGTTGGAATTACTAGAAAACTGACTAATGTTGCTGCTGAG 1320
QY 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCAAGAAACAAGCTTAAGCTGACA 1500
DB 1441 AAAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCAAGAAACAAGCTTAAGCTGACA 1500
QY 1501 TCAAGAGAAAGTCACAAAGGCTTGAAGGCAGTGAATAAGCCAGCCAGAGAAAGATCT 1560
DB 1501 TCAAGAGAAAGTCACAAAGGCTTGAAGGCAGTGAATAAGCCAGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGACTAGAAAAATTTTATGCTATCGAA 1620
DB 1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGACTAGAAAAATTTTATGCTATCGAA 1620

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QY 1621 GAAATGAAGAACACAGGAAGTACTCATGTCGGAATTTCCAGAAAACTGACTAATGTGCC 1680
DB 1621 GAAATGAAGAACACAGGAAGTACTCATGTCGGAATTTCCAGAAAACTGACTAATGTGCC 1680
QY 1681 ACTGTGCGAATGTGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
DB 1681 ACTGTGCGAATGTGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGAAACAAATATACTCG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTGAAGAAACAAATATACTCG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACACTGGAATATTAACAGATGATTTCTGATTAAGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACACTGGAATATTAACAGATGATTTCTGATTAAGAA 1860
QY 1861 GAAAACAGATGAAGTGTGTAAGAAAAATGAATTTCTGAGCTTCTTATGTTGAAGAA 1920
DB 1861 GAAAACAGATGAAGTGTGTAAGAAAAATGAATTTCTGAGCTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCATTTTGATGATGAAAAATAGTACGTTGCGGAAAGAAATGCCATGTAAGACTG 1980
DB 1921 GAAAAAGCATTTTGATGATGAAAAATAGTACGTTGCGGAAAGAAATGCCATGTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAACATGAGAGCCAGCTTAAGAAAAAAGAAAAAAGAAAAA 2040
DB 1981 GAGCTAGACACAATGAACATGAGAGCCAGCTTAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 12
US-10-212-679-303
; Sequence 303, Application US/10212679
; Publication No. US20030125536A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-303

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTGTTGAGGTGATTCATGCGCGTGTCTTCTGTGAGAAAGCAATTTGGTCTC 60
DB 1 ATGTGTGTTGAGGTGATTCATGCGCGTGTCTTCTGTGAGAAAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGGTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTGCTGATGAAGCACTCGAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACAGACGACTGCTGATGAAGCACTCGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACTG 240
DB 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGAGCAACTG 240

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QY 241 GGGCTTCTGGAGACCAAGCACTCTGCTATGAAACACTCAAGAAAGATGGGCAAG 300
DB 241 GGGCTTCTGGAGACCAAGCACTCTGCTATGAAACACTCAAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGAGATGGGGCTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGGAGCGGCAAGAGATGGGGCTGG 360
QY 361 GGAAGCTACAGTACAGTGTCTTCATGAGCCAGGATCCAGTCCGTGGAGAAATCTG 420
DB 361 GGAAGCTACAGTACAGTGTCTTCATGAGCCAGGATCCAGTCCGTGGAGAAATCTG 420
QY 421 GAAAGCTCCAGAGAGTGTCTGCTGGGGGTTAAAGTCCCAAGAAAGATCTCATGCTG 480
DB 421 GAAAGCTCCAGAGAGTGTCTGCTGGGGGTTAAAGTCCCAAGAAAGATCTCATGCTG 480
QY 481 CTCAGGACACTGACGTCGAAACAAGAGGACAAGCAAAAGAGAGCTGCTCATCTGGCC 540
DB 481 CTCAGGACACTGACGTCGAAACAAGAGGACAAGCAAAAGAGAGCTGCTCATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAATGATPAAACTCTGTGAGACAGAGATCTCACTTAAT 600
DB 541 TCTGCAATGGGAATTCAGAAATGATPAAACTCTGTGAGACAGAGATCTCACTTAAT 600
QY 601 GTCTCTGACAAACAAAAGAGAGCACTCTGATPAAAGCCGTACATCCAGAAAGTAA 660
DB 601 GTCTCTGACAAACAAAAGAGAGCACTCTGATPAAAGCCGTACATCCAGAAAGTAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGATPAGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCACTGATCCAAATTTCCAGATGATPAGAAAT 720
QY 721 ACCACTCTGACACTGATCTATPAAATGAAATPAAATPAAATGAGCAAGCACTCTTA 780
DB 721 ACCACTCTGACACTGATCTATPAAATGAAATPAAATPAAATGAGCAAGCACTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAACAGCATGCGCTCACACACTGTTACTTGGTGA 840
QY 841 CATGACCAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAGAGGAAATTTAAATGCA 900
DB 841 CATGACCAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAGAGGAAATTTAAATGCA 900
QY 901 CTGGATAGATGAGAGAGAGCTGCTCATATCTTGTGATGTTGTGATGAGCAAGTATA 960
DB 901 CTGGATAGATGAGAGAGAGCTGCTCATATCTTGTGATGTTGTGATGAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATPATTGATATCTTCTCAAGATCTATCTGAGACG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATPATTGATATCTTCTCAAGATCTATCTGAGACG 1020
QY 1021 GCCAGAGATGCTGTTCTACTCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATGCTGTTCTACTCATCATCATGTAATTTGCAAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAAGATGCTPAAAAATCTCTTGAAGAAAGCAATCCAGAAACAAGCTTAAAG 1140
DB 1081 AAAAGAAAAAGATGCTPAAAAATCTCTTGAAGAAAGCAATCCAGAAACAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGCTGAAATATGCCCAGGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAGGAGCTGAAATATGCCCAGGAGAA 1200
QY 1201 ATGTCTCAAGAAACCAAGAAATPAAATGAGATGAGAGGTTGAAGAAAGAAAG 1260
DB 1201 ATGTCTCAAGAAACCAAGAAATPAAATGAGATGAGAGGTTGAAGAAAGAAAG 1260
QY 1261 AAGCATGAAAGATATATGAGATTACTGAGAAACCTGACTAATGATGCTGAGC 1320
DB 1261 AAGCATGAAAGATATATGAGATTACTGAGAAACCTGACTAATGATGCTGAGC 1320

QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
DB 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGCAACACTGAAAAATCGCAATTT 1380
QY 1381 CCTGACAAAGAGATGAGATGATCAGAAATTTGGCAATTTAGTTCTGCTCAAGAA 1440
DB 1381 CCTGACAAAGAGATGAGATGATCAGAAATTTGGCAATTTAGTTCTGCTCAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCACTGAAATATGCCCAGGAGAAAGATCT 1560
DB 1501 TCAGAGAAAGATCACAAGAGCTTGAAGGCACTGAAATATGCCCAGGAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATAGATGATGATGAGAGCTGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATTAATAGATGATGATGAGAGCTGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAAGAGCAGGAAATCTCATGTCGATTCAGAAAACTGACTAAATGATGCC 1680
DB 1621 GAAATGAAAGAGCAGGAAATCTCATGTCGATTCAGAAAACTGACTAAATGATGCC 1680
QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGCAACACTGAAAGC 1740
DB 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGCAACACTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAATGAGATGATCAGAGAGCAACAAATGATCTCG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAATGAGATGATCAGAGAGCAACAAATGATCTCG 1800
QY 1801 AAGCAATTTTGTGAGAGAGAGCAACCTGGAATATTAACAGATGATGATGATGAA 1860
DB 1801 AAGCAATTTTGTGAGAGAGAGCAACCTGGAATATTAACAGATGATGATGATGAA 1860
QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTCTCTTATGTTGAA 1920
DB 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGCTTCTCTTATGTTGAA 1920
QY 1921 GAAAAAGACATCTGATGAAAAATGATGATGCGGGGAGAAATTCGCAATGCTPAAAGC 1980
DB 1921 GAAAAAGACATCTGATGAAAAATGATGATGCGGGGAGAAATTCGCAATGCTPAAAGC 1980
QY 1981 GAGCTGAGACATGAGAAACATCAGAGCCAGCTPAAAAATGAAAAATGAAAAA 2040
DB 1981 GAGCTGAGACATGAGAAACATCAGAGCCAGCTPAAAAATGAAAAATGAAAAA 2040

RESULT 13
US-10-144-678A-375
; Sequence 375, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalo, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaelir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassole, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Metanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-144-678A-375

Query Match      100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGTGATGAGTTGATTCATGCGCGCTCTCTTCTGTGAAGCAATTTGGTCTC 60
DB      1 ATGTGTGATGAGTTGATTCATGCGCGCTCTCTTCTGTGAAGCAATTTGGTCTC 60

QY      61 AGGAGCAAGATGGGCAAGTGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGTGTGCTGCGCTGCTCCCTGCTGCAAGGAGCGGCAAG 120

QY      121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGCTATGAAGACATCAGAGCAAG 180
DB      121 AGCAAGTGGGCACTTCTGAGACAAGCAAGCACTGCTATGAAGACATCAGAGCAAG 180

QY      181 ATGGGCAAGTGTGCGCGCCCTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAG 240
DB      181 ATGGGCAAGTGTGCGCGCCCTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAG 240

QY      241 GGGCTTCTGAGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAAAGATGGGCAAG 300
DB      241 GGGCTTCTGAGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAAAGATGGGCAAG 300

QY      301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGCAAGTGGGCTGG 360
DB      301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGCAAGTGGGCTGG 360

QY      361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGGAGAGATCTG 420
DB      361 GGAAGCTAGAGTACAGTGTCTTCAATGAGCCCAAGGTACCAAGTGGAGAGATCTG 420

QY      421 GACAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGCAGAAAGATCTCATGCTATG 480
DB      421 GACAAGCTCCACAGAGCTGCTGTGTGGGTAAAGTCCCGCAGAAAGATCTCATGCTATG 480

QY      481 CTCAGGAGACCTGACGTGAACAAGAGACAAGCAAAAGAGACTGCTTCAATCTGGCC 540
DB      481 CTCAGGAGACCTGACGTGAACAAGAGACAAGCAAAAGAGACTGCTTCAATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCAGAGTAAAGTAAATCTCTGCTGAGACAGATGCTCAATTAAT 600
DB      541 TCTGCCAATGGGAATTCAGAGTAAAGTAAATCTCTGCTGAGACAGATGCTCAATTAAT 600

QY      601 GTCCTTGACAAACAAAAGAGACAGCTGTATTAAGGCGGTACAAATGCCAGAAAGTGA 660
DB      601 GTCCTTGACAAACAAAAGAGACAGCTGTATTAAGGCGGTACAAATGCCAGAAAGTGA 660

QY      661 TGTGCGTTAATGTTGTGTAACATGCACTGATCCAATATTCAGATGATGGAAT 720
DB      661 TGTGCGTTAATGTTGTGTAACATGCACTGATCCAATATTCAGATGATGGAAT 720

QY      721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATGAGCAATGCTCTTA 780
DB      721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATGAGCAATGCTCTTA 780
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QY      781 TATGGTGTGATATGGAATCAAAAAACAAGATGGCTTCACACCACTGTACTGTGTGA 840
DB      781 TATGGTGTGATATGGAATCAAAAAACAAGATGGCTTCACACCACTGTACTGTGTGA 840

QY      841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900
DB      841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGA 900

QY      901 CTGATAGATATGAAGAGCTGCTCATACTTGTGCTATGTGTGATGATCAGCAATTA 960
DB      901 CTGATAGATATGAAGAGCTGCTCATACTTGTGCTATGTGTGATGATCAGCAATTA 960

QY      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
DB      961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020

QY      1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB      1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

QY      1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAAACTTAAG 1140
DB      1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAAACTTAAG 1140

QY      1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATAGCCAGCCAGAGAA 1200
DB      1141 CTGACATCAGAGAAAGTCACAAAAGTTCAAAAGCAAGTAAATAGCCAGCCAGAGAA 1200

QY      1201 ATGTCTCAAGAAACAGAAATTAATAGATGTGTATAGAGAGTTGAAGAAATGAAG 1260
DB      1201 ATGTCTCAAGAAACAGAAATTAATAGATGTGTATAGAGAGTTGAAGAAATGAAG 1260

QY      1261 AAGCATGAAGATTAATATGTGGATTTATAGAAAACTGACCTAATGTGTCTCTGTGCG 1320
DB      1261 AAGCATGAAGATTAATATGTGGATTTATAGAAAACTGACCTAATGTGTCTCTGTGCG 1320

QY      1321 AATGGTATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATCAGCAATTT 1380
DB      1321 AATGGTATATGATTAATTTCTCAAGAGAAAGACAGAACCTGAAATCAGCAATTT 1380

QY      1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440
DB      1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440

QY      1441 AAAACAGATGCCAAAATACCTTCTGAAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
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QY      1501 TCAGAGAAAGATCACAAAAGCTTGAGGCACTGAAAAATGGCCAGCAGAGAAAAAGATCT 1560
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QY      1561 CAAGAACCAAGAAATTAATAGATGTGTATAGAGACTAGAAAAATTTTATGCTATCGAA 1620
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QY      1621 GAAATGAAGAACACAGGAAGTACTCATGTGCGATTTCCAGAAAACTGATCTAATGTGTGC 1680
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QY      1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAGAC 1740
DB      1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAGAC 1740

QY      1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGAAACAAATGATATCTCAG 1800
DB      1741 CAGCAATTTCTGACACTGAGATGAAGATATCAAGTGAAGAAACAAATGATATCTCAG 1800

QY      1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAGATTTGATTCATGA 1860
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QY 1861 GAAAAAGATAGATGTTGTTGAAAAATGATTTCTGAGCTTCTCTAGTTGTAGAAA 1920
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Db 1921 GAAAAAGATCTTTGATGAAAAATAGTACGTTGCGGAGAAATTCATGCTAGACTG 1980
QY 1981 GAGCTGACACATGAAACATGAGAGCAGCTTAAAAATTTTTTTTTTTTTTTTTT 2040
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Db 1981 GAGCTGACACATGAAACATGAGAGCAGCTTAAAAATTTTTTTTTTTTTTTTTT 2040

RESULT 14
US-10-033-527-7
; Sequence 7, Application US/10033527
; Publication No. US20030170631A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513C1
; CURRENT APPLICATION NUMBER: US/10/033,527
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-033-527-7

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTTGATTCATGCGGCTCTCTTCTGTGAAAGCATTGGTCTC 60
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Db 1 ATGGTGGTGGAGTTGATTCATGCGGCTCTCTTCTGTGAAAGCATTGGTCTC 60
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Db 181 ATGGGCAAGTGGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGT 240
QY 241 GGGGCTTCTGAGACCAAGCACTGCTGTAAGAACATCAGAGCAAGTGGCAAG 300
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Db 241 GGGGCTTCTGAGACCAAGCACTGCTGTAAGAACATCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTCTGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGTGGGCTTGG 360
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|
|
Db 301 TGGTGTCTGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGTGGGCTTGG 360
QY 361 GGAGCTAGATGATGATGCTTCTGAGAGCCAGGATACAGTCCGTGGAGAGATCTG 420
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Db 361 GGAGCTAGATGATGATGCTTCTGAGAGCCAGGATACAGTCCGTGGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGGTAAAGTCCCGCAAGAAAGATCTCATCTG 480
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Db 421 GACAACTCCACAGAGCTGCTGCTGGTAAAGTCCCGCAAGAAAGATCTCATCTG 480
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Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAAGAGACTGCTACATCTGGCC 540
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Db 601 GTCTTGAACAACAAAAGAGACAGCTCTGATTAAGCCGTACATCCAGAGATGAA 660
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Db 661 TGTGCTTATGTTGCTGGAACAATGCACTGATCCAAATTTCCAGATGAGTAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAAGGCCAAAGCACTGCTTA 780
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|
|
Db 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAAGGCCAAAGCACTGCTTA 780
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|
Db 781 TATGCTGATATGATGATCAAAAACAAAGCATGCGCTCAACCACTGTTACTGGTGA 840
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|
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Db 841 CATGACCAAAACAGCAAGTGGTGAATTTTATCAAAAAGCCGAATTTAATGCA 900
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Db 901 CTGATATGATGAGAGAGCTGCTCATACTGCTGTAATGTTGATGATCAGCAATAT 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGGAACAGAG 1020
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Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGGAACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
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Db 1021 GCCAGAGATATGCTGTTCTGATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
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Db 1081 AAGAAAAACAGATGCTAAATATCTCTGAAAAACAGATCCAGAACAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGCAAGTAAATAGCCAGCAAGAAA 1200
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Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGCAAGTAAATAGCCAGCAAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATGATGATGATGAGAGTGGAAAGAAATGAA 1260
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|
Db 1201 ATGTCTCAAGAACCAAAATTAATGATGATGATGAGAGTGGAAAGAAATGAA 1260
QY 1261 AAGCATGAAAGTATATGTTGGAATTAATGAAAACTGACTAATGTTGCTGCTG 1320
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|
|
Db 1261 AAGCATGAAAGTATATGTTGGAATTAATGAAAACTGACTAATGTTGCTGCTG 1320
QY 1321 AATGTGATATGATTAATTTCTCAAAAGAGAGAGCACTGAAATATGCAATTT 1380
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|
|
Db 1321 AATGTGATATGATTAATTTCTCAAAAGAGAGAGCACTGAAATATGCAATTT 1380
QY 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGCAATTAATTTCTGATCAAAAG 1440
|
|
|
Db 1381 CCTGACAAAGAGTGAAGATATCAAGAAATTTGGCAATTAATTTCTGATCAAAAG 1440
QY 1441 AAACAGATCCAAATATCTCTGAAAAACAGAACTCCAGAACAGACTTAAGCTGACA 1500
|
|
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Db 1441 AAACAGATCCAAATATCTCTGAAAAACAGAACTCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGATGCAAAAAGCTTGAAGGCACTGAAATGCGCACAGCAAGAAAGAT 1560
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Db 1501 TCAGAGAAAGATGCAAAAAGCTTGAAGGCACTGAAATGCGCACAGCAAGAAAGAT 1560
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Db 1561 CAAGAACCAGAAATAAATAGATGATAGAGACTAGAAAAATTTATGCTATCGAA 1620
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Db 1621 GAAATGAAGAAGACGGAAGTACTCATGTCGGAATTCGCCAGAAAACTGTACTAATGATGCC 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAAAGACAGAACACTGTAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAAAGACAGAACACTGTAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGAGTACGACGACAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGAGTACGACGACAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAAGACGAACTGTAAATTTACAGATGAGATTTCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAAGACGAACTGTAAATTTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAAACAGATAGAGTGTGTAATAATGAATTTCTGAGCTTTCTCTTAGTTGTAAGAA 1920
Db 1861 GAAAAACAGATAGAGTGTGTAATAATGAATTTCTGAGCTTTCTCTTAGTTGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCGCAATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTCGCAATGCTAAGACTG 1980
QY 1981 GAGCTGACACATGAAACTCAGACCCAGCTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2040
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RESULT 15
US-10-294-025-375

/ Sequence 375, Application US/10294025
/ Publication No. US20030185830A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Stolk, John A.
/ APPLICANT: Kalos, Michael D.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C29
/ CURRENT APPLICATION NUMBER: US/10/294,025
/ NUMBER OF SEQ ID NOS: 1038
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 375
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-294-025-375

Query Match 100.0%; Score 2040; DB 6; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCGTGTGAGTTTATTCATGCGCGGCTGCTCTTCTGTGAAGAGCATTTGTCTTC 60
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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
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Job time : 1665.77 sec

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:12:24 ; Search time 248.436 Seconds
(without alignments)
4025.047 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New.*
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2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170.6	8.4	1041	US-10-131-826A-21	Sequence 21, App1
2	84.6	4.1	14770	US-10-821-234-268	Sequence 268, App
3	71.4	3.5	1870	US-10-750-185-34429	Sequence 34429, A
4	66	3.2	2048	US-10-955-054A-16	Sequence 16, App1
5	61	3.0	343	US-11-108-172-795	Sequence 795, App1
6	60.2	3.0	4270	US-10-714-781A-54	Sequence 54, App1
7	60.2	3.0	5004	US-10-714-781A-77	Sequence 77, App1
8	58.8	2.9	6928	US-10-714-781A-60	Sequence 60, App1
9	56	2.7	2505	US-11-186-283-9	Sequence 9, App1
10	56	2.7	3026	US-11-186-283-7	Sequence 7, App1
11	52	2.5	6549	US-11-186-284-92	Sequence 92, App1
12	50.6	2.5	5054	US-10-821-234-123	Sequence 123, App
13	50.4	2.5	3025	US-11-186-283-3	Sequence 3, App1
14	50.4	2.5	3025	US-11-186-283-1	Sequence 1, App1
15	49.8	2.4	1790	US-11-000-463-671	Sequence 671, App
16	49.4	2.4	1936	US-10-750-185-55958	Sequence 55958, A
17	45	2.2	2487	US-10-689-742-165	Sequence 165, App
18	42.8	2.1	28524	US-10-689-561-13292	Sequence 13292, A
19	42.4	2.1	1108	US-10-689-742-209	Sequence 209, App
20	42	2.1	1454	US-10-750-185-57501	Sequence 57501, A
21	41.8	2.0	340000	US-11-102-978-3	Sequence 3, App1
22	40.6	2.0	201	US-10-995-561-32576	Sequence 32576, A
23	40.6	2.0	387780	US-10-995-561-13259	Sequence 13259, A

24	40.2	2.0	765	US-11-000-463-199	Sequence 199, App
25	40	2.0	2668	US-10-131-826A-511	Sequence 511, App
26	39.6	1.9	201	US-10-995-561-46034	Sequence 46034, A
27	39.6	1.9	201	US-10-995-561-46035	Sequence 46035, A
28	39.6	1.9	201	US-10-995-561-46036	Sequence 46036, A
29	39.6	1.9	191091	US-11-121-086-60	Sequence 60, App1
30	39.6	1.9	237326	US-11-157-389-2	Sequence 2, App1
31	39.4	1.9	3819	US-10-131-826A-405	Sequence 405, App
32	39.4	1.9	6189	US-10-909-125-825	Sequence 825, App
33	39.2	1.9	103931	US-11-117-187-193	Sequence 193, App
34	39.2	1.9	159781	US-11-121-086-92	Sequence 92, App1
35	39	1.9	496	US-10-131-826A-533	Sequence 533, App
36	39	1.9	187745	US-11-121-086-83	Sequence 83, App1
37	38.8	1.9	1332	US-10-131-826A-443	Sequence 443, App1
38	38.8	1.9	2036	US-10-996-217A-8	Sequence 8, App1
39	38.8	1.9	179597	US-11-121-086-91	Sequence 91, App1
40	38.8	1.9	268685	US-10-933-025-22	Sequence 22, App1
41	38.6	1.9	755	US-10-131-826A-153	Sequence 153, App
42	38.6	1.9	75007	US-10-995-561-13194	Sequence 13194, A
43	38.4	1.9	1878	US-10-750-185-56104	Sequence 56104, A
44	38.4	1.9	2150	US-10-955-054A-98	Sequence 98, App1
45	38.2	1.9	201	US-10-995-561-32049	Sequence 32049, A

ALIGNMENTS

RESULT 1
US-10-131-826A-21
Sequence 21, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Elvarroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 21
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-131-826A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
 Best Local Similarity 63.7%; Pred. No. 2,9e-29;
 Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGGCTTCATGAGACCCAGGATCCAGGTCGTGAGAGATGTGAGACAGGTCACAGAGC 437
 DB 300 TGGCTTCGATTTCCCAATACCCCACTTAACCGTTCATCTGAAGATCCACAGAGC 359
 QY 438 TGGCTGTGGGTAAAGTCCCAAGAAATCTCATGTGATGCTGAGGACACTGAGCT 497
 DB 360 TGTCTTACATGTGTATCTAGAGAACTGAA---GTACCTTGTGCTCAGGTATTATGACGC 416
 QY 498 GAACAGAAAGAGACAGACAAAGAGACTGTCTACATCTGAGCTTGGCAATGGAAATTC 557
 DB 417 CATATAGAGAGACAGAGAGAAAGACCGCCCTACATTTGGCCTGTGCCACTGGCCAAAC 476
 QY 558 AGAAGTAGTAAATCTCTGTGAGACAGAGATGTCAACTTAATGTCTTGAACAACAAAA 617
 DB 477 GGAATGTGTACATCTCTGTGTGTCAGAAAGATGTGAGCTTACCTTGGACCGTGAAGA 536
 QY 618 GAGACAGCTGTGATTAAGCCGTACAGATGCCAGAAATGATGTGCTTATGTGTCT 677
 DB 537 CAGGACACCTGTGATCAAGGCTGTACACTGAGGAGAGGCTTGTGCAACTCTTGTGCT 596
 QY 678 GGAACATGGACCTGATCCAAATTTCCAGATGATGTGAAATATCACTCTGCACTACGC 737
 DB 597 GCAAAATGGGCCCAATCAAAATTTACGATTTCTTTGAGAGACGCTCTGCACTACGC 656
 QY 738 TATCTTAATGAAGATTAATTAATGGCAAGACAGCTCTTATGATGTGATATGCA 797
 DB 657 TGTGTATTAATGAAGATACATCCATGATGAAAAATCTTTTTCATGTATCAAAATTTGA 716
 QY 798 ATCAAAAAACAAG 810
 DB 717 AGAATGACAGCAAG 729

RESULT 2
 US-10-821-234-268
 ; Sequence 268, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 268
 ; LENGTH: 14770
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-821-234-268

Query Match 4.1%; Score 84.6; DB 6; Length 14770;
 Best Local Similarity 49.9%; Pred. No. 1.9e-09;
 Matches 213; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 511 AAGCAAAAGAGGACTGCTCTACATCGGCTGTGCCAAATGGGAATTCAGAGTAGTAANA 570
 DB 1879 AAGAAAGATTTATCTCTCTTATGTGTGCGCAAAATATGGAAGCTTGAAGTCCCAAT 1938
 QY 571 CTCCTGTGACAGAGATGTCACTTAATGTCTTGAACAACAAAAGAGACAGCTCTG 630
 DB 1939 CTCCTGTCAAGAAAAGTCACTCTCAAGATGTGCTGTGGAGAGAGGGCTTACACACATG 1998
 QY 631 ATTAAGGCGCTTCAATGCGAGGAAGATGATATGTGCTTATGTGCTGGAACATGCACT 690
 DB 1999 CATGTAGCTGCACATTAATCATATATCAAGAAAGGCGCTTCTCTTTTGGACAGAGGCG 2058
 QY 691 GATCCAAATATTCAGATAGTATGAAATATACACTGTGACCTATCTATATATGAA 750
 DB 2059 TCACCTCAGCAGCGCGCAAGAAATGTTATACCACTGTCAATGTCTGCCAAAAGAAC 2118
 QY 751 GATTAATTAATGGCAAGACACTGTCTTATATGTGTGCTGATATGATCAAAAAACAAG 810
 DB 2119 CAGATGACATATGCGCAACTGTGCTGGAATATGTGTGATGATGCAAGCAGTTACCGG 2178
 QY 811 CATGCTCTCACACACTGTACTTGTGTGTATCATGACAAAAACAGCAAGTGTGAATTT 870
 DB 2179 CAAGGAATGTCTTCCGTCCATCTCCAGCTCAGAAAGGCGACGTGACATGTGTGCTG 2238
 QY 871 TTAATCAAGAAAAAGCGAATTTAATGCACTGATATGATATGAAAGCACTGCTCAT 930
 DB 2239 CTCCTGTGAGAAATGCAATGTGAATCTGAGCAATTAAGAGCGGCTTACCCCATTCAT 2298
 QY 931 CTGCTG 937
 DB 2299 TTGGCTG 2305

RESULT 3
 US-10-750-185-34429
 ; Sequence 34429, Application US/10750185
 ; Publication No. US2005026063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: Patencin version 3.1
 ; SEQ ID NO 34429
 ; LENGTH: 1870
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880438718
 US-10-750-185-34429

Query Match 3.5%; Score 71.4; DB 6; Length 1870;
 Best Local Similarity 72.1%; Pred. No. 7.8e-07;
 Matches 93; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 916 AGACTGCTCTCATCTGCTGTATGTGTGATACAGCAATATGATGACCTTCTACTT 975
 DB 1634 AGAAGAGCCCTCATCTGCTGTCAAGTATGATACAGCAATATGATGATGATGATGAT 1693
 QY 976 GAGCAAAATATGATGATCTTCAAGATCATCTGACAGACGCGCAGAGATGTGT 1035
 DB 1694 CAGCAAGGTGTGACATCTTTCTCAAGATGTTTTGTGATGACGCGGAGAAATATGCT 1753
 QY 1036 GTTCTAGT 1044

Db 1754 GTTATTAGT 1762

RESULT 4

US-10-955-054A-16
Sequence 16, Application US/10955054A
Publication No. US20050266420A1
GENERAL INFORMATION:
APPLICANT: PUSZTAI, LAJOS
APPLICANT: SYMMANS, W. FRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC-880US
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 2048
TYPE: DNA
ORGANISM: Homo sapiens
US-10-955-054A-16

Query Match

Best Local Similarity 3.2%; Score 66; DB 6; Length 2048;
Best Local Similarity 56.4%; Pred. No. 1.3e-05;
Matches 123; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 523 ACTGCTTACATCTGGCCTCTGCCAATGGAATTCAGAGTAGTAAATCTCTGCTGAC 582
Db 1296 AGTCACTGTCGTTGGCTGTAGTAAAGCTACACAGATTTGTCAAAATGCTGCTGAT 1355
QY 583 AGACGATGTAATTAATGTCCTTGACACAAAAGAGACAGCTGTGATTAAGCCGTA 642
Db 1356 TGTGAGGTGATGTAATGATTAATGATTTGATGGAATGAGAACACCTGCTTTATGCTGTA 1415
QY 643 CAATGCAGGAAGATGATGCGTTAATGTTCTGSAACATGACCTGATCCAAATATT 702
Db 1416 CATGGAATATATGTGAATGTGTAAGATGCTCTTGAAAGATGGGGCTGATCCAAATTT 1475
QY 703 CCAGATGATGATGAAATACCACTGCTGACTACGCTAT 740
Db 1476 GAAACTGACTGTGATATATTTCTATGATGATCTAGCTGT 1513

RESULT 5

US-11-108-172-795/c
Sequence 795, Application US/11108172
Publication No. US20050260177A1
GENERAL INFORMATION:
APPLICANT: XU, JIANGCHUN
APPLICANT: LODES, MICHAEL J.
APPLICANT: SECRIEST, HEATHER
APPLICANT: BENSON, DARIN R.
APPLICANT: MEASHER, MADELEINE JOY
APPLICANT: STOLK, JOHN A.
APPLICANT: WANG, YUJUN
APPLICANT: JIANG, YUJUN
APPLICANT: SMITH, CAROLE L.
APPLICANT: KING, GORDON E.
APPLICANT: WANG, AIJUN
APPLICANT: CLAPPER, JONATHAN D.
APPLICANT: SKEIKY, YASIR A. W.
APPLICANT: FANGER, GARY R.
APPLICANT: VEDVICK, THOMAS S.
APPLICANT: CARTER, DARRICK
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,360

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 09/922,217

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 09/833,263

PRIOR FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR FILING DATE: 2000-08-28

PRIOR APPLICATION NUMBER: US 09/609,448

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: US 09/575,251

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 09/519,444

PRIOR FILING DATE: 2000-03-06

PRIOR APPLICATION NUMBER: US 09/504,629

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: US 09/480,321

PRIOR FILING DATE: 2000-01-10

PRIOR APPLICATION NUMBER: US 09/476,296

PRIOR FILING DATE: 1999-12-30

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1130

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 795

LENGTH: 343

TYPE: DNA

ORGANISM: Homo sapiens

US-11-108-172-795

Query Match

Best Local Similarity 3.0%; Score 61; DB 7; Length 343;
Best Local Similarity 64.5%; Pred. No. 8.7e-05;
Matches 91; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 778 TTATATGCTGATATTCGATCAAAACAAAGCATGGCTCACACCACTGTTACTTGGT 837
Db 342 TCACATGATGAACAAATATTTGAAGATGACGCAAGATGATATGACGCACTGTTACTTGGT 283
QY 838 GTACATGAGCAAAAACAGCAAGTCGTAATTTTATGCAAGAAAAGCAATTTTAAAT 897
Db 282 GTGAGTCGAAGAAAGTGAAGATGATGTAATTTTATTAAGAAAAGCAATGTAAT 223
QY 898 GCACGTGATGATGTAAGAGG 918
Db 222 GCCATTGATTATCTTGGCAAG 202

RESULT 6

US-10-714-781A-54
Sequence 54, Application US/10714781A
Publication No. US20050255127A1
GENERAL INFORMATION:
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: MINKE, JULES MARTEN
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
FILE REFERENCE: 574313-3161.5
CURRENT APPLICATION NUMBER: US/10/714,781A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 10/679,520
PRIOR FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: 10/374,953
PRIOR FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 10/116,298
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,923
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 10/676,502
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/FR02/01200
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 54
LENGTH: 4270
TYPE: DNA


```

; ORGANISM: West Nile virus
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (1760) ..(3811)
US-10-714-781A-54

```

Query Match	3.0%	Score 60.2;	DB 6;	Length 4270;
Best Local Similarity	47.9%	Pred. No. 0.00036;		
Matches 173; Conservative	0;	Mismatches 188;	Indels 0;	Gaps 0

OY	524	CTGCTCTCATCTGGCCTCTGCGCATTGGGAATTTCAGAAAGTATATAAACTCCCTGCTGGACA	583
Db	977	CTTGCTCTCATGATCGCGGTGTGAGAGACGACTACAAATATGTGAAAGATCTGTGTGAAGA	1033
OY	584	GACGATGTCACCTTAATGTCTTGA.CAA.CMAAAAGAGGACAGCTCTGATTAAGGCGCTAG	643
Db	1037	ATAACTATGTAAACAAATGTTCTTTACAGGCGAGGCTTACTCTTGTGTGGCAGCTT	1099
OY	644	AATGCCAGAGAGATGAATGTGCGTTAATGTCTGTGAACATGGACCTGATCCAAATATTC	703
Db	1097	ACCTTAA.CMAAGTTAATTTGGTTAAACTCTTATGTGCTCATTCGGCGGATGTAGATATTT	1155
OY	704	CAGATGATTAATGGAAATACCACTTCGCGACTAGGCTATCTATATAAGATTAATTAATGG	763
Db	1157	CAAAACGCGATCGTTAACTCCTCTACATATAGCCGATCAAAATATTAATAACAAATGG	1211
OY	764	CCAAAGCACTGCTCTTATATGTGTGCTGATATCGATCAAAAACAAAGCATGGCCTCACAC	823
Db	1217	TTAAACTTCTATTGAA.CMAAGGTGCTGATACGACTTGTGCGATTAACATGGAGCTACTTC	1277
OY	824	CACGTGTACTTGGTGTACATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAA	883
Db	1277	CTTAAATATGTCGTGTACATCTGGAAATATGGAATATGTAGCACACACTTAATAAAAAA	1337
OY	884	A 884	
Db	1337	A 1337	

RESULT 7
US-10-714-781A-77
Sequence 77, Application US/10714781A
Publication No. US20050255127A1
GENERAL INFORMATION:
APPLICANT: LOOSMORE, SHEENA MAY
APPLICANT: MINK, JULES MARTIN
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
FILE REFERENCE: 574313-3161.5
CURRENT APPLICATION NUMBER: US/10/714,781A
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: 10/679,520
PRIOR FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: 10/374,953
PRIOR FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 10/116,298
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,923
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 10/676,502
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/FR02/01200
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 77
LENGTH: 5004
TYPE: DNA
ORGANISM: Canarypox virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1864) . (2187)
US-10-714-781A-77

Query Match	3.0%;	Score 60.2;	DB 6;	Length 5004;
Best Local Similarity	47.9%;	Pred. No. 0.00039;		
Matches 173; Conservative	0;	Mismatches 188;	Indels 0;	Gaps 0

QY	524	CTGCTTACATCTGGCCCTCTGCAATGAGAAATTCAGAAGTAGTAAATCTCCGCTGGACA	583
Db	1304	CTTGCTGCAATGATCGCGGTGTTGAGAGACGACTCAAAATATGTGAAAGATCTGTTGAAAG	1364
QY	584	GACCATGTCAACTTAATGTCTCTTGACAACAAAAAGAGACAGCTCTGATTAAGGCCGTAC	643
Db	1364	ATAACTATGTAAACAATGTCTTTTACACGGAGGCTTACTCTTTGTGTTGGCAGCTT	1423
QY	644	AATCCAGGAAGATGAATGTGCGTTTAATGTTGCTGGAACTATGGCATCCAAATATTC	703
Db	1424	ACCTTAACAAAGTTAAATTGTGTTAAACTTTAATTTGGCTCATTCGGCGGATGTGATATT	1483
QY	704	CAGATGAGTATGAAAAATACACTCTGCACACTACGCTATCTAATATAGATAAATTAAATGG	763
Db	1484	CAAAACAGGATCGGTTAACTCTCTTACATATAGCCGTATCAATTAATAATTTTAACAATGG	1544
QY	764	CCAAAGCACTGCTCTTATATGTGTGCTGATATCGAATCAAAAAACAAGCATGGCCCTCACAC	823
Db	1544	TTTAACTTCTATTGAACAAAGTGCTGATATCTGACTTGCTGGATTAACATGGAGCACTTC	1604
QY	824	CACGTTCATCTTGTGTACATAGACAAAAACGAAATCGTGAATTTTAAATCAAGAAA	883
Db	1604	CTTTAATGATCGCTGTACAATCTGGAAATATTTGAAATATGTAGCACACTTAATAAAAAA	1664
QY	884	A 884	
Db	1664	A 1664	

```

      RESULT 8
      US-10-714-781A-60
      ; Sequence 60, Application US/10714781A
      ; Publication No. US20050255127A1
      ; GENERAL INFORMATION:
      ; APPLICANT: LOOSMORE, SHEENA MAY
      ; APPLICANT: MINKE, JULES MARTIN
      ; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
      ; FILE REFERENCE: 574313-3161.5
      ; CURRENT APPLICATION NUMBER: US/10/714, 781A
      ; CURRENT FILING DATE: 2003-11-17
      ; PRIOR APPLICATION NUMBER: 10/679,520
      ; PRIOR FILING DATE: 2003-10-06
      ; PRIOR APPLICATION NUMBER: 10/574,953
      ; PRIOR FILING DATE: 2003-02-26
      ; PRIOR APPLICATION NUMBER: 10/116,298
      ; PRIOR FILING DATE: 2002-04-04
      ; PRIOR APPLICATION NUMBER: 60/281,923
      ; PRIOR FILING DATE: 2001-04-06
      ; PRIOR APPLICATION NUMBER: 10/676,502
      ; PRIOR FILING DATE: 2003-09-30
      ; PRIOR APPLICATION NUMBER: PCT/FR02/01200
      ; PRIOR FILING DATE: 2002-04-05
      ; NUMBER OF SEQ ID NOS: 85
      ; SOFTWARE: PatentIn Ver. 3.2
      ; SEQ ID NO 60
      ; LENGTH: 6928
      ; TYPE: DNA
      ; ORGANISM: West Nile virus
      ; FEATURE:
      ; NAME/KEY: CDS
      ; LOCATION: (2005) .. (4059)
      ; US-10-714-781A-60

```

Query Match	2.9%	Score 58.8;	DB 6;	Length 6928;
Best Local Similarity	47.0%	Pred. No. 0.00091;		
Matches 217;	Conservative 0;	Mismatches 242;	Indels 3;	Gaps 1
QY	524	CTGCTCTACATCTGGCCCTCTGGCAATGGGAATTCAAGAAAGTAGTAAACTCTCTCTGGACA		583

Db 1128 CTCCTCTTGAAATGCGTGTAAATGTTCAAGAAATCCAGAGCTATATAAATCTTGATGAGTT 1187
QY 584 GAGAGTGTCACTTAATATGCTTGGACAACAAGAGAGAGAGCTGTGATTAAGCCGTAC 643
Db 1188 ATGAGAGCTAAACCTGTAGTACTGAATGCACA--ACTTCTGTCTGCATGATGCGGTGT 1244
QY 644 AATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAAACATGGCACTGATCCAAATATTC 703
Db 1245 TGAAGAGCGACTCAAAATATGATGAATATCTGTTGAAGAAATTAATGTAACAAATGTTTC 1304
QY 704 CAATGATGATGAAATATACACTCTGCACTACGCTATCTTAATGAAGATAAATTAATG 763
Db 1305 TTAAACGCGAGGCTTACTCCCTTGTGTGGAGCTTACCTTAACAAGTTAATTTGG 1364
QY 764 CCAAGACATGCTCTTAATATGATGCTGATATCGAATCAAAAAACAAGATGCGCTCAAC 823
Db 1365 TTAAACTTATTTGGCTCATCTTCGCGGATGATGATATTTCAACACGAGATCGGTTAACTC 1424
QY 824 CACTGTACTTGTGTACATAGAGCAAAACAGCAAGTCGTAATTTTAAATCAAGAAA 883
Db 1425 CTCTACATATAGCCGTATCAAAATTAATTAACAATGTTAACTTAATGAACAAAG 1484
QY 884 AAGCGAATTTAAATGCACTGATGATGATGAAAGAGCTGCTCATCTGCTGATGTT 943
Db 1485 GTGCTGATCTGACTTGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1544
QY 944 GTGATTCAGCAAGTATATGTCAGCTTCTTACTTGAAGCAAAATA 985
Db 1545 CTGGAATATTTGAATATGATGACACTTAAAAAATA 1586

RESULT 9
US-11-186-283-9
; Sequence 9, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-9

Query Match 2.7%; Score 56; DB 7; Length 2505;
Best Local Similarity 46.3%; Pred. No. 0.0026;
Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;
QY 524 CTGCTTACATCTGGCTCTGCAATGGAATTCAGAGTAAATCTCTCTGAGACA 583
Db 308 CAGCTTCGACACTGCGCGTTTACAAGAGACGCCGGAATTAATCACTTCACTGTGACACA 367
QY 584 GAGAGTGTCACTTAATATGCTTGTGACAAACAAAAGAGACAGCTTGAATAAAGCCGTAC 643

Db 368 GCGAGCAGATGTTTCAGCAAGTGGATATAGGTGGCTTCACAGCCCTCCACATAGCTGCA 427
QY 644 AATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTC 703
Db 428 TAGCTGGAACACCAGAGGCTGCGAAGTGTCTGCTCAACATGGGGCCAATGTGAATGTTTC 487
QY 704 CAGATGATGATGAATATACCTCTGCACTAGCGCTATCTTAATGAAGATAAATTAATG 763
Db 488 AAGATCCGCTCTTCTTACCCCACTGCACATGACCTGACTTAATGAGCAGACAGGTAA 547
QY 764 CCAAGACATGCTCTTAATATGATGCTGATATGCAATCAAAAAACAAGATGCGCTCAAC 823
Db 548 CCAATGCTCTTTGAAGTTTGGTGTGATGTCAATGTAACCGGTGAAGTTGGGACAGGC 607
QY 824 CACTGTACTTGTGTACATAGCAAAAAACAAGTCGTAATTTTAAATCA----- 878
Db 608 CTCTGACCTGGGCTCTGCAAGAGGCTTCTTCAACATGTAAGAACCTCTGTGAAAGAG 667
QY 879 -GAAAAACGAAATTTAAATGCACTGATGATGATGAAAGAGCTGCTTCATCTGCTG 937
Db 668 GAGCAAGCAGATGTGAACGCTCAGAGCAATGAAACCAAGTCCCTCTGCACTTCTGTT 727
QY 938 TATGTTGTGATCAGCAAGTATATGTCAGCTTCTTACTTGAAGCAAAATATGATGATCTT 997
Db 728 CTGATTTGGAACCAACATATATGATGATGATGATGATGATGATGATGATGATGATG 787
QY 998 CTCAG 1003
Db 788 CTCAG 793

RESULT 10
US-11-186-283-7
; Sequence 7, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3026
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(2565)
US-11-186-283-7

Query Match 2.7%; Score 56; DB 7; Length 3026;
Best Local Similarity 46.3%; Pred. No. 0.0028;
Matches 225; Conservative 0; Mismatches 255; Indels 6; Gaps 1;
QY 524 CTGCTTACATCTGGCTCTGCAATGGAATTCAGAGTAAATCTCTCTGAGACA 583
Db 368 CAGCTTCGACACTGCGCGTTTACAAGAGACGCCGGAATTAATCACTTCACTGTGACACA 427
QY 584 GAGAGTGTCACTTAATATGCTTGTGACAAACAAAAGAGACAGCTTGAATAAAGCCGTAC 643

Db 428 GCGAGACGATGTTGAGCAAGTGGATACGGTGGCTCACAGCCCTCCACATAGTGCAA 487
Qy 644 AATGCCAGAAATGATGATGCTTAATGTTGCTGGAACATGACACTGATCCAAATATTC 703
Db 488 TAGCTGAGACACCCAGAGGCTGCAAGAGTCTGTACACATGGGGCAATGGAAATGTTG 547
Qy 704 CAGATGATGGAATTAATGACCTGCTGACCTAGCCTATCTATAATGAAGTAATTAATG 763
Db 548 AAGATGCCCTCTTCTTCCACCCCTGACATTCGACCTCTATGAGGACAGACAGTAA 607
Qy 764 CCAGACACTGCTCTTATATGTTGCTGATGATGATCAATCAAAAAACAAGATGCTGCAC 823
Db 608 CCAAGTCTCTTTGAAGTTGGTGTGATGTCAATGATTAAGCGTGAAGTTGGGACAGGC 667
Qy 824 CACTGTACTTGTGTGATGATGAGCAAAAAACAGCAATCGTGAATTTTATCA----- 878
Db 668 CTCTGACCTGGCTCTGCAAAAGGCTTCTTCAACATTTGAAACCTCGTGAAGAA 727
Qy 879 -GAAAAAGCAATTTAAATGCACTGGATGATGAAAGAACTGCTCATCTACTGCTG 937
Db 728 GAGGCAAGCAGATGTGAAGCTCAGACATGAACAACAGCTCCCTGCACTTCTGTT 787
Qy 938 TATGTTGTGATGACGAAGTATAGTACGCTTCTACTTGAAGCAAAATATTGATCTT 997
Db 788 CTCGATTTGGACACCAATATATGAGCTACTGCTCCAGATGACTTAGAGTCCAGC 847
Qy 998 CTCGAG 1003
Db 848 CTCACG 853

RESULT 11
US-11-186-284-92

/ Sequence 92, Application US/11186284
/ Publication No. US2005026493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamatkar, Shubhangt
/ APPLICANT: Monahan, John B.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ TITLE OF INVENTION: THERAPY OF COLON CANCER
/ FILE REFERENCE: MP01-029P2RM
/ CURRENT APPLICATION NUMBER: US/11/186,284
/ PRIOR FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/301,822
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 92
/ LENGTH: 6549
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (240)...(4904)
US-11-186-284-92

Query Match 2.5%; Score 52; DB 7; Length 6549;
Best Local Similarity 46.8%; Pred. No. 0.03;
Matches 163; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy 491 CTGAGTGAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGCCCTGCAATG 550
Db 2626 CTGCTGTGTCGGGCAAAACAGAGAGGGGTTCCACCTTTGTTTGTGACAGCCGACG 2685
Qy 551 GGAATTCAGAAATAGTAAATCTCTGCTGACAGACGATGTCATTAATGCTTTGACA 610
Db 2686 GGCATTGGCAGATTGTATGACTGCTGTGGAACGGGGCTGTGATGTAACCTTAAGTACA 2745
Qy 611 ACAAAAAGAGACAGCTCTGATTAAGGCCCTGCAATGCCAGAAATGATGTGCTTAA 670
Db 2746 ACCAAGGCCGAGCGCCCTCATGTGTGCTTGTGAAGGACCTTGACACCGGGAAT 2805
Qy 671 TGTTCGTGAACATGAGCACTGATCCAAATATTCAGATGATGGAATTAATCACTGTC 730
Db 2806 TCTCTCTTTCAAAAGTGTGACGCCCTTTCTTCTTATGACAAAGAGGTCTGTACATTA 2865
Qy 731 ACTAGCTATCTATATGAAATTAATTAATGACCAAGCAAGCTGCTTATATGTGCTG 790
Db 2866 GCTGGGCTTGTGTGAAGGTCAAGGGCAGTGTCCAGTATCTGTTGAAGAAAGAGCTG 2925
Qy 791 AATGGAATCAAAAAACAAGCATGGCTTCACACCACTGTTACTTGCTG 838
Db 2926 CAATGACCAAGACAGACAAAGATGGCCGACACCTTGGACCTGCTG 2973

RESULT 12
US-10-821-234-123

/ Sequence 123, Application US/10821234
/ Publication No. US2005025114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andermani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 123
/ LENGTH: 5054
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-123

Query Match 2.5%; Score 50.6; DB 6; Length 5054;
Best Local Similarity 44.4%; Pred. No. 0.056;
Matches 203; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

Qy 526 GCTTACATCTGGCCTTGGCCAATGGGAATTCAGAGTAGTAAATCTCTGTGACAGA 585
Db 519 GCCTTACATCTGGCAGCCAAAGAACGCCACATGATGATCAGGAAGCTGCTCAGTCT 578
Qy 586 CGATGCACTTAATGTCTTGAACAACAAAAGAGACAGCTCTGATTAAGGCCGTACAA 645
Db 579 AATGCCAGCCGGAAGGTGTGACAGCTCTGGAAAAACGCTTACATTATCCAGCGCT 638
Qy 646 TGCAGGAAGATGAATGTCGTTAATGTTGCTGGAACATGAGGACCTGATCCAAATATTC 705
Db 639 CAGGCTGCTTCAAGCTGTGCAAGTTCTTCTGCAACACAAAGCCCTAAACCTCAAA 698
Qy 706 GATGATGAAATATACCACTGTCATGCTATCTATATGAAGATTAATTAATGAGCT 765
Db 699 GATTTGATGGAATATACCGTGTGCTGTGTAACAAAATGTCACAGTGAATCTGT 758
Qy 766 AAGACCTGCTTATATGTTGCTGATGATGATCAAAAAACAAGCATGCTCACACA 825
Db 759 CACTTCTCTGATGATGAGCAGATGTCAATTCAGAGAAAGTGAAGAACTGCT 818
Qy 826 CTGTACTTGTGTATGATGAGCAAAAAACAAGTCGTGAATTTTATCAAGAAAAA 885

Db	819	CTATGCTGSCCTGTGAGATTGGCAGCTTAAACGCTGTGGAAGCTTTAATTTAAAAAGGCT	878
Oy	886	GCGAATTTAAATGCACTGATAGATATGSAAGAGCTGCTTCATATCTTGATATGTTGT	945
Db	879	GCAGACCTTAAACCTTGTAGATTCCTCTTGATTCACATGCTTACATTATTCAAACTCTCA	938
Oy	946	GGATCAGCAGATATAGTCAGCCCTTCACTTGAGCAAA	982
Db	939	GAAATTCAGAGATTCAAAGCTTTCATTTATCAAAA	975

RESULT 13

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US-11-186-283-3
/ Sequence 3, Application US/11186283
/ Publication No. US20050255520A1
/ GENERAL INFORMATION:
/ APPLICANT: Raju, Jayaseelan
/ TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
/ FILE REFERENCE: IN1-068CP2
/ CURRENT APPLICATION NUMBER: US/11/186,283
/ CURRENT FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/626,173
/ PRIOR FILING DATE: 2003-07-24
/ PRIOR APPLICATION NUMBER: US/09/947,199A
/ PRIOR FILING DATE: 2001-09-05
/ PRIOR APPLICATION NUMBER: US 60/111,938
/ PRIOR FILING DATE: 1998-12-11
/ PRIOR APPLICATION NUMBER: US 09/291,839
/ PRIOR FILING DATE: 1999-04-14
/ PRIOR APPLICATION NUMBER: US 09/458,457
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 2505
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(2505)
/ US-11-186-283-3

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Query Match	2.5%	Score 50.4	DB 7	Length 2505
Best Local Similarity	44.0%	Pred. No. 0.047		
Matches 213; Conservative	0	Mismatches 271	Indels 0	Gaps 0

Qy	522	ACGCTCTACATCTGGCCCTCTGGCAATGGGAATTCAGAAAGTAAAGTAAATCTCTGGCGAC	562
Db	307	ACAGCCCTTGATTTTACAGATTACAGATTAACAGATTAATGCAATTAATGATCATCTTCTGGCTTAC	366
Qy	583	AGACGATGTCACTTATATGTCTCTTGCACAACAAAAAAGAGAGACGCTCTGATTAAGGCCGTA	642
Db	367	AGTGAAGCTGATTAACAGAGGTTGGATTAACGTTGGCCCTCATCTGCCCTCCATATTGCTACA	426
Qy	643	CAATGCCAGGAAAGATGATATGTCGTTAATGTTTCTGGAACATGGCATCGATCCAAATATT	702
Db	427	ATATGCTGGCCACTATAGAGCTGCTGATGCTGTGTTGCAACATGGAGCTAATGTCAATATT	486
Qy	703	CCAGATGATGATGGAATTAACCATCTGCATACGCTATCTTAATGAAAGTAAATTAATG	762
Db	487	CAAGATGACGTTTTTTTTCTACTCCATTGCAATTAATGAGCGTCTATTTGACATGAAACAGTA	546
Qy	763	GCCAAAGACACTGCTCTTATATGATGTCGATATCGAATCAAAAACAAAGCATGGCCATCA	822
Db	547	ACTCGCCTTCTTTTGAAATTTGGTGTGTAATGTAATGATGGTGAAGTTGGAGATAGA	606
Qy	823	CCACTGTTAATTGGGTGTACATGACAAAAACGAAAGTCGTAATATTTTAATCAAGAA	882
Db	607	CCCTCCACTAGCATCTGCAAAAAGGATCTTGATTAATTGCAAAATCTTGATGGAAGAA	666
Qy	883	AAAGCGAATTTAATGCACTGGATGATATGGAAGACCTGCTCTCATATCTTGCTGTATGT	942

D_b 667 GGCAGCAGAAGATGTGAATGCTCAAGTAAATGAACCATGTCCTCCACTCCATTCTGG 726
Q_y 943 TGTGATCAGCAAGTATTAAGTCAGCCCTTCTAATTGAGCAAAATATTTGATATCTTCTCAA 100
D_b 727 TCTCGATTTTGACACCATGATATTAAGTATCTGCTGCCAAAAGATTTGGAAAGTTCAA 786
Q_y 1003 GATC 1006
D_b 787 CTC 790

RESULT 14

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US-11-186-283-1
; Sequence 1, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jayaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI -068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ. ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48)..(2552)
US-11-186-283-1

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Query Match	2.5%;	Score 50.4;	DB 7;	Length 3025;
Best Local Similarity	44.0%;	Pred. No. 0.051;		
Matches 213;	Conservative 0;	Mismatches 271;	Indels 0;	Gaps 0;

Qy	522	ACTGCTCTCATCTGGCTCTGCCAATGGGAATTCAGAGTAGTAAATCTCTGCTGAC	562
Db	354	ACGCTTTCATTTTAGCGATTTACAGAGTATATCAGATTGATCAGCTTCTCTGCTTAC	413
Qy	583	AGACGATGCACTTAATATGTCCCTTACACAAAAGAGGACGCTCTGATAAAGCCGTA	642
Db	414	ATGGAGCTCATATACAGAGTTGATACGGTGGCTCAGTGCCTTCATATTGCTACA	
Qy	643	CAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATT	702
Db	474	ATAGCTGGCACCCTAGAGGCTGCTGATGTGCTGTTGGCAATGAGCTAATGTCAATATT	533
Qy	703	CCAGATGAGTATGGAATATCCACTCTGCATACGTATCTATATGAAGTAAATTAATG	762
Db	534	CAGAGTACGTTTTTTTCACTCCATTCATTTTCAGGTACTATGTGACATGAAACAGTGA	593
Qy	763	GCCAAAGCAGTCTCTTATATGAGGCTGATATGCAATCAAAAAACAAGCATGGCCTACA	822
Db	594	ACTGCGCTTCTTTTGAATTTGGTGCTGATGTAAATGTAAGTGTGAAGTTGAATAGA	653
Qy	823	CCACTGTTACTTGTGTACATGAGCAAAAAACAGCAAGCTGTGAATTTTATATCAAGAA	882
Db	654	CCCTTCACCTAGCATCTGCAAAAAGGATCTTGAATTTGCAAAAACCTTGATGGAAGAA	713
Qy	883	AAAGCAATTAATGACCTGGATGATATGAAAGACCTGCTCATACTTCTGTATGT	942

Db 714 GGCAGCAAGCAGATGTGATGCTCAAGTAATGAAGACCAGTCCCATCTCATTTCTGT 773
QY 943 TGTGATCAGCAAGTATAGTCCCTTCTACTTGAGCAAAATATGATATCTTCTCA 1002
Db 774 TCTCGATTGGACACCATATATATTAAGTATCTGTCGAAGGATTTGGAAGTTCAA 833
QY 1003 GATC 1006
Db 834 CCTC 837

RESULT 15

US-11-000-463-671
; Sequence 671, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FaalSeq for Windows Version 3.0
; SEQ ID NO 671
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-671

Query Match 2.4%; Score 49.8; DB 7; Length 1790;
Best Local Similarity 48.4%; Pred. No. 0.056;
Matches 138; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 537 GGCCTTGCCATGGGAATTGAGAGTAGTAAACTCTGCTGAGACAGATGCACT 596
Db 209 GGGCCCTGAAACCGAGACTGTGATGAGAAAGACTATGTGCCAAGGAGAAAGATGT 268
QY 597 TAATGCTTGAACAACAAAGAGAGAGAGCTGATTAAGCCCGTCAATGCCAGAGAGA 656
Db 269 CAACCGGACACTGAGAGGTGAAAGAACTCTTCAATTAGCAGCATTTGGGCGAGCT 328
QY 657 TGAATGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATATG 716
Db 329 TGAATCTCGAATTTCTGCTGTAAGAGAGAGAGATATTAATGCTCCAGATAACATCA 388
QY 717 AATATCACTCTGCACTAGCTATCTATTAATGAAGATTAATGAGCAAGCACTGCT 776
Db 389 TATTACTCTCTCTGCTGCTGTATGAGGCTCATGTTCTCTGTGAAATTCCTCT 448

QY 777 CTTATATGCTGCTGATATCGAATCAAAAACAGCATGGCCCTCAC 821
Db 449 GTCAAGGCTGCTGATTAAGACTGTGAAGGCCCAAGATGACTGAC 493

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Job time : 252.436 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2005, 07:36:50 : Search time 8221.6 Seconds
(without alignments)
11609.127 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040
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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
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6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1105	54.2	6098	4	HSMB09270
2	592.4	29.0	633	3	BM763453 K-EST0044
3	581.4	28.5	621	3	BM763942 K-EST0045
4	508	24.9	729	5	BU930826 AGENCOURT
5	478.6	23.5	544	1	AL703938 DKFZp6865
6	472.8	23.2	865	2	BF676987 602084215
7	376.4	18.5	505	5	BQ43731 AGENCOURT
8	357.8	17.5	910	5	BQ43731 AGENCOURT
9	357.2	17.5	910	5	BQ43731 AGENCOURT
10	351.2	17.2	2677	4	CR660726 Pongo pyg
11	348.8	17.1	843	1	AU120666
12	345.8	17.0	5130	11	DO053800 Homo sapi
13	343.4	16.8	909	7	CR994478 CR994478
14	324	15.9	5483	4	BM469654 AGENCOURT
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16	323	15.8	874	6	CD358418 AGENCOURT
17	316.2	15.5	5130	11	DO053801 Pan trogl
18	305.2	15.0	793	7	CO884999 BovGen 13
19	300.2	14.7	381	7	CR747857 CR747857
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21	289.6	14.2	739	8	HSMB01761 DN831905 MGC2.2.1.
22	283.8	13.9	1079	3	BM548157 AGENCOURT

23	272	13.3	539	1	AA910780
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25	269.4	13.2	760	5	BU568215 AGENCOURT
26	267.2	13.1	754	3	BI871077 603394250
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28	261.2	12.8	537	3	BM511319 1146C10.Y
29	256	12.5	1486	11	DO052688 Homo sapi
30	251.2	12.3	1347	4	AK084890 Mus muscu
31	251.2	12.3	1758	4	AK017783 Mus muscu
32	250.8	12.3	1661	4	AK087771 Mus muscu
33	250.8	12.3	582	3	BP280827 BP280827
34	237.8	11.7	513	11	DO048070 Homo sapi
35	235	11.5	423	5	BU584403 3967290F5
36	235	11.5	583	3	BP316828 BP316828
37	230.4	11.3	289	1	AA533501 nt96a04.8
38	225.6	11.1	521	8	DN995247 TC106315
39	223.8	11.0	802	5	BQ432733 AGENCOURT
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44	217.6	10.7	1054	4	AK015948 Mus muscu
45	216.8	10.6	856	3	BI830348 603073084

ALIGNMENTS

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LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
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Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; consortium of the German Genome Project.
This clone (DKFZp686J0529) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686J0529
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES
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/clone="DKFZp686J0529"
/issue_type="testis"
/clone_lib="686 (synonym: h1ccc3). Vector pSport1_sfi1 host DH10B; sites SfiI + SfiI B"
/dev_stage="adult"
/note="putative transcript"

ORIGIN
Query Match 54.2% Score 1105; DB 4; Length 6098;
Best Local Similarity 88.2%; Pred. No. 3.7e-259;

Matches 1243; Conservative 0; Mismatches 95; Indels 71; Gaps 1;

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QY 1 ATGGGTGTTGAGGTGATTCATCCATGCGGGTCCCTCTTCTGTGAAAGAACCATTTGGTCTC 60
Db 441 ATGTGACTGAGGTGTTGTCATATGCGCGCTGCTGTGTGAAGAGCATTCGATCTTC 500
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGCAAGGAGACGGCAAG 120
Db 501 AGGAGCAAGATGGGCAAGTGTGCTGCAACCGCTTCCTCCCTGCTGCAAGGAGACGGCAAG 560
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGCTATGAAAGCACTCAGAGCAAG 180
Db 561 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGCTATGAAAGTGTCTCAGAGCAAG 620
QY 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGGCAAGCG 240
Db 621 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGGCAAGCG 680
QY 241 GGGGCTTCTGAGACCAAGCACTGCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 300
Db 681 GGGGCTTCTGAGACCAAGCACTGCTGCTATGAAAGCACTCAGAGCAAGTGGGCAAG 740
QY 301 TGGTGTCCCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGCAAGTGGGCGCTTGG 360
Db 741 TGGTGTCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGGCAAGTGGGCGCTTGG 800
QY 361 GGAGCATAGAGTACGATGCTTCAATGAGCCCAAGTACCAAGTCCGATGAGAGTCTGG 420
Db 801 GGAGCATAGAGTACGATGCTTCAATGAGCCCAAGTACCAAGTCCGATGAGAGTCTGG 860
QY 421 GACAACTCCACAGAGCTGCTGGTGGTGAAGTCCCAAGAGAGATCTCATCTGCTATG 480
Db 861 GACAACTCCACAGAGCTGCTGGTGGTGAAGTCCCAAGAGAGATCTCATCTGCTATG 920
QY 481 CTCAGGGAACACTGACCTGAAACAAGAGCAAGCAAAAGAGCTGCTTCAATCTGGCC 540
Db 921 CTCAGGGAACACTGACCTGAAACAAGAGCAAGCAAAAGAGCTGCTTCAATCTGGCC 980
QY 541 TCTGCCAATAGGGAATTCAGAGTGAATTAATCTCTGCTGCAAGAGATCAACTTAAT 600
Db 981 TCTGCCAATAGGGAATTCAGAGTGAATTAATCTCTGCTGCAAGAGATCAACTTAAT 1040
QY 601 GTCTCTGCAACAACAAAAGAGAGCAGCTGATTAAGGCGCTAACATGCGAGAGATGAA 660
Db 1041 GTCTCTGCAACAACAAAAGAGAGCAGCTGATTAAGGCGCTAACATGCGAGAGATGAA 1100
QY 661 TGTGCTTAATGTTGCTGCAACAATGCACTGATCAAAATATTCAGATGATGGAAT 720
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QY 721 ACCACTCTGCACTAGCTATCTTAATGAAGATTAATTAAGGCAAGCAAGCTCTTA 780
Db 1161 ACCACTCTGCACTAGCTATCTTAATGAAGATTAATTAAGGCAAGCAAGCTCTTA 1220
QY 781 TATGTGCTGATATCCAAATCAAAAAGAGATGGCTCAACACCTGTTACTTGGTGA 840
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QY 841 CATGACAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 1281 CATGACAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 1340
QY 901 CTGGATAGATATGGAAGAGCTGCTCATATCTTGTGATGTTGTTGATCAGCAATTA 960
Db 1341 CTGGATAGATATGGAAGAGCTGCTCATATCTTGTGATGTTGTTGATCAGCAATTA 1400
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Db 1401 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGCAGAG 1460
QY 1021 GCCAGAGAGTATGCTTCTTCTAGTCAATCATGATGAATTTGCCAGTTACTTCTGA 1080
Db 1461 GCCAGAGAGTATGCTTCTTCTAGTCAATCATGATGAATTTGCCAGTTACTTCTGA 1520

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Db 1630 AAGCATGAAGTAAATCTGTGGGATTAATCCAGAAAACTGACTAATGGTCCAGTGTGAC 1689
QY 1321 AATGGTGAATTAATGATTAATTTCTCAAAAGGAAGAGAGCAACCTGAAATGACAAATTT 1380
Db 1690 AATGGTGAATTAATGATTAATTTCTCAAAAGGAAGAGAGCAACCTGAAATGACAAATTT 1749
QY 1381 CCTGACAAACGAAAGTGAAGATATCACAG 1409
Db 1750 CCTGACAACTGAAGAAATGAAGATATCACAG 1778

RESULT 2
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LOCUS K-EST0044791 S13KMS5 Homo sapiens CDNA clone S13KMS5-16-All 5',
DEFINITION mRNA sequence.
ACCESSION BM763453
VERSION BM763453.1 GI:19093068
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 633)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
COMMENT
TITLE
JOURNAL
CONTACT
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
High quality sequence stop: 633.
Location/Qualifiers
1 633
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/tissue_type="myeloma"
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/lab_host="Top10P"
/clone_id="S13KMS5"
/notes="Vector: PCMS; Site 1: EcoRI; Site 2: NotI. The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then deapped intact mRNA was
labeled with DNA-RNA linker including BcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.

```

coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 29.0%; Score 592.4; DB 3; Length 633;
Best Local Similarity 96.7%; Pred. No. 8.3e-134;
Matches 616; Conservative 0; Mismatches 17; Indels 4; Gaps 1;

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DB 1 CAAGCAAAAGAGACGCTCTTACATCTGCGCTTCCCAATGGGAATTCGAACTAGTAA 60
QY 570 ACTCGTGTGACAGACGATGTCATCTTATGCTTGAACAACAAAGAGACGCTCT 629
DB 61 ACTCGTGTGACAGACGATGTCATCTTATGCTTGAACAACAAAGAGACGCTCT 120
QY 630 GATTAAGGCGGTACCAATGCGAGAGATGATGCTTATGCTTGAACATGCGAC 689
DB 121 GATTAAGGCGGTACCAATGCGAGAGATGATGCTTATGCTTGAACATGCGAC 180
QY 690 TGATCCAAATATCCAGATGATGATGATGATGATGATGATGATGATGATGATG 749
DB 181 TGATCCAAATATCCAGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 750 AGATAATTAATGCGCAAGCACTGCTTATGCTTATGCTTATGCTTATGCTTATG 809
DB 241 AGATAATTAATGCGCAAGCACTGCTTATGCTTATGCTTATGCTTATGCTTATG 300
QY 810 GGATGCGCTCACACCACTGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 869
DB 301 GGATGCGCTCACACCACTGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 360
QY 870 TTTAATCAAGAAAAAGCAATTTAATGATGATGATGATGATGATGATGATGAT 929
DB 361 TTTAATCAAGAAAAAGCAATTTAATGATGATGATGATGATGATGATGATGAT 420
QY 930 ACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 989
DB 421 ACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 990 TGTATCTTCAAGATCTATCTGACAGACGCGCAGAGATGCTGTTTCTAGTATCA 1049
DB 481 TGTATCTTCAAGATCTATCTGACAGACGCGCAGAGATGCTGTTTCTAGTATCA 536
QY 1050 TCATGTAATTTGCGCACTTACTTCTGATCAACAAAGAAAAAGATGCTTAAATCTCTTC 1109
DB 537 TCATGTAATTTGCGCACTTACTTCTGATCAACAAAGAAAAAGATGCTTAAATCTCTTC 596
QY 1110 TGAACCAAGCAATCCAGAACAGACTTAAAGCTGACA 1146
DB 597 TGAACCAAGCAATCCAGAACAGACTTAAAGCTGACA 633
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DEFINITION K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-A11 5',
ACCESSION BM763942
VERSION BM763942.1 GI:19093557
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kim.N.S., Hahn.Y., Oh.J.H., Lee.J.Y., Ahn.H.Y., Chu.M.Y., Kim.M.R.,
```

TITLE
JOURNAL
COMMENT

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@email.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-25-A11"
/issue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"

/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI. The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tabacco acid pyrophosphatase (TAP). The dephosphorylated RNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10F⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 28.5%; Score 581.4; DB 3; Length 621;
Best Local Similarity 96.8%; Pred. No. 4.1e-131;
Matches 605; Conservative 0; Mismatches 16; Indels 4; Gaps 1;

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QY 510 CAAGCAAAAGAGACGCTCTTACATCTGCGCTTCCCAATGGGAATTCGAACTAGTAA 569
DB 1 CAAGCAAAAGAGACGCTCTTACATCTGCGCTTCCCAATGGGAATTCGAACTAGTAA 60
QY 570 ACTCGTGTGACAGACGATGTCATCTTATGCTTGAACAACAAAGAGACGCTCT 629
DB 61 ACTCGTGTGACAGACGATGTCATCTTATGCTTGAACAACAAAGAGACGCTCT 120
QY 630 GATTAAGGCGGTACCAATGCGAGAGATGATGCTTATGCTTGAACATGCGAC 689
DB 121 GATTAAGGCGGTACCAATGCGAGAGATGATGCTTATGCTTGAACATGCGAC 180
QY 690 TGATCCAAATATCCAGATGATGATGATGATGATGATGATGATGATGATGATG 749
DB 181 TGATCCAAATATCCAGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 750 AGATAATTAATGCGCAAGCACTGCTTATGCTTATGCTTATGCTTATGCTTATG 809
DB 241 AGATAATTAATGCGCAAGCACTGCTTATGCTTATGCTTATGCTTATGCTTATG 300
QY 810 GGATGCGCTCACACCACTGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 869
DB 301 GGATGCGCTCACACCACTGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 360
QY 870 TTTAATCAAGAAAAAGCAATTTAATGATGATGATGATGATGATGATGATGAT 929
DB 361 TTTAATCAAGAAAAAGCAATTTAATGATGATGATGATGATGATGATGATGAT 420
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QY 930 ACTTGCTGATGTTGGATGCAAGATAGTACAGCTTCTTATGACAAATATGTA 989
 DB 421 ACTTGCTGATGTTGGATGCAAGATAGTACAGCTTCTTATGACAAATATGTA 480
 QY 990 TGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATATGCTGTTCTATGATCA 1049
 DB 481 TGTATCTTCTCAAGATCTATCTGACAGACGGCCAGAGATATGCTGTTCTATGATCA 536
 QY 1050 TCATGTAATTTGGCAGTACTTCTTCTGACATCAAGAAAAAGATGCTATAATCTCTTC 1109
 DB 537 TCATGTAATTTGGCAGTACTTCTTCTGACATCAAGAAAAAGATGTAATAATCTCTTC 596
 QY 1110 TGAAGACAGCAATCCAGAACAGAC 1134
 DB 597 TGAAGACAGCAATCCAGAACAGAC 621

RESULT 4
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 LOCUS AGNCOURT_10425351 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:6668956
 DEFINITION 5', mRNA sequence.
 ACCESSION BU930826
 VERSION BU930826.1 GI:24119645
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2943 row: 0 column: 04
 High quality sequence stop: 555.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6668956"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccgcgcgcgc); Site 2: SfiI
 (ggcgccatggcc); 5' and 3' adaptor were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCCATATGAGCC-3'
 and 3' adaptor sequence:
 5'-ATCTAGAGCGCAGGCGCGCCAGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN
 Query Match 24.9%; Score 508; DB 5; Length 729;
 Best Local Similarity 94.8%; Pred. No. 4.1e-113;
 Matches 548; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
 QY 579 GGACAGACGATGCTCACTTAATGCTCTTGAACAACAAAAGAGACAGCTCTGATAAG-- 636
 DB 3 GGACAGACGATGCTCACTTAATGCTCTTGAACAACAAAAGAGACAGCTCTGATAAGGT 62

QY 637 -----GCCGTACAAATGCCAGGAAGATGATGCCGT 668
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 QY 669 AATGTTGCTGGAACATGGCAGCTGATCAATATATCCAGTGAATGGAATATACACTCT 728
 DB 123 AATGTTGCTGGAACATGGCAGCTGATCAATATATCCAGTGAATGGAATATACACTCT 182
 QY 729 GCACCTACGCTATCTATATGAAGATTAATGATGCGCAAGACAGCTCTTATATGATGTC 788
 DB 183 GCACCTACGCTATCTATATGAAGATTAATGATGCGCAAGACAGCTCTTATATGATGTC 242
 QY 789 TGATATGCAATCAAAAAACAAGCATGGCTCACACATGTTACTTGGTGTATGATGACA 848
 DB 243 TGATATGCAATCAAAAAACAAGCATGGCTCACACATGTTACTTGGTGTATGATGACA 302
 QY 849 AAAACAGCAAGTCTGTAATTTTATATCAAGAAAAAGCAATTTAAATGCACTGGATAG 908
 DB 303 AAAACAGCAAGTCTGTAATTTTATATCAAGAAAAAGCAATTTAAATGCACTGGATAG 362
 QY 909 ATATGAAAGAGCTGCTCTCATATCTTGTGATGTTGTGATGATGACAGATATAGTACGCT 968
 DB 363 ATATGAAAGAGCTGCTCTCATATCTTGTGATGTTGTGATGATGACAGATATAGTACGCT 422
 QY 969 TCTACTTGAAGCAAAATATGATGATATCTTCAAGATCATCTATGACAGACGGCCAGAGA 1026
 DB 423 TCTACTTGAAGCAAAATATGATGATATCTTCAAGATCATCTATGACAGACGGCCAGAGA 482
 QY 1029 GTATGCTGTTTCTAGTCAATCATCATGATTAATTTGCCAGTTACTTCTGACTCAAGAAAA 1088
 DB 483 GTATGCTGTTTCTAGTCAATCATCATGATTAATTTGCCAGTTACTTCTGACTCAAGAAAA 542
 QY 1089 ACAGATGCTAAATAATCTCTTCTGAAAAACGACATCTCAG 1126
 DB 543 ACAGATGCTAAATAATCTCTTCTGAAAAACGACATCTCAG 580

RESULT 5
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 LOCUS DKFP686B1728_r1 686 (synonym: hicc3) Homo sapiens cDNA clone
 DEFINITION DKFP686B1728_5', mRNA sequence.
 ACCESSION AL703938
 VERSION AL703938.1 GI:19687293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 544)
 Ockenwelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weill,B. and
 Wiemann,S.
 EST (Ockenwelder,B., Obermaier,B., Mewes,H.W., Weill,B. and
 Wiemann,S.)
 Unpublished (2001)
 CONTACT: MIPS

JOURNAL
 TITLE MIPS
 COMMENT Ingleaeder Janderst.J., D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de,
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German genome Project. No 31 sequence
 available.
 This clone (DKFP686B1728) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
 Location/Qualifiers
 1..544
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES
 source

ORIGIN

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/db_xref="taxon:9606"
/clone="DKFZP686E1728"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/notes="Vector: pTriplex2; site_1: sfilA; site_2: sfilB;
cDNA-collection"

Query Match      23.5%; Score 478.6; DB 1; Length 544;
Best Local Similarity 93.6%; Pred. No. 6.1e-106;
Matches 510; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 649 CAGGAAGATGAATGCTGCTTAATGTCGGAACATGGCCTGATCCAAATATTCAGAT 708
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Db 1 CAGGAAGATGAATGCTGCTTAATGTCGGAACATGGCCTGATCCAAATATTCAGAT 60
    |||||

QY 709 GAGTATGAAAAATCACTCTGCACTACGCTATCTATATGAGATTAATTATGSCCAA 768
    |||||
Db 61 GAGTATGAAAAATCCGCTTACACTA-TCTATCTACATGAGATTAATTATGSCCAA 119
    |||||

QY 769 GCATCTCTTATATGTCGCTGATATGCAATCAAAAAACAGATGGCTCACACACTG 828
    |||||
Db 120 GCATCTCTTATATGTCGCTGATATGCAATCAAAAAACAGATGGCTCACACACTT 179
    |||||

QY 829 TTAATTGGTGTACATGACGAAAAACGCAAGTGTGAAATTTTATCAAGAAAAAGCG 888
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QY 889 AATTAAATGACTGTATGATATGAGAGAGAGTCTCTCATATCTGCTGATGTTGTGA 948
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QY 949 TCAGCAAGTATGATGAGCTCTTCTACTTGAAGCAAAATTTGATGATCTTCAAGATCTA 1008
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Db 300 TCAGCAAGTATGATGATGATCTTCTACTTGAAGCAAAATTTGATGATCTTCAAGATCTA 359
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QY 1009 TCTGACAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATGATTAATTCGCGTTA 1068
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Db 360 TCTGACAGAGCGCCAGAGAGTATGCTGTTTCTAGTCATCATCATGATTAATTCGCGTTA 419
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QY 1069 CTTTCTGACTACAAAGAAAAACAGATGCTTAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
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Db 420 CTTTCTGACTATTAAGAAAAACAGATGCTTAAATCTCTCTGAAAAACAGCAATCCAGAA 479
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QY 1129 CAAGACTTAAAGCTGACATCAGAGAGAGTCACAAAAGTTCAAGAGCAGTGAATAAGC 1188
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Db 480 CAAGACTTAAAGCTGACATCAGAGAGAGTCACAAAAGTTCAAGAGCAGTGAATAAGC 539
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QY 1189 CAGCC 1193
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Db 540 CAGCC 544
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RESULT 6
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DEFINITION mRNA sequence.
ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
            1 (bases 1 to 865)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov

```

FEATURES

Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LCCM1067 row: m column: 03
 high quality sequence stop: 642.
 Location/Qualifiers
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 83"
 /notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
 site_1: sfil (ggcgccgcgcgc); site_2: sfil
 (ggcctatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence:
 5'-ATTCTAGAGCGCGCGCGCCGACATG-AT (30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

```

Query Match      23.2%; Score 472.8; DB 2; Length 865;
Best Local Similarity 97.4%; Pred. No. 1.8e-104;
Matches 491; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 635 AGGCGTACATGCGCCAGAGAGTATGCTGTTATGTTGCTGAACATGGCATGATC 694
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Db 69 AGGCGTACATGCGCCAGAGAGTATGCTGTTATGTTGCTGAACATGGCATGATC 128
    |||||

QY 695 CAATATTCAGATGATGATGAAATATACACTCTGCACTACGCTATCTATATGAAGATA 754
    |||||
Db 129 CAATATTCAGATGATGATGAAATATACACTCTACACGCTATCTATATGAAGATA 188
    |||||

QY 755 AATTATGCGCCAAAGAGACTCTTATATGAGTGTGATATCGAATTAATAAACAGACATG 814
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Db 189 AATTATGCGCCAAAGAGACTCTTATATGAGTGTGATATCGAATTAATAAACAGACATG 248
    |||||

QY 815 GCTTCACACACTGTTACTTGGTGTACATGAGCAAAAAACAGCAAGTGTGAATTTTAA 874
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Db 249 GCTTCACACACTGTTACTTGGTGTACATGAGCAAAAAACAGCAAGTGTGAATTTTAA 308
    |||||

QY 875 TCAAGAAAAACGAAATTTAAATGCACTGATATGATGAAGAGCTGCTCATACTTG 934
    |||||
Db 309 TCAAGAAAAACGAAATTTAAATGCGCTGATATGATGAAGAGCTGCTCATACTTG 368
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QY 935 CTGTATGTTGTGATGATGAGAGTATAGTACGCTTCTATTTAGCAAAATATTTGATAT 994
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Db 369 CTGTATGTTGTGATGATGAGAGTATAGTACGCTTCTATTTAGCAAAATATTTGATAT 428
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QY 995 CTTTCTCAAGATCTATCTGAGAGAGCGCCAGAGAGTATGCTGTTTCTACTCATCATCAG 1054
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Db 429 CTTTCTCAAGATCTATCTGAGAGAGCGCCAGAGAGTATGCTGTTTCTACTCATCATCAG 488
    |||||

QY 1055 TAATTGGCAGTTACTTTCTGACTCAAGAAAAACAGATGCTAAATCTCTTGAAA 1114
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Db 489 TAA-TTGGCAGTTACTTTCTGACTCAAGAAAAACAGATGCTAAATCTCTTGAAA 547
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QY 1115 ACAGCAATCCAAACAAGCTTAA 1138
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Db 548 ACAGCAATCCAAACAAGTCTCAA 571
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RESULT 7
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LOCUS BX492731 505 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP781C0523 r1 781 (synonym: hlc4) Homo sapiens cDNA clone
ACCESSION BX492731
VERSION BX492731.1 GI:32004516
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 505)
Bloecker,H., Bloecker,M., Mewes,H.W., Well,B., Amid,C., Oesanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Bloecker,M., Mewes,H.W., Well,B., Amid,C., et al.)
Unpublished (2003)
CONTACT: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by GFP (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 31 sequence available.
This clone (DKFZP781C0523) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubneweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clonezspd.de.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP781C0523"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1_sfl; Site_1: sflIA; Site_2: sflIB;
cDNA-collection"

ORIGIN
Query Match 18.5%; Score 376.4; DB 5; Length 505;
Best Local Similarity 92.7%; Pred. No. 6.6e-81;
Matches 395; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 325 TGCAGGGGAGCGGCAAGCAAGTGGCGCTTGGGAGACTACATGAGCTTTC 384
DB 80 TGGCTGGGAGCGGCAAGCAAGTGGCGCTTGGGAGACTACATGAGCTTTC 139
QY 385 ATGAGCCGAGGTAACGCTCGGTGGAAGATCTGGAAGCTCCAGAGCTGCTGG 444
DB 140 ATGAGCCGAGGTAACGCTCGGTGGAAGATCTGGAAGCTCCAGAGCTGCTGG 199
QY 445 TGGGTAAGTCCCGCAAGAAAGATCTCATGTCATGCTGAGGACACTGCAAG 504
DB 200 TGGGTAAGTCCCGCAAGAAAGATCTCATGTCATGCTGAGGACACTGCAAG 259
QY 505 AAGGACAAAGCAAGAGAGCTGCTTACATCTGGCTTGGCCATGGGAATTCAGAGTA 564
DB 260 AAGGACAAAGCAAGAGAGCTGCTTACATCTGGCTTGGCCATGGGAATTCAGAGTA 319
QY 565 GTTAAATCTGCTGTCAGAGAGATGTCATTAAATGCTTGAACAAAAGAGGAA 624
DB 320 GTTAAATCTGCTGTCAGAGAGATGTCATTAAATGCTTGAACAAAAGAGGAA 379
QY 625 GCTGTGATTAAGGCGGTACATGTCAGAGAGATGTCATTAAATGCTTGAACAT 684
DB 380 GCTGTGATTAAGGCGGTACATGTCAGAGAGATGTCATTAAATGCTTGAACAT 439
QY 685 GGCAGTGAATCAAAATTTCCAGATGATGGAATACACTTGGACTACGCTATCAT 744
DB 440 GGCAGTGAATCAAAATTTCCAGATGATGGAATACCGCTTACATGCTATCTAC 499

RESULT 8
BQ441373
LOCUS BQ441373
DEFINITION AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 817)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLOUTCH
cDNA Library Preparation: CLOUTCH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6103855"
/lab_host="DH10B (TI phase-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SflI (ggcgccctggcc); Site_2: SflI (ggccatcattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 clones contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN
Query Match 17.5%; Score 357.8; DB 5; Length 817;
Best Local Similarity 92.7%; Pred. No. 2.7e-76;
Matches 431; Conservative 0; Mismatches 27; Indels 7; Gaps 5;
QY 1408 AGAATTTGGGATTAAGTTTCTGACTACAAAGAAAAAGATGCCAAATTAATCTTCTGAA 1467
DB 319 AGAATTTGGGATTAAGTTTCTGACTACAAAGAAAAAGATGCCAAATTAATCTTCTGAA 378
QY 1468 AACACCAACCCGAGCAAGACTTAAGCTGATCAAGAGAAAGATCACAAGGCTTGA 1527
DB 379 AACACCAACCCGAGCAAGACTTAAGCTGATCAAGAGAAAGATCACAAGGCTTGA 438
QY 1528 GGCAGTGAAGATGGCAGCAGAGAAAGATCTCAAGAACCGAATTAATTAAGATGGT 1587
DB 439 GGCAGTGAAGATGGCAGCAGAGAAAGATCTCAAGAACCGAATTAATTAAGATGGT 498
QY 1588 GATAGAGAGCTAAGAAATTTTATGCTATCGAAGAAATGAAGAACCGAAGTACTCAT 1647
DB 499 GATAGAGAGCTAAGAAATTTTATGCTATCGAAGAAATGAAGAACCGAAGTACTCAT 558

QY 1648 GTCCGATCCGAGAAAACCTGACTAATGTCGACCTGTCGACATGATGAATGAATTA 1707
DB 559 GTCCGATCCGAGAAAACCTGACTAATGTCGACCTGTCGACATGATGAATGAATTA 618
QY 1708 ATTCTCTCAAGAGAGAGACAGAACCTGAAAGCCAGCAATTTCTGACACTGAG-AATGA 1766
DB 619 ATTCTCTCAAGAGAGAGAGACAGAACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGA 678
QY 1767 AGAGTATCAGAGT-GAGCAACAAATGATAC-TCAGAGCAATTTTGTGAGAA--CAGA 1822
DB 679 AAGATATCCAGAGAGAGAGCAACAAATGATCTTCAAGAACCAATTTTGTGAGAAACAGA 728
QY 1823 AACCTGGAATATATACAGA--TGAGATTCCTGATTCATGAGAA 1865
DB 739 CACCTGGAATTTTACCCGATGAGATCTGATCCTGAGAA 783

RESULT 9
BX437445 910 bp mRNA linear EST 03-MAY-2004
LOCUS BX437445 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP006Y104
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX437445
VERSION BX437445.2 GI:46959477
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 910)
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30771569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5500.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0CAP006Y104&c=5500.r.
FEATURES
source Location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP006Y104"
/rissue_type="THYMUS"
/clone_id="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 17.5%; Score 357.2; DB 5; Length 910;
Best Local Similarity 69.6%; Pred. No. 3.9e-76;
Matches 501; Conservative 1; Mismatches 209; Indels 9; Gaps 1;

QY 223 AGTGGCAAGCAACTGGCGCTTTGAGACACAGCACTCTCTATGAAGACATTC 282
DB 100 AAGAGCGAAGAGACATGAGTGTCTCTGAAGCCCGCTGCGCCATGAAGAGATT 159
QY 283 AGAACAAGATGGGCAAGTGTGCTGCACCTGCTCCCTGCGCAGGGGAGCGCGCAG 342

DB 160 TTTAGTAAGAGGCGAAGTGGCTTGGGCTCCTTGGCCGCGGCGAGAGACAC--- 216
QY 343 AGCAAGTGGCGGCTTTGGGGAAGCTACATGACAGTGCCTTCAATGAGCCAGATCAC 402
DB 217 -----GCGGAGAGCGGGGCGAGCGGGGAGAGGCGCTTACGAGCCGCGCTACAC 270
QY 403 GTCCCTGAGAGAAAGATTGGAACAGCTCCACAGAGCTGCTGTGGGGGTAAATGCCAGA 462
DB 271 GTCCGAGACCGAGATTGCGAAGATGCAAGAGCTGCCAGCGCGGGTAAATGTGGGAAA 330
QY 463 AAGATCTCATGCTGATGCTGACAGGACACTGACGTGACCAAGAGAGACAGCAAGAGAG 522
DB 331 GTCCGACAGATCTTTTGTCTGAGAGAAATGCTTGAAGATGAGACAAATGAACAG 350
QY 523 ACTGCTTACATCTGGCTCTGCGCAATGGAAATTCAGAAATGATAAACTCCTGTGAC 582
DB 391 ACGGCTTACATTTGGCTGTGCGCAATGGTCACTCCAGAAATGATACCTCCTGTGAC 450
QY 583 AGACGATGTCACCTTAATGCTTGAACAACAAAGAGACAGCTGTGATTAAGGCGCTA 642
DB 451 AGAAATGTCACCTCAATGCTGTGACCAAGAAACAGACAGCTGTGATGAAGGCTGA 510
QY 643 CAATGCGAGAGATGATGATGCTGATGATGCTGATGATGATGATGATGATGATGAT 702
DB 511 CAATGCGAGAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 570
QY 703 CCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 762
DB 571 GCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 630
QY 763 GCCAAGACCTGCTTATATGATGATGATGATGATGATGATGATGATGATGATGAT 822
DB 631 GCAACCAAGCTCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 690
QY 823 CCAGTGTACTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882
DB 691 CCACTTTTACTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
QY 883 AAGCAATTTTAAATGACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 942
DB 751 AAGCAATTTTAAATGACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 810

RESULT 10
CR860726 2677 bp mRNA linear HTC 12-NOV-2004
LOCUS CR860726 Pongo pygmaeus mRNA; cDNA DKFZp459F0427 (from clone DKFZp459F0427).
DEFINITION CR860726
ACCESSION CR860726
VERSION CR860726.1 GI:55732274
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pongo.
1 (bases 1 to 2677)
Blocker, H., Boeher, M., Brandt, P., Mewes, H.W., Well, B., Amid, C.,
Osaenger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GfP (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp459F0427) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459F0427
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES		Location/Qualifiers	
source		1..2677	
		/organism="Pongo pygmaeus"	
		/mol_type="rRNA"	
		/db_xref="taxon:9600"	
		/clone="DKFZp459P0427"	
		/issue_type="cortex"	
		/clone_1ib="459 (synonym: pcorl). Vector pSport1_sfi; host	
		DH10B; sites Sfi1A + Sfi1B"	
		/dev_stage="adult"	
		/note="hypothetical protein (Homo sapiens), differentially	
		spliced"	
gene		1..2677	
		/gene="DKFZp459P0427"	
CDS		176..973	
		/gene="DKFZp459P0427"	
		/codon_start=1	
		/product="hypothetical protein"	
		/protein_id="CAH92841.1"	
		/db_xref="GI:55732275"	
		/translation="MGVRSFLAACRRBMTAKRNRKNDKXGSRVVRKDLGMTHK	
		AIIAGDVNLTLSILLGANDVNDKRRRTAHLCAHGRPVVADLVARKRLMID	
		SENRTALIAVOCQEAIVCASIIIEHGADPNVDMGTALHAIINENISMGKLLAY	
		GADIBARSGSHISLLAVNRKEENVAFLLKKPDLTAIDNFGTALIAARNGSTS	
		VYVOLLQHNIDVFCDISGMTAEDYAAASKFOATRLRNDIRARAKA"	
ORIGIN			
Query Match		17.2%; Score 351.2; DB 4; Length 2677;	
Best Local Similarity		53.1%; Pred. No. 1.5e-74;	
Matches 887; Conservative 0; Mismatches 748; Indels 37; Gaps 5;			
Qy	378	TGCCTTCATGAGCCAGGATACACGCTCGTGAGAGATCTGACACGCTCACAGAC	437
Db	250	TGGCTTCTCAAAATTCGGGATACCGATCCGCGAGAAAGATCTGGGATATCCAAAGC	309
Qy	438	TGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATGTCATGCTCAGGACATGACGT	497
Db	310	TGCCATCGCCGGTGAATGAACAAGCTGTGAGAGACATCTTGCTGGGCTGATGACGT	369
Qy	498	GAAACAAGAGACAAAGACAAAGAGCTGCTACACTCGGCTCTGCCAATGGGAATTC	557
Db	370	GAATGACAGGACAAAGAAACAGAGCTGCTTACATTTGGCGTGTGCGCCATGGCCGTC	429
Qy	558	AGAAGTAGTAATAACTCTGCTGGACAGAGATGCACTTAATGTCTTGAACAACAAA	617
Db	430	GGGAGTGTGAGCTGATTTGGTGCCAGAAATGCCGGCTTAACCTGACGACGTAAGAA	489
Qy	618	GAGGACGCTGTGATTAAGGCGGTACATGCGCAGAAAGATGAATGTGCGTTATGTTGT	677
Db	490	CAGGACGCTGTGATCAAGGCTGTACATGTCAAGAAAGCATTTGTGACATCTGTCT	549
Qy	678	GGAACATGGACCTGATCCAAATATTCGAGATGATGGAATACACTCTGCACTACGC	737
Db	550	GGAACATGGCGCGGACCCAAATGTTAGAGATATGATGCAACACGCGCTCTGCATATGC	609
Qy	738	TATCTATTAAGAAATAATTAATGSCAAAGCATGCTCTTAATATGATGCTGATATGCA	797
Db	610	CATTGATTAATGAGATATATCAATGSCAAGAAAACTGCTTGCATATGTGCAATTTGA	669
Qy	798	ATCAAAAAACAGCATGCGCTCACACACTGTTACTTGTGATACATGACAAAAACAGA	857
Db	670	ACGAACAAAGCCAGGCGTGACATCATCATCTTTACTCGCTGTAAATAGAAAAAAGAGA	729
Qy	858	AGTCGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCACTGATGATGAGAG	917
Db	730	AATGTGGAGATTTTGTGAAGAAAAACAGATTTTAACTGCAATGATTAATTTTGAAG	789
Qy	918	GACTGCTCATPCTTGCTGTATGTTGTGATCAGCAAGTATGACGCTTCTACTTGA	977
Db	790	AACAGCCTCATPCTTGCTGTATGTTGTGATCAGCAAGTATGATGCTTCTTCTTGA	849
Qy	978	GCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACGCGCAGAGATGCTGT	1037

Db	850	GCACATATATGACGCTTTTGGCAAGATATATCTGGATGAGACTGCAAGAAAGCATGACGTC	909
Qy	1038	TTCTAGTCATCATCTGTAATTTTGGCAGTACTTCTGACTCAAGAAAAACATGTCT	1097
Db	910	TGCTTCTAAGTTTCAAGAA-----CAAGCTTGAAGATGAC	946
Qy	1098	AAAAATCTTCTGAAAAACAGCAATCCAGAACCAAGCTTTAAAGTGCATCAGAGAAAGA	1157
Db	947	ATCAGAGGAGAGCAAGAAAGCTTTGAAGATGTGAAGTACGACCCAGAGTTGAAAGA	1006
Qy	1158	GTCAAAAGTTTCAAGGACGTAAATATGACGCGCAGAGAAAAATGTCTCAAGAACAGA	1217
Db	1007	---AAAAATGAAGAAATCCAGAAATTAAGAAAAATGAAGATGTCAAGAAACGTACATGCTGA	1063
Qy	1218	AATTAATTAAGATGATGTAATGAGAGTTGAAGAAATGAAGAACATGAAGTAATA	1277
Db	1064	TGACAGTACAGTTATTAATGATGATGATGATTAATTCACAAATTAAGAACAGAAA	1123
Qy	1278	TGTGGATTTACTAGAAAACTGACTAATGTTGTCACTGCTGGCAATGGTATATGATTT	1337
Db	1124	ACCTGATAGTCATCAATTTCCAGAGAGAGAAATGACAAATTTGATAGCTTGCAGAAA	1183
Qy	1338	AATTCCTCAAGAGAGAGAGAACACTGAAAAATCAGCAATTTCTGACACAGAAAG--T	1395
Db	1184	AACCTCTAATGAAGAAAGAGAGATTTATTAAGTTAAAGCCAAATATATTTCAAGGAT	1243
Qy	1396	GAAAGATATCACAGAAATTTGCAATTTAGTTTCTGACTCAAGAAAAACAGATGCAAAA	1455
Db	1244	GATCTTAATGATATACCTGGGTCATCTGAAAAACCTCAGAGAGATGATGCTTAAC	1303
Qy	1456	TACTCTTCGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACATCAGAGAGAGATCA	1515
Db	1304	TCTGATGATTAAGATTTTATGTTACTCATGTAACAAAGTGAAGAAAGATGTAAGATTT	1363
Qy	1516	CAAAGCTTGAGGCGAGTGAAGAAATGGCCAGACGAGAAAAAGTCTCAAGAACCAAGATA	1575
Db	1364	GTTACCTTATGAATCAAGAAATCAAGATGCAAGCTGATGTAAGATGATTAAGATTA	1423
Qy	1576	AATAAGATGATGATGAGAGCTTAAGAAATTTATGCGTATGAGAAATGA--AGAAC	1633
Db	1424	AAATGTTACTGTGAACAATTAAAGTAAATTTCAAAAAATGAATTAATTTTGCATA	1483
Qy	1634	ACGGAAGTACTCATGTCGGATTTCCAGAAAACTGACTAATGATGTCCTGCGCAATG	1693
Db	1484	CTACAAAAGATCTATCTGAAACAAACAAACCAATCAAGTTAGAGATCAGAAATCTT	1543
Qy	1694	GTGATGATGATTAATTCCTCAAGAAAGACAG-----AACCTGAAAGCAAGCAA	1746
Db	1544	GAAAGAAAAAAACCTCTGTATTTGAGATTCATCTTACAAACAAGAAAGAAAGAA	1603
Qy	1747	TTTCTGACACTGAGAAATGAAGAGATATCAAGTGCAGAACAAATGATATCTAGAAAGCA	1806
Db	1604	ATTAAGCTGAAGATTTGTATGAAGAAAGATACAGAAAGTTAAATTAATGAGAGCAG	1663
Qy	1807	TTTTGTGAAGAACAAACACTGAATATTTACAGATGAGATTTCTGATTCATGAAGAAA	1866
Db	1664	TATAGACACAAACTGAAGTGAAGAAAAACAATTAACTGACCTCAATCATTTGGAAGTG	1723
Qy	1867	CAGATGAAGTGTGAAAAAAATGAATTCGAGCTTCTCTTAATGTTGAAGAGAAAA	1926
Db	1724	GCATTGAAGACTGTAAAGATTAATCAATCAGAAATTCATATCTCATGAAAAAGAAAGA	1783
Qy	1927	GACATCTTGCAATGAAGAAATGATCGTTGGGGAAGAAATTTGCCATGCTAAGATGAGCTA	1986
Db	1784	GACCGGTGACAGAAAAATCACTTGAATGGGAGTGAATTTGCCAGACTGAGCTGGAATA	1843
Qy	1987	GACCAATGAACATCAGAGCAGCTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA	2038
Db	1844	GACCAATTAACATCAGACAGAGAACTGAAAAATTAATTAATTTCAAGATA	1895

RESULT 11
AUI20666

LOCUS AUI20666 843 bp mRNA linear EST 01-AUG-2002
DEFINITION AUI20666 HEMBI Homo sapiens cDNA clone HEMBI001175 5', mRNA
sequence.
ACCESSION AUI20666
VERSION AUI20666.1 GI:10935901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 843)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Makinaka, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isozaki, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isozaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kibarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..843
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBI001175"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_1ib="HEMBI1"
/note="Vector: pME18SFL3"

ORIGIN
Query Match 17.1%; Score 348.8; DB 1; Length 843;
Best Local Similarity 69.2%; Pred. No. 4.4e-74;
Matches 492; Conservative 0; Mismatches 210; Indels 9; Gaps 1;
1;
223 AGTGCAGAGCAAGCTGGGCGCTTGTGAGACCAAGCACTCTGTATGAAGACATC 282
119 AGAGCCGAGAGACATGAGGTGTCTCTGAAGCCCGTCCCTGGCCATGAAGAGATT 178
283 AGGACCAAGATGGGCAAGTGTCTGCTCCCTGCTGCGGGGAGCCGCAAG 342
179 TTTAGTAAAGGCGCAAGTGGCTCTTGGCTCTTGGCGCGGCGAGAGCAAGC--- 235
343 AGCAAGTGGGCGCTTGGGAGACTACATGACAGTGCCTTATGAGAGCCAGGTACAC 402
236 -----GCGGAGGCGGGGCGAGCGCGGGAGGGGCGCTACTCGAGCCGCTACAC 289
403 GTCCGTGAGGAAGATCTGACAAAGCTCCAGAGCTCTGTGGGTAAAGTCCCCACA 462
290 GTCCGAGACCGAGATCTCGGCAAGATCCAAAGCTGCCAGCGGGGTATGTGGGAAA 349
463 AAGGATCTCATGTCTCTCAGGAGCACTGACGTGAACAAGAGCAAGAAAAGAG 522
350 GTGCGAGAGATCTTTGTCTAGGAGAAATGGCTTAAAGATGAGACAAAGTGAACAG 409
523 ACTGCTCATCTGCGCTCTGCGCAATGGAAATTCAGAGTAGTAAACTCCCTGTGAGC 582
410 AGGCTCTCATTTGGCTCTGCGCAATGTGTATCCAGAGTAGTAACTCTCTGTTGAGC 469
583 AAGCATGTCAACTTATGTCTTTCAGCAACAAAAGAGAGAGAGCTGTGTAAGAGCCGTA 642
470 AAAAAATGCGACACTCATGTCTGTGCAACGAAAAGAGAGAGAGCTGTGTAAGAGCTGTA 529
643 CAATGCAAGGAAGATGAATGTGTAAATGTGTCTGGAACATGAGCACTATCAATATT 702

Db 530 CAATGCCAGGAAGAGAAATGTGCAACTATTCTGTCTGTAAGAACATGCTCATCAATCTT 589
Qy 703 CCAGATGAGTATGAAATCCACTGTGACCTATCTATATGATGAATTAATTAATG 762
Db 590 GCGGATGTCCATGCGAACACACTGCTCTTCACTATGTGTCTATATGAGACATATCAGTA 649
Qy 763 GCCAAGACATGCTCTTATATGTGTCTGATATGCAATCAAAAAACAGATGCGCTCAC 822
Db 650 GCAACAAAGCTGCTTTTGTATATGATGCAAAATATTTGAAGCAAAAAACAGATGACCTNACA 709
Qy 823 CCAGTGTACTTGGTGTATACATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAA 882
Db 710 CCACCTTTTACTTCTGAGTATGAGAAAAAGCAGCAATATGTGATTTTAAATTAAGAA 769
Qy 883 AAGGCAATTTAATGACCTGATATGATATGAGAGAGACTCTCTCATCTT 933
Db 770 AAGCAAAATGTAAATGCTTAAATATAGTTGGAAGAGAGTCAACACTAATTT 820

RESULT 12
DQ053800
LOCUS DQ053800
DEFINITION Homo sapiens KIAA1074 gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION DQ053800
VERSION DQ053800.1 GI:66899747
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 5130)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeille, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) Plos Biol. 3 (6), E170 (2005)
15869325
JOURNAL
PUBMED
REFERENCE 2 (bases 1 to 5130)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeille, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submision
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source
1..5130
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/gene="KIAA1074"
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ORIGIN
Query Match 17.0%; Score 345.8; DB 1; Length 5130;
Best Local Similarity 71.4%; Pred. No. 3.8e-73;
Matches 455; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
281 TGAAGAAAGATTTTGTGTAAGAGGCGAGTGGCTCTTGGCGCGCGCGGA 61
Db 2 TGAAGAAAGATTTTGTGTAAGAGGCGAGTGGCTCTTGGCGCGCGCGGA 61
Qy 341 AGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACC 400
Db 62 GGAGCAGCGCGGAGAGCGCGGCGAGCCGCGGAGAGGCGGCTTACTGACGCCGCTACC 121

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QY 401 ACGTCCGTGAGAGAGTCTGACAAAGCTCCAGAGCTGCTGTTGGGTAAAGTCCCA 460
DB 122 AGGTCCGAGACCGAGATCTCGGCAATCCAAAGCTCCAGCGGGGTAAATGGCCA 181
QY 461 GAAAGATCTCATGCTGATGCTCAAGGACATGACCTGAAACAAGAGACAAAGAA 520
DB 182 AAGTGCAGAGATCTCTTTGCTCAGAGAAATGGCTTGAACGATAGACAAAGATGACA 241
QY 521 GAGCTGCTACATCTGGCTCTGCAATGGGAATTCAGAAAGTAAATCTGCTGG 580
DB 242 GAGGCTCTACATTTGGCTGTGCAATGGTATCCAGAAAGTAACTCTCTGGTGG 301
QY 581 ACAGACATGTCATCTTAATGTCCTTGACAAACAAAAGAGACAGCTGATTAAGCCG 640
DB 302 AAGGAAATGCGACGCTCAATGCTGTGACAGAGAAAACAGACAGCTGTGATGAAGCTG 361
QY 641 TACATGCGACAGAAATGAAATGTCGTTAATGTTGCTGGAACATGGCACTGATCAATA 700
DB 362 TACAAATGCCAGAGAAATGTAATGCAATATCTGCTAGAAACATGGTCTGATCCAAATC 421
QY 701 TTCCAGATGAGTATGGAATATCCATCTGCACTGCACTGATCTATATTAAGATTAATTA 760
DB 422 TTGCGGATGTCATGGCAACATGCTCTTCACTATGCTGTATTAATGAGACATATCAG 481
QY 761 TGGCCAAAGCATGCTCTTATATGTCGTGATTCGATCAATCAAAAACAGACATGCTCA 820
DB 482 TAGCAACAAGAGCTCTTTGTATGATGCAAAATTTAGACAAAACAGAGATGACTCA 541
QY 821 CACCATCTTACTTGTGTATGATGAGCAAAAACAGCAAGTCGTGAATTTTATATCAAGA 880
DB 542 CACCATTTTACTTGTGATGATGAGAAAAACAGCAAAATGTTGTAATTTTATATAAGA 601
QY 881 AAAAGCGAATTTAATGCACTGGATGATATGGAAG 917
DB 602 AAAAGCAATGTAAATGATGATGATGGAAG 638

RESULT 13
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LOCUS CR994478 RZPD no. 9016 Homo sapiens cDNA clone RZPD9016M101 5',
DEFINITION mRNA sequence.
ACCESSION CR994478
VERSION CR994478.1 GI:6828363
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 909)
Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
and Korn, B.
Human T-Lymphocytes library
Unpublished (2005)
Contact: Inge Airlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: RZPD9016M101.
RZPDLIB: (Human T-Lymphocytes) RZPD LIB No. 9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016 Contact:
Inge Airlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=RZPD9016M101
contact RZPD (product- support@rzpd.de) for further information.
Primer name: ges_4 , Primer sequence: CGGATACCAATTCACACAG.

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                cisue_type="T-Lymphocytes"
                dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="RZPD no.9016"
                /note="Vector: pQE80LSN cloned; Site_1: SalI; Site_2:
                NotI; vector:
                http://www.rzpd.de/info/vectors/pQE80LSN cloned.p1c.shml
                ; 1st strand cDNA was prepared from mRNA obtained from
                human T-Lymphocytes with a NotI - oligo(dT) primer [5'
                GACTAGTCTAGATGCGACGCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
                Double-stranded cDNA was ligated to SalI adaptors,
                digested with NotI and cloned into the NotI and SalI sites
                of the pQE80LSN cloned vector"

ORIGIN
Query Match 16.8%; Score 343.4; DB 7; Length 909;
Best Local Similarity 69.3%; Pred. No. 9,4e-73;
Matches 500; Conservative 0; Mismatches 211; Indels 10; Gaps 2;

QY 223 AGTGGCAAGACAGACGTGGGCGCTTCTGGAGACACAGACCTGTATGAAGACATC 282
DB 92 AGAGCCGAGAGAGACATGAGGTGTCTGAGAGCCGGGTGCTGGGCCATGAAAGATT 151
QY 283 AGGAAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGTGCAAGGGGAGCGGCAAG 342
DB 152 TTATGTAAGAAAGGCGAGTGGCTTGGGCTCTTGGCGGCGGCGGAGAGAGCAGC--- 208
QY 343 AGCAAGTGGGCGCTTGGGAGACATGACATGACATGCTTATGAGGCCAGTACAC 402
DB 209 -----GGGGGAGGGGGGCGAGCGGGGGGCGGCTTATCCAGCGCTGCTACAC 262
QY 403 GTCCGTGAGAGATCTGGACAAAGCTCCACAGAGCTGCTGTGGGGTAAATGCCACAG 462
DB 263 GTCCGAGACCGAGATCTGGGCAAGATCCCAAAAGCTGCCAGCGGGGTAAATGGCGAA 322
QY 463 AAGATCTTCATGTCATGCTCAAGGACATGACGTGAACAGAGACAGCAAGCAAGAGAG 522
DB 323 GTGACAGAGATCTTTTGTCTCAGGAAGATGAGCTTGAACATGATAGACAAATGAA 382
QY 523 ACTGCTTACATCTGGCTCTGCAATGGGAATTCAGAAATGTAATAATCTCTGCTGAC 582
DB 383 ACGGCTTACATTTGGCTGTGCAAGATGCTATCCAGAAATGTAATCTCTGCTGAC 442
QY 583 AGACATGTCATTTAATGCTTGAACAAACAAAAGAGACAGCTGTGTAAGGCCGTA 642
DB 443 AGAAATGCCAGCTCAATGCTGTGACAGAAACAGAGACAGCTGTGTAAGGCCGTA 502
QY 643 CATTGCGAAGAGATGATGTCGTTAATGTTGCTGGAACATGACATGATCAATATT 702
DB 503 CATTGCGAAGAGAGATGATGTCGTTAATGTTGCTGGAACATGATGATCAATATT 562
QY 703 CAGATGATGATGAAATTCACCTGACATGCTGATGCTGATGATGATGATGATGATG 762
DB 563 GCGAGATGCCAGAGCAACATGCTCTTCACTATGCTGTGTTAATGAGAGACATACAGTA 622
QY 763 GCGAAGACATGCTCTTATATGTCGTGTAATGCAATC-AAAAACAAGAGGCTGAC 821
DB 623 GCAACAAGCTCTTTTGTATGATGCAATATTTAGAACAAACAAAGAGATGACCTCAC 682
QY 822 ACCACTGTTACTTGTGTATGATGACAAACAGCAAGTCGTGAATTTTATCAAGAA 881
DB 683 ACCACTTTTACTTGTGATGATGAGAAAGAGAGCAATGTTTATTAAGAA 742
QY 882 AAAAGCAATTTAATGCACTGATGATGATGAAAGAGTCTCTCATATCTGCTGATG 941
DB 743 AAAAGCAATTTAATGCACTGATGATGATGAAAGAGTCTCTCATATTTTCAAGATA 802

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QY 942 T 942
Db 803 T 803

RESULT 14
LOCUS BC063888
DEFINITION Homo sapiens cDNA clone IMAGE:30389199, with apparent retained intron.
ACCESSION BC063888
VERSION BC063888.1 GI:39645658
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Teshigahara, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gilmwood, J., Schmutz, J., Myers, R.M., Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smalys, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 5483)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabos-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butcherfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lise Prabhu, Parvaneh Seedi, Jr Santos, Angelique Scherch, Ureila Skalska, Duane Smalls, Jeff Scott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRK Plate: 141 Row: O Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein
This clone has the following problem: retained intron.

FEATURES
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/note="Vector: PCMV-SPORT6.1"

ORIGIN
Query Match 15.9%; Score 324; DB 4; Length 5483;
Best Local Similarity 94.1%; Pred. No. 8.5e-68;
Matches 348; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

QY 1658 CAGAAACCTGACTTAATGCTGACACCTGCGCATATGATGATTAATTCCTCAA 1717
Db 1 CAGAAACCTGACTTAATGCTGACACCTGCGCATATGATGATTAATTCCTCAA 60
QY 1718 GGAAGACGAAACACCTGAAAGCAGCAATTTCTGACACTGAGATGAGATTCACA 1777
Db 61 GGAAGACGAAACACCTGAAAGCAGCAATTTCTGACACTGAGATGAGATTCACA 120
QY 1778 GTGACGACAAATATGATCTGACAGCAATTTTGTGAAGACGACCTGAAATTTAC 1837
Db 121 GTGATGACAAATATGATCTGACAGCAATTTTGTGAAGACGACCTGAAATTTAC 180
QY 1838 AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1897
Db 181 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
QY 1898 AGCTTCTCTTACTGTTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1957
Db 239 AGCTTCTCTTACTGTTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 298
QY 1958 AAGAAATTCCTGCTTAAGACGAGCTGACACATGAAATGACCTGACCTAATA 2017
Db 299 AAGAAATTCCTGCTTAAGACGAGCTGACACATGAAATGAAATGACCTGACCTA 358
QY 2018 AAAAAAAAAA 2027
Db 359 AAAAAAAAAA 368

RESULT 15
LOCUS BM469654
DEFINITION AGENCOURT_6444673 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585453
LOCUS 5', mRNA Sequence.
ACCESSION BM469654
VERSION BM469654.1 GI:18518696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC <http://mgc.ncl.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabos-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LLM12351 row: m column: 06
High quality sequence stop: 680.

